1

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
--- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
--- SÜBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION (G-149 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macropus rufus (Red kangaroo) (Megaleia rufa).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6CC7262429CD6B64 CRC64;
                                                                               Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368.197-207(1995).
-i. FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
-i. SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPRO01894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
Probon; P0001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antlb.ctic; Amidation; Multigene family; Signal.
SIGMAL 30 130 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1;
Pred. No. 0.017;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PROTEGRIN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
                                        STRAIN=RED DUROC;
MEDLINE=95354835; Pubmed=7628604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X84096; CAA58892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 EGGRLCYCRPRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 AA; 16604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.3
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P32194; 1PG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
107
136
138
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP1_NACRU
P42142:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSPI_MACRU
1D HSPI_MACRU
1D HSPI_MACRU
DT 01-NOV
DD 01-NOV
DE SPERM
GN PRMI.
GN MACROP
OC MANMAI
OX NCBLIA
RN [1]
RN SEQUEN
RX TISSUE
RX TISSUE
RX TISSUE
RX TESUE
RX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            αq
οy
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-149 PROVIDE AMIDE GROUP).
GF4BA98429CD6ED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEGRIN 3.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 1; Length 149;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X83267; CAA58240.1; -.. EMBL; X84095; CAA58891.1; -.. EMBL; X84695; CAA58891.1; -.. HSSP; S3457; S34587. InterPro: IPRO1894; Ted1. InterPro: IPRO1894; Cathelicidin. IPRO5066; Cathelicidins; 1.. PROSTIE; PS00946; CATHELICIDINS. 1.. PROSTIE; PS00946; CATHELICIDINS. 1; INTERPROSTIE; S900947; CATHELICIDINS. 1; INTERPROSTIE; S19014; Antibiotic; S19014; Anidation; Multigene family. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                               Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                      STRAIN-RED DUROC;
MEDLINE-95354835; PubMed-7628604;
                                                                                                                                                                                          TISSUE-Leukocyte;
MEDLINE-93327946; PubMed-8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEGRIN 5 PRECURSOR (PG-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 RGGGLCYCRRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                     SEQUENCE OF 131-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
138
148
149 AA;
               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PG5_PIG
P49934;
01-0CT-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PG5_PIG

ID PG5,

AC P499

DT 01-(

DT 01-(

DE PRO'

GN NPG

OC EUK,

OC EUK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

ö

Gaps

```
RESULT
                                                                                                                                                         g
                                                                                                                                                                                                                                                                                          HID DESCRIPTION OF STREET AND DESCRIPTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            the European Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-1- PUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DAN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBSCELLULAR LOCATION: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
                                                                                                                                                                                                                                                                                                                                                            protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 59; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                               Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY.
SEOUENCE 59 AA; 8230 MW; 78FIAE592B4B2FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Testis; DNA condensation; Nuclear protein.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L35332; AAA74598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8514 MW;
                                                                                                                                                                                                                                                           EMBL; L35447; AAA74616.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenolestes fuliginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=37696;
                                                                                                                                                                                                                                                                                                                                                               Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSP1_CAEFU P42131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
HSP1_CAEFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMAYOGENEIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DitterPro; IPR000221; r.v. ...
Pfam; PF00260; protamine_Pl; 1.
PROSITE; PS00048; PROTAMINE_Pl; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Chromosomal protein; Nucleosome protein.
Testis; DNA condensation; Nuclear protein.
TNIT_MET 0 0 BY SIMILARITY.
TNIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                            Dasyurus viverrinus (Southeastern quoll), and Dasyurus hallucatus (Satanellus/northern quoll). 
Eukaryota: Metazoca; Chordata; Craniata; Vertebrata; Euteleostomi; 
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 1; Length 60; Pred. No. 0.24;
                         Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                        Indels
                       Score 45; DB 1;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                           HSP1_DASVI STANDARD; PRT; 60 AA. P42135; P42133; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 AA
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341; AAA56795.1; -. IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L35340; AAA74599.1; -.
                       49.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%;
69.2%;
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 32, (Rel. 32, 1) (Rel. 32, 1) (Rel. 35, 1)
                                                                                                                  13
                                                                                                                                                               53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 RGRRRGYSRRYS 54
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM PROTAMINE P1.
                                                                                                                  1 RGGRLSYSRRFS
                                                                                                                                                               41 RGRRRGYSRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSP1_MACAG
P42137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSP1_MACAG
                                                                                                                                                                                                                                                        HSP1_DASVI
```

```
EMBL;
    ò
                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                       Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259.7-14(1995).
-!- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UNCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                         Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Macropus agilis (Agile wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                           49.5%; Score 45; DB 1; Length 60; 69.2%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY.
SEQUENCE 60 AA; 8338 MW; 96255C818921EB85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                       EMBL; L35451; AAA74615.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                             Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                             MEDLINE-95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 36, Created)
(Rel. 36, Last sequ
(Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antechinomys laniger.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM PROTAMINE P1.
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-60701;
                                   NCBI_TaxID=9313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP1_ANTLA
018745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSP1_ANTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orserd and the statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome b, 12S rRNA, and protamine P1 gene trees.";
J. Manmal. Evol. 4:217-236(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in R.J., Dixon G.H.;
protamine Pl genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=N.lorentzii, D.albopunctatus, D.geoffroil, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
                                                                                                                                               EMBL; AF001587; AAB91377.1; -.
InterFro; IPR000221; Protamine_P1.
Pfam, PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromcsomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Winkfein R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neophascogale lorentzii (Long-clawed marsupial mouse),
Dasyurus albopunctatus (Native cat),
Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                            E021567627E562B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm; MEDLINE-92215351; PubMed-7700877; Retief J.D., Krajewski C., Westerman M., Winkfein R "Molecular phylogeny and evolution of marsupial proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 1;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antechinus swainsonii, Phascolosorex dorsalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                     Testis; DNA condensation; Nuclear protein.
INIT_WET 0 BY SIMILARITY
SEQUENCE 61 AA; 8409 MW; E021567627F56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dasyurus spartacus (Native cat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF010267; AAB69297.1; -. AF010272; AAB69302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L35338; AAB95429.1; -. EMBL; L35339; AAA74601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.2.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || | | |||||:|
FGRRGYSRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP1_ANTSW S3
P4213C; P42146;
01-NOV-1995 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
HSP1_ANTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRM1
```

61 AA.

PRT;

STANDARD;

```
HSP1_SARHA
P42151:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP1_DASRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                               A PARTIES OF COURSE OF STREET AND SECOND SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S rrMx, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DORING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                Promit Provided Protesting Protesting Protesting Processing Protesting Protes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parantechinus bilarni (Broad-footed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
NCBI_TaxID=32555;
                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1; Length 61; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                           Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   condensation; Nuclear protein.
0 0 BY SIMILARITY.
51 AA; 8421 MW; C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000221; Protamine_P1. Pfam; PF00260; protamine_P1; 1.
                                                         InterPro; IPR000221; Protamine_P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00048; PROTAMINE_P1; 1.
EMBL; AF010274; AAB69304.1; -. EMBL; AF010275; AAB69305.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF010277; AAB69307.1; -.
                                                                                                                                                                                                                                                                                                                                                 49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.5%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AA; 8421 MW;
                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 RGRRRGYSRRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRRFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Testis; DNA INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP1_PARBI
018768;
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
HSP1_PARBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         SPECIES-S.harrisii; TISSUE-Sperm;
MEDLINE-9521531; Pubmed-7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMATIN OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=D.maculatus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12s TRRA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN SPERM DUBING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and
Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                         Dasyurus maculatus (Tiger quoll).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                 Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 61; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP1_DASRO STANDARD; PRT; 62 AA. P42144; P42149; 01-NOV-1995 (Rel. 32, Created) 1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                              Sarcophilus harrisii (Tasmanian devil), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.24
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF010276; AAB69306.1; -. Pro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L35324; AAA74608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                            NCBI_TaxID=9305, 9281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGRRRGYSRRYS
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERM PROTAMINE P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID DT DT OC OC OC OC
```

ö

RESULT 12

43

us-09-485-571-25.rsp

```
HSP1_ANTST
P42129;
                                                                                                                                                                                                                                                                                                                                             INIT_MET SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSP1_ANTST
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                          Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259-7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.-I- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phascogale tapoatafa (Common wambenger),
Sminthopsis crassicaudata (Fat-tailed dunnart),
Myrmecoblus fasclatus (Numbat), and
Thylacinus cynocephalus (Tasmanian wolf).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Murexia.
NCBI_TaxID=37736, 9293, 9301, 55782, 9275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
 Dasyuromorphia; Dasyuridae; Dasykaluta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 62;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 62 AA: 8585 MW; 99C02857DF087FC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSPI_MURLO STANDARD; PRT; 62 AA. P42140; P42150; P42154; P42140; P42159; P42154; P42140; P42159; P42154; P42140; P421995; P421 32, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SPECIES-M.fasciatus, and T.cynocephalus;
MEDLINE-97368867; Pubmed-9225481;
Krajewski C., Buckley L., Westerman M.;
                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95215351; PubMed-7700877;
                                                              MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%;
            NCBI_TaxID=33560, 9291, 9299;
                                                                                                                                                                                                                                                                                                   EMBL; L35325; AAA74605.1; -. EMBL; L35326; AAA74607.1; -. EMBL; L35337; AAA74603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
 Mammalia; Metatheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | | ||||||:|
RGRRRGYSRRRYS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murexia longicaudata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
HSP1_MURLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Sperm;
MEDLINE-95215351; PubMed=7700877;
MEDLINE-95215351; PubMed=7700877;
Metief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
Molecular phylogeny and evolution of marsupial protamine PI genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DORING THE RALDID PHASE OF SPERMATOGENESIS. THEY COMPACT
SFERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                    Proc. R. Soc. Lond., B, Biol. Sci. 264:911-917(1997).

-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antechinus stuartii (Brown marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
99C02857CBB73429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
"DNA phylogeny of the marsupial wolf resolved.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U87140; AAB91328.1; -.
InterPro; PRRODG21; PROCAmine_P1.
Pfam; PF00260; protamine_P1; I.
PROSIZE; PS00048; PROTAMINE_P1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             condensation; Nuclear
                                                                                                                                                          -!- SÜBCELLULAR LOCATION: NUCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L35336; AAA74600.1; -.
EMBL; L35327; AAA74606.1; -.
EMBL; L32743; AAA9478 1; -.
EMBL; U87139; AAB91327.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AA; 8566 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 HGRRRGYSRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_T'axID-9283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Testis; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal
```

```
DR EMBL, L35335; AAB95428.1; -.

DR InterPro; IPR000221; Protamine_Pl.

DR Pfam; PF000260; protamine_Pl.

DR PROSTTE; PS00048; PROTAMINE_Pl.; 1.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

BY SEQUENCE 63 AA; 8722 MW; D4FF992DAAB56D61 CRC64;

SQ SEQUENCE 63 AA; 8722 MW; D4FF992DAAB56D61 CRC64;

Best Local Similarity 69.2%; Pred. No. 0.25;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

A4 RGRRSCYSRRRS 13

Db 44 RGRRRCYSRRRS 56
```

Search completed: February 12, 2002, 12:39:52 Job time: 805 sec

us-09-485-571-25.rspt

```
February 12, 2002, 12:38:40 ; Search time 232.64 Seconds
(without alignments)
11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                      473505
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                   US-09-485-571-25
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPTREMBL_17:*
                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                           Run on:
```

11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*

sp_plant:*

Result Query No. Score Match Length DB ID 1 52 57.1 173 2 0987A8 2 47 51.6 92 12 073508 5 47 51.6 93 12 073509 6 47 51.6 93 12 073514 7 47 51.6 93 12 073514 8 47 51.6 93 12 073514 9 47 51.6 93 12 073527 10 47 51.6 93 12 073527 11 47 51.6 93 12 073529 12 07353 potato viru 13 47 51.6 93 12 07353 14 46 50.5 94 12 073525 15 041 12 086541 16 45 50.5 231 5 016689 17 45 50.5 231 5 016689 18 45 49.5 61 6 096LD9 19 45 49.5 61 6 096LD9 10 47 51.6 0941486 11 486 50.5 231 5 016689 12 041486 potato viru 13 47 51.6 94 12 073525 14 46 50.5 231 5 016689 15 45 49.5 61 6 096LD9 16 45 49.5 61 6 096LD8 17 45 49.5 61 6 096LD8 18 45 49.5 61 6 096LD8 19 45 49.5 61 6 096LD8 10 47 50.6 61 6 096LD8 10 47 50.6 61 6 096LD8 10 47 61.0 073525 11 6 45 49.5 61 6 096LD8 12 07351 potato viru 13 47 51.6 04 12 073525 14 6 50.5 231 5 016689 15 041486 potato viru 16 45 49.5 61 6 096LD8 17 45 49.5 61 6 096LD8 18 45 49.5 61 6 096LD8

Q9tuc2 sminthopsis Q9dq0 bettongia p Q9tuc4 sminthopsis Q9dq2 lagorcheste Q9icw2 kalanchoe l Q9icw2 manchoe l Q9icw2 manchologis Q9ty3 neisseria m Q9fy4 mashidopsis Q9fy6 serbidopsis Q9fy6 serbidopsis Q9fy6 sercopyrum p Q99fx1 thermoplasm Q90y12 thermoplasm Q99y13 templylococ Q99fx1 thermoplasm Q999y1 templylococ Q99fx1 thermoplasm Q999y1 templylococ Q99fx1 thermoplasm Q999y1 templasm	Q9yek7 aeropyrum p Q90110 bombyx mori Q9f934 bifidobacte Q9sns6 oryza sativ O39296 equine herp O17484 plodia inte
09TUC2 09GL00 09GL02 09GL02 09ICW8 09ICW8 09JCW2 09SV3 09SV10 09SV10 09SV7 09SV56 09SV7 09PV09 099K16 099K16 099K16 099K16 099K10 099K10	a a oo
62 6 62 6 63 6 63 6 63 6 1001 12 1101 12 1102 12 1293 2 1293 2 1293 2 1351 11 135 2 60 12 136 13	118 1 138 12 287 2 427 10 747 12 1016 5
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	addadda
υ ω ω α α α α α α α α α α α α α α α α α	444444
22 22 22 22 22 22 22 22 22 22 22 22 22	0010m45.

ALIGNMENTS

RESULT	.n. 1
S a S	OGETAR PRELIMINARY; PRT; 173 AA. 09ETAR:
T T	01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
I I	(TrEMBLrel. 16, Last
OE GN	HYPOTHÈTICAL 18.9 KDA PROTEIN. ORFS8.
os	Corynebacterium equil (Rhodococcus equi).
90	Plasmid pREAT701 (p33701), and Plasmid virulence.
ဗ	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
88	Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
N N	
RP	SEQUENCE FROM N.A.
RC C	CC33701; PLASMID=PREAT701 (P33701);
RA	Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
RL	(FEB-2000) to the EMBL/GenBank/DDBJ d
RN	[2]
RP	SEQUENCE FROM N.A.
S S	STRAIN "ATCC33701, AND 103; PLASMID-PREAT701 (P33701), AND VIRULENCE;
RX	PubMed=11083803;
RA	
RA	Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
ΚA	Dan H Prescott J.F.;
RT	"DNA sequence and comparison of virulence plasmids from Rhodococcus
Ϋ́	equi Auce 33/01 and 103.";
R.	Infect. Immun. 68:6840-6847(2000).
DR G	EMBL; AP01204; BAB16667.1;
ž :	EMBL, AFILOSU/; AAGZI/OI.I.
× ×	Hypothetical protein; Plasmid.
S S	SEQUENCE 173 AA; 18851 MW; F18A637BCA404053 CRC64;
One	Query Match 57.1%; Score 52; DB 2; Length 173;
Mai	vative 4; Mismatc
Qy	2 GGRLSYSRRRFSTSTGR 18

ö

qq

```
11K PROTEIN (FRAGMENT).
                      Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          073512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
073512
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 12; Length 92;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 12; Length 93;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                 STRAIN-IDAMO;
Cavileer T.D., Corsini D.L., Berger P.H.;
Cavileer T.D., Corsini D.L., Berger P.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF023877; AABB1273.1; -.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Hypothetical protein.
SEQUENCE 92 AA; 10319 MW; B0A9AC70B579A980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN-ASCHERSLEBEN;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15643; CAA75702.1; -.
InterPro; IPR002568; Carla_C4.
InterPro; IPR01623; Carla_C4; 1.
SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POTATICAL 10.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 07, TrEMBLrel. 07, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.90,
Best Local Similarity 52.90,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 GGRSKYARRRRAIAAGR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 52.9
les 9; Conservative
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               073509 F
073509;
01-AUG-1998 (
01-AUG-1998 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              073508
                                                                                          038024;
                                                                      038024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
O73508
1D O73508
O77508
D7 O77508
O77
                                RESULT
038024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
073509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
NCBL_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                      Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 93;
                                                  [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MATORIN-ASCHERSLEBEN;
Matorisek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15615; CAA75706.1; -.
Interpro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4, 1.
NON_TER 93
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-EARLA;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; F15611; CAA75698.1; -.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4: 1.
NON TER 93
                                                                                                                                                                                                                            SEQUENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                    Score 47; DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 12;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 AA.
                                                                                                                                                                                                                                                                                                       Pred. No. 1.8;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         073514 PRELIMINARY;
073514;
01-302, 1998 (TrEMBLrel. 07, Cr
01-30N-2001 (TrEMBLrel. 17, Le
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                      52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%;
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.9°,
Best Local Similarity 52.9°,
Conservative
                                                                                                                                                                                                                                                                                                                                                                 2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                      ||| :|:|:| : | ||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLSYSRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| :|:|:| | ||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=KARLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12169;
```

us-09-485-571-25.rspt

Page

ö

Gaps

```
11K FROTEIN (FRAGMENT).

Obtato virus S.
Viruses: SSRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virusės; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_SaxID=12169;
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 12; Length 93; Pred. No. 1.8; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 12; Length 93; Pred. No. 1.8; 4; Mismatches 4; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-KOBRA;
MATOUSEK J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15614; CAA75704.1; -.
InterPro; IPR002568; Carla_C4.
Pfam: PF01623; Carla_C4.
NON_TER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15610; CAA75696.1; -.
InterPro; IPR002568; Carla_C4.
Pfam: PF01623; Carla_C4: 1.
NON_TER 93
SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 93 AA; 10565 MW; 11BD8D5D69865A75 CRC64;
                                                                                                                                                                                                                                   01-AUG-1998 (TrEWBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOY-1998 (TrEMBLrel. 08, Created)
01-NOY-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
      Mismatches
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.6%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                 2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| :|:|:| | ||
38 :GRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGRLSYSRRFSTSTGR 18
                                                                       38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| :|:|:| : | ||
38 GGRSTYARKRRARSIGR 54
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-VITAVA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potato virus S.
      6
                                                                                                                                                                                             073531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 093139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093139
                                                                                                                                                       σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
093139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
073525
                                                                                                                                                       RESULT
                                                                                                                                                                              073531
                                                 οy
                                                                                    g
                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID DT STAND THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11. FROTALIN (FRAGMENT).
Potato virus S.
Viruses: ssRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                     Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 93;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-VITAVA;
Matcusek J., Schubert J., Dedic P.;
Matcusek J., Schubert J., Dedic P.;
Submitted (VOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, Y15609, CAA75694.1; -.
InterPro; IPR002568; Carla_C4.
PFf01623; Carla_C4; 1.
NON_TER P910529; Carla_G4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matcusek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15616; CAA75708.1; -
InterPro; IPR002568; Carla_C4.
Ffam; PF01623; Carla_C4; 1.
NON_TER 93
SEQUENCE 93 AA; 10507 MW; AC2FE2A0F98645C9 CRC64;
EMBL; Y15612; CAA75700.1; -.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93 93
SEQUENCE 93 AA; 10538 MW; 11BD9CBC9997BBB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
                                                                                                                                                   51.6%; Score 47; DB 12;
illarity 52.9%; Pred. No. 1.8;
Conservative 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 12;
Pred. No. 1.8;
4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.6%; Score 47; DB 12; 52.9%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AA.
                                                                                                                                                                                                                                                                                                                                                                                         93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%;
52.9%;
                                                                                                                                                                                                                                     2 GGRLSYSRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                              38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.6
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | | :|:|:| | || 38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-VITAVA;
                                                                                                                                                                                                                                                                                                                                                                                073527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               073529
073529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
073529
                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                073527
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S T B S
                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
```

ö

Gaps

ö

Gaps

```
XX STRAIN-C57BL/G5. TISSUE-TESTIS;

XX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arakawa T., Hara A., Fukunishi Y., Konon H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konon H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

XA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

XA Fleischmann W., Satubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

XA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

A Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Willming L.,

XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

XA Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO15647; BAB29915.1; -.
MGD; MGI:1923059; 4930488L21Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 12868 MW; 665940B7EF891419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGRLSYSRRFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA po
NCBI_TaxID=12169;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S-RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       041486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           016689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   041486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΙD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            öλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDCINE=93033173; PubMed=1413539;

MEDCINE=93033173; PubMed=1413539;

Foster G.D., Mills P.R.;

Foster G.D., Mills P.R.;

Foster G.D., Mills P.R.;

Foster G.D., Mills P.R.;

EMBL; S45593; AAB23462.1; -..

EMBL; S45593; AAB23462.1; -..

EMBL; S45593; Carla_G4.1:

Pfam; PF010523; Carla_G4; L.

SEQUENCE 94 AA; 10680 MW; 2241BD8D5D69865A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
                                                                                                                                                    Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 12; Length 94; Pred. No. 1.8; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB 12; Length 94; Pred. No. 1.8; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                            SEQUENCE ...
STRAIN-KOBRA;
Matousek J., Schubert J., Dedic P.;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15625; CAA75721.1; ...
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10665 MW; 5236BDFD583C830A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                      01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 11K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 AA
          94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.6%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, 11 KDA PROTEIN.
                                                          (TremBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.5.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| :|:|:| | ||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4930488L21RIK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4930488L21RIK.
                                073525;
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                086541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      965060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
0286541
10 086541
07 01.NOV
DT 01.NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              086541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Оþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
ö
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                               positive-strand viruses, no DNA stage; Carlavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                       ö
51.6%; Score 47; DB 11; Length 117; 69.2%; Pred. No. 2.2; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 12; Length 94; Pred. No. 2.6; 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Joung Y.H.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U74376; AAB65087.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro: IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10649 MW; C8CCDFF10F00A10A CRC64;
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AA.
                                                                                                                                                                                           94 AA
                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.5%;
52.9%;
                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
         Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                        46 GGRLSHSHQEFST 58
```

```
ö
                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-BRISTOL N2;

MEDLINE-94150718; bubmed-7906398;

MEDLINE-94150718; bubmed-7906398;

MISON R., Ainscough R., Anderson K., Baynes C., Berks M.,

MISON R., Ainscough R., Anderson K., Eavello A., Fulton L.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Waterston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

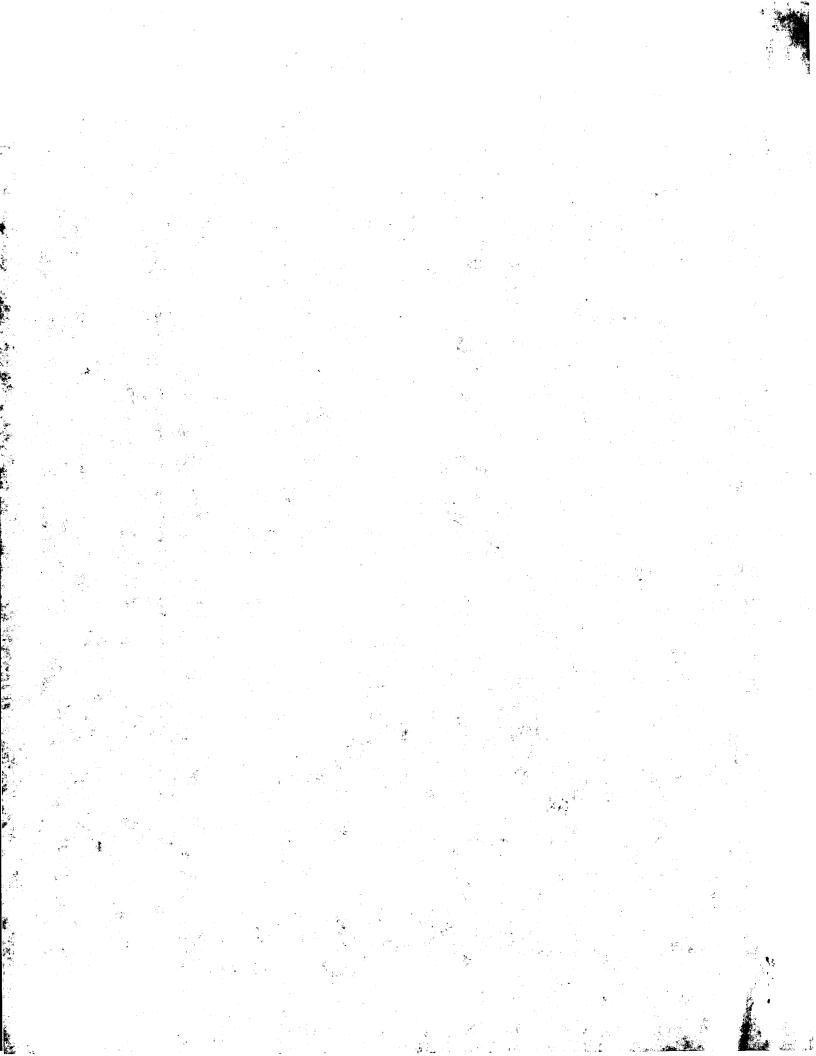
Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mp of contiguous nucleotide sequence from chromosome III of C.

"In Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.5%; Score 46; DB 5; Length 231; Best Local Similarity 47.1%; Pred. No. 6.7; Matches 8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF016678; AAB66149.1; -.
SEQUENCE 231 AA; 26411 MW; FDF4DBE1DE511EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Jones K., Kramer J.;
Submitted (AuG-1997) to the EMBL/GenBank/DDBJ databases.
016689;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-HAR-2001 (TrEMBLrel. 16, Last annotation update)
K07E8.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRRFSTSTG 17
                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
   õ
```

Search completed: February 12, 2002, 12:38:40 Job time: 753 sec

q



us-09-485-571-26.rag

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:30:32; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec		ú
2, 12:	RSR 17	ext 0.
, 2003	71-26 GISYRI	Gabe
ry 12	485-5' RVSYR	62 10.0
Februa	US-09-485-571-26 91 1 KWSFRVSYRGISYRRSR 17	BLOSUM62 Gapop 10.0 , Gapext 0.5
	Title: Perfect score: Sequence:	Scoring table:
Run on:	Title: Perfect s Sequence:	coring
ž.	SPE	Š

522463 Total number of hits satisfying chosen parameters:

522463 seqs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databas

A_Geneseq_1101:*	1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*	2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*	3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*	4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*	5: /SIDS8/gcgdata/geneseq/genesegp/AA1984.DAT:*	6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*	7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*	8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*	9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*	<pre>10: /SIDS8/gcgdata/geneseq/genesegp/AA1989.DAT:*</pre>	<pre>11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*</pre>	IDS8	<pre>13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*</pre>	<pre>14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*</pre>	<pre>15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*</pre>	<pre>16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*</pre>	<pre>17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*</pre>	18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*	<pre>19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*</pre>	20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*	21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*	22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*	
se Se																							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Tachyplesin deriva	Peptide which may	Tachyplesin deriva	Antimicrobial tach	Tachyplesin analog	Antimicrobial tach	Generic tachyplesi	Tachyplesin analog	Antimicrobial tach	Antimicrobial tach	Antimicrobial tach
SUMMARIES	OI.	AAW99413	AAY93617	AAW99414	AAR75806	AAY69610	AAR75819	AAY69609	AAY69617	AAR75807	AAR75808	AAR75816
	DB	20	21	20	16	21	16	21	21	16	16	16
	Query Match Length DB	17	17	17	17	17	17	17	17	17	17	21
ď	Query Match	100.0	100.0	6.7	86.8	86.8	82.4	82.4	82.4	81.3	81.3	81.3
	Score	91	91	88	79	79	75	75	75	74	74	74
	Result No.	-	7	æ	4	ស	9	7	80	6	10	11

Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells

ial tial tilysac	Tacyplesin-1. Tac Tacyplesin, an an Cationic peptide t Cationic peptide T Tacyplesin (TP),	ਰਲ ਵਾ	Tacyplesin-III. T Antimicrobial tach Antimicrobial tach Antimicrobial tach Tachyplesin analog Tachyplesin analog Tachyplesin analog Tachyplesin analog Tachyplesin analog	Hrappari
AAR75810 AAR75822 AAP91671 AAR06266 AAR06861	AAR38489 AAR75805 AAW66465 AAY91764 AAY69608	AAR75817 AAR75817 AAR75803 AAR23114	AAR38491 AAR75820 AAR75814 AAK69611 AAK69612 AAY69615 AAY69615	AARO6862 AAR23113 AAR3490 AAR75811 AAW66466 AAR91765 AAR75815 AAR75812
16 10 11 13	231	13 11 19 19 19 19 19 19 19 19 19 19 19 19	14 16 21 21 21 21	11 11 11 11 11 11 11 10
. 35 17 17 17 17	11 11 11 11 11	39	71 71 71 71 71 71	71 71 71 71 71 71
81.3 80.2 78.0 78.0 78.0		0000	74.7 73.6 73.6 73.6 73.6 73.6	71.4 71.4 71.4 71.4 71.4 70.3 70.3
74 73 71 71 71	17 17 17 17 17	71 71 70 68 68	68 67 67 67 67	00 00 00 00 00 00 00 00 00 00 00 00 00
, 112 114 115 116 117	18 19 20 22 23	25 25 26 28 28 28	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	788844444 78884 7884 7844444

ALIGNMENTS

```
Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                           Kaczorek M;
                                                                          Tachyplesin derivative peptide SM1726.
                AAW99413 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                           Grassy G,
                                                                                                                                                                                                    98WO-FR01757.
                                                                                                                                                                                                                      97FR-0010297
                                                      08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                         Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                             WPI; 1999-190034/16.
                                                                                                                                                                                                                                        (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                   06-AUG-1998;
                                                                                                                                                                                                                      12-AUG-1997;
                                                                                                                                                              WO9907728-A2
                                                                                                                                                                                 18-FEB-1999.
                                                                                                                                            Synthetic.
                                    AAW99413;
RESULT
AAW99413
```

; 0

Gaps

ö

Indels

100.0%; Score 91; DB 21; 100.0%; Pred. No. 1.7e-08; iive 0; Mismatches 0;

Length 17;

```
1 kwsfrvsyrgisyrrsr 17
                                                                                                                      1 KWSFRVSYRGISYRRSR 17
                                                 Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calas B,
                                                                                                                                                                                                                                                                                       AAW99414;
                                                                                                                                                                                                                                AAW99414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                 ô
                        This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivitals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, machanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition useful for cancer treatment and prevention, contains enticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                            Score 91; DB 20;
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93617 standard; peptide; 17
     8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-FR02939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     1 kwsfrvsyrgisyrrsr 17
                                                                                                                                                                                                                                                                                                                                                                                     KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Temsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93617
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer
         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
```

g

:

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivitatals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                       Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derivatives of antibiotic peptides lacking disulfide bridges \, used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88; DB 20; L. Pred. No. 5.3e-08; 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaczorek M;
                                                                                                                                                                    Tachyplesin derivative peptide SM2307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grassy G,
AAW99414 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 rwsfrvsyrgisyrrsr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 96.7
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1997;
                                                                                                                 08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999.
```

AAR75806

```
Sequences AAV69610-Y69611 and AAV69617 represent tachyplesin analogues
used in an exemplification of the present invention, in which the
contains tachyplesin cysteine residues are replaced with Ala, Leu and
Asp, respectively. Tachyplesin (AAV69608) is a naturally occurring
antimicrobial peptide which contains two disulphide bonds which help
comming the reflary structure. The invention relates to novel
peptide analogues of tachyplesin (Y696912-AAX69614, AAX69616) in which
the cysteine residues at positions 3, 7, 12 and 16 of the native
the cysteine replaced by the hydrophobic amino acids isoleucine,
actoryplesin are replaced by the hydrophobic amino acids isoleucine,
the same maino acid being
present at all four positions. Despite being unable to form
intramolecular disulphide bonds, the analogues are functional as
antimicrobial agents. The tachyplesin analogues are seful for
controlling fungal and viral activity in agricultural and medical
applications and for controlling plant viruses. They can also be
cypressed in transgenic plants, preferably wheat, sorghum, sunflower,
soya or especially maize plants, preferably wheat, sorghum, sunflower,
soya or especially maize plants to provide resistance to pathogenic fungi
                                                                                                                                                                                                                                                                                               New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 21; Length 17;
Pred. No. 1.6e-06;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR75819 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page -; 17pp; English.
                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.8%;
                                                                                             97US-0962034
                                                                                                                                   97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence given in column 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|||:|||:|||:|
| kwafrvayrgiayrrar 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                       WPI; 2000-126327/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                     31-OCT-1997;
                                                                                             31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9516776-A1
                US6015941-A.
                                                      18-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Matich
                                                                                                                                                                                                                    Rao AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75819
δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium araminearum, Fusarium monliforme, Sclerctinia sclerotiorum, Sclerctinia trifoliorum and Aspergilus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analogue; generic; antimicrobial; disulphide bond; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                        Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79; DB 16; Length 17
Pred. No. 1.6e-06;
4; Mismatches 0; Indels
                                                                                                                                   Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY69610 standard; peptide; 17 AA.
            AAR75806 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                       94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                              93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rao A;
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachyplesin analogue, TPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||:|||:|||:|
| kwafrvayrgiayrrar 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.8
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                          WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                       19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                            17-DEC-1993;
                                                                                           07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachyplesin
antifungal;
                                                                                                                                                                                                                                                                                                               22-JUN-1995
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                             infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY69610;
                                                 AAR75806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
```

ö

Gaps ;

AAY6961

ò g

```
WPI; 2000-126327/11
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6015941-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2000
                                                                                                                                                                                                                                                                   and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY69617;
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rao AG;
                          Rao AG;
                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                            AAY69617
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= lle, Val, Met, Phe, Tyr
/note= "The molecule has the same amino acid at all four
  of the above positions"
                                                                                                                                         AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                        Gaps
                                                                                            New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                   Score 75; DB 16; Length 17; pred. No. 7e-06; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic tachyplesin (TP) analogue antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
/note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ile, Val, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          AAY69609 standard; peptide; 17 AA.
                                     (PION-) PIONEER HI-BRED INT INC.
                                                                                                                           Claim 1; Paqe 35; 45pp; English.
                                                                                                                                                                                                                                                                      82.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0962034
                                                                                                                                                                                                                                                                                76.5%;
                   93US-0168809
  94WO-US14619
                                                          Rao AG, Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                           1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                      || ||| ||| |||| ||| |
| kwkfrvkyrgikyrrkr 17
                                                                           WPI; 1995-231570/30
                                                                                                                                                                                                                                          17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6015941-A.
                     17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2000
  19-DEC-1994;
                                                          Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                              AAY69609
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                         animals
                                                                                                                                                                                                                                                                                                                                                                            g
   ò
```

```
This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disuplande bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY69614, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants, to provide resistance to pathogenic fungi
                                                                                                                                                                                                    New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 21; Length 17;
Pred. No. 7e-06;
); Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY69617 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 23; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC
(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0962034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.4%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tachyplesin analogue, TPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
```

S

Page

ö

us-09-485-571-26.rag

```
Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FE3-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putmar RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75308;
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animals
                                                                                                                                                                         animals
                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75808
                                                                                                                                                                                                                                                                                                                                                         οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 × 0 0 0 0 0 0 0 0 0 0 × 0
                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                            Sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala, Leu and Asp, respectively. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y66912-AAY66014, AAY66016) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be controlling maize plants to provide resistance to pathogenic funging and viruses. Note: The present sequence is not shown in the sequence given in column 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                             fundi
                            New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 75; DB 21;
Pred. No. 7e-06;
0; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR75807 standard; peptide; 17 AA.
                                                                                                  Example 1; Page -; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.4%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 82.4
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-231570/30.
WPI; 2000-126327/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
```

ò 셤

```
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerotinia sclerotionum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Evsarium monilforme, Sclarottinia sclerotiorum, Sclerottinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74; DB 16; Length 17; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 16; Length 17;
Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75808 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                        17 AA;
```

13;

Matches

δλ g Synthetic.

AAR75816;

AAR75816

RESULT

```
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hoemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                           New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibitor; antimicrobial; plant pathogen; fungi;
Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74; DB 16;
Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75822 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 31; 45pp; English.
                                                                                                                                                                                                       (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rao A;
                                                                                                                                                                          93US-0168809
                                                                                                                                                                                                                                       Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.3
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rao AG,
                                                                                                                                                                                                                                      Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                 WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tachyplesin;
infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1995
                                                                                 W09516776-A1
                                                                                                                                                                          17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putman RJ,
                                                                                                              22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                      infection
                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hosemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monificame, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
           ö
                                                                                                                                                                                                                                                                 Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 16; Length 21
Pred. No. 1.3e-05;
.; Mismatches 3; Indels
           Indels
           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                           Antimicrobial tachyplesin peptide derivative.
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
                                                                                                                                                   AAR75816 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 34; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR75810 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                          1 KWSFRVSYRGISYRRSR 17
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                      W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1993;
                                                                                                                                                                                                               07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-1995
```

Query Match Best Local S Matches 13

Sequence

animals.

AAR75810;

3. .

AAR75810

a

RESULT

g ŏ

ö

Gaps

0

```
The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemocytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LPS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for trachobronchial infections, urhary tract infections, bedsores, burns, complications.
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antivirus agents of polypeptide - useful as antivirus agents for vesicular stomatitis virus or human immuno-deficiency virus
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                                                               Length 17;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            Score 71; DB 10; L
Pred. No. 3.2e-05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 11;
Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vesicular stomatitis virus; HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 3.16 7.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06266 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 309; 12pp; Japanese.
                Claim 2; Page 27; 39pp; English.
                                                                                                                                                                                                                                                                                              78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89JP-0166811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88JP-0239051.89JP-0166811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                              1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                             Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tachypeus tridentatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-241996/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiviral peptide
                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP02167230-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEF-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR06266;
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR06266
     qq
                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                         AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monliforme, Sclerothina sclerotiorum, Sclerothina trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                          Score 73; DB 16; Length 1,
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New lipo:polysaccharide- binding polypeptide(s) - useful for treating bacterial infections and immune and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New lipopolysaccharide-binding polypeptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miyazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label-OTHER
/note="Arg-OH or Arg-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP91671 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohno M,
                                                                             Claim 1; Page 36; 45pp; English
                                                                                                                                                                                                                                                                                                                           80.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=OTHER
/note="H-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88WO-JP00823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87JP-0206258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                           1 kwrfrvryrgieyrrer 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           horseshoe crab haemocytes
                                                                                                                                                                                                                                                                                                                                                            13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iwanaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3..16
WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-068854/09.
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond 3
Disulfide-bond 7
Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horseshoe crab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8901492-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP91671;
                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                            Query Match
```

ö

Matches

õ g

Search completed: February 12, 2002, 12:30:33 Job time: 366 sec

, Appl Appli Appli

Appli Appli Appli Appli Appli Appli Appli

Appli Appli Appli Appli Appli Appli Appli

```
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
APPLICANT: Roo, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                                                                                                                                                                             Sequence 12, 1
Sequence 12, 1
Sequence 3, Ap
                        Sequence 1, A Sequence 7, A Sequence 8, A Sequence 8, A Sequence 13, Sequence 17, Sequence 17, Sequence 17, Sequence 5, A Sequence 5, A Sequence 23, A Sequence 24, A Seque
                                                                                                                                                                                                                                                                Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB 1; Le
Pred. No. 4.7e-07;
4; Mismatches 0;
US-08-282-030-7
US-08-426-550-4
US-08-426-550-4
US-08-282-030-8
US-08-168-809-8
US-07-856-0268-13
US-07-856-0268-14
US-07-856-0268-14
US-07-856-0268-23
US-07-856-0268-23
US-07-856-0268-23
US-08-426-550-5
US-08-459-400-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEFRONE: 515-245-3555
TELEFRAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08168809
Patent No. 5580852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.8
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
NO
      118
118
118
118
118
118
118
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
    667.0
667.0
667.0
667.0
665.4
663.7
663.7
663.7
663.7
663.7
673.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-168-E09-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-168-809-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21, Appl
1, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2, Appli
3, Appli
3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13, Appl
19, Appl
2, Appli
10, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Appli
                                                                                                                                                                            (without alignments)
3.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/packfiles1.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-08-962-034-2
S-08-168-809-6
S-08-168-809-15
S-08-168-809-15
S-08-168-809-21
S-07-926-965-1
S-07-876-883-1
S-07-876-883-1
S-08-168-809-4
S-08-168-809-4
S-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-08-168-809-16
5-08-168-809-2
5-07-876-883-3
5-08-426-550-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -08-168-809-13
-08-168-809-19
-07-876-883-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-168-809-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-876-883-4
                                                                                                                                                                                                                                                                                                                                                                                               212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                     February 12, 2002, 12:32:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                       US-09-485-571-26
91
1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                          rotal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score:
                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0B
0B
                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                  Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No.
```

ö

Gaps

```
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
APPLICANT: RAILOR STRUCTURE G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/962,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 3;
Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/168,809
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Redistration NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08168809
Patent No. 5580852
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: SPTUIL, W. MURTEY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWXFRVXYRGIXYRRXR 17
                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.4
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
ZIP: 27622-1107
COMPUTER READABLE FORM:
                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                     APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INIBITIORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Rao, A. Gururaj

APPLICANT: RAO, A. GURURAJ

TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN

TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 2

ADDRESSEE: Bell Seltzer IP Group of Alston & Bird

STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUETE S0309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 1; I
Pred. No. 2.1e-06;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michaell J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEFAN: 515-245-3595
TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                               Sequence 18, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-962-034-2
; Sequence 2, Application US/08962034
; Patent No. 6015941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 17 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWKFRVKYRGIKYRKR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
        1 KWAFRVAYRGIAYRRAR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                       CITY: Des Moines
STATE: IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3605 Gl
CITY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-168-809-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                 US-08-168-809-18
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                 අ
```

Gaps ; 0

```
Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE JF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE JF INVENTION: INTIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
Sequence 15, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 74; DB 1; Lengtn 41, Pred. No. 3.9e-06;
                                                                                                                                                                                                                                                                                                                                                                    SOFWHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORIEY/AGENT INFORMATION:
NAME: Roch, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01/3R US
TELECHONUSICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFRAX: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.3%;
ilarity 76.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTEETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Lac 13; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-168-809-15
                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: DIRIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                       Score 74; DB 1; Length 1/;
Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 1; Length 17; Pred. No. 3.1e-06; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROLL, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELECHONE: 515-245-3595
TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.3%;
76.5%;
                                                                                                                                                         81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 81.3 Best Local Similarity 76.5 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                  1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
         single
                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
                           linear
                                                                              ; ANTI-SENSE: NO
US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO
US-08-168-809-7
                         TOPOLOGY: 11
MOLECULE TYPE:
                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-168-809-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                RESULT 5
US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

ô

```
Sequence 1, Application US/07926965
; Sequence 1, Application US/07926965
; Patent No. 5416194
; GENERAL INFORMATION:
    APPLICANT: NAKAMORI; IWANAGA, SADAAKI;
    APPLICANT: NAKAMORI; MIYAZAKI, KYOSUKE
    TITLE OF INVENTION: NOVEL POLYPEPTIDE AND METHOD FOR
    TITLE OF INVENTION: PREPARING THE SAME
    NUMBER OF SEQUENCES:
    ADDRESSEE: BIERMAN & MUSERLIAN
    STREEP: 600 THIRD AVENUE
    CITY: NEW YORK
    STATE: NEW YORK
    COUNTRY: USA
                                                                                                Length 17;
                                                                                                80.2%; Score 73; DB 1; I
76.5%; Pred. No. 4.6e-06;
Live 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 19.048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: HORSESHOE CRAB
STRAIN: TACHYPLEUS TRIDENTATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
                                                                                                                                                                              1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE
                                                                                                                     Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE: CELL TYPE: F
  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10016
                    ; ANTI-SENSE:
US-08-168-809-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANELLE
                                                                                                                                                                                                                                                                                                  US-07-926-965-1
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 1; Length 35; Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 50309

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29.342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                              0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Reth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 01731
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 35 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 515-245-3634 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.3
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 700 Capit
CITY: Des Moines
                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οχ
```

ì

```
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Ankiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
                                                                                APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                           ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
STATE: IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 71; DB 1; 1
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: Now York
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0173R US
                                                                                                                                                                                                                                                                                                                                                                         COMFUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                         ; Sequence 4, Application US/08168809
; Patent Nc. 5580852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08426550 ; Patent No. 5710128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ROCH, MIChael J.
RECISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                             50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE:
US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
IDENTIFICATION METHOD:
OTHER INFORMATION: WHEREIN CYS-3 AND CYS-16 CAN
OTHER INFORMATION: FORM A DISULFIDE BOND, AND CYS-7 AND CYS-12 CAN FORM A DISULE
OTHER INFORMATION: BOND; WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE AMIDATED; WHERE
OTHER INFORMATION: OR ALL OF THE RESIDUES CAN BE PROTECTED WITH PROTECTIVE GROUP
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
TITLE OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                 Score 71; DB 1; Length 17;
Pred. No. 9.7e-06;
); Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71; DB 1; Length 17; Pred. No. 9.7e-06; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New YOLK

STATE: New YOLK

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC COMPALIBLE
COMPUTER: DATENTION DATE

SOFTWARE: PATENTION DATA:
CURRENT APPLICATION NUMBER: US/07/876,883

TITING DATE: 19920429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24,576
3R: 7568-003
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07876883
Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELECHONE: 212 790-9990
TELETAX: 212 869-9741
TELETAX: 212 869-9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                           ö
                                                                                                                                                                 78.0%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                  1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                         1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                             Query Match
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-876-883-1
                                                                                                        US-07-926-965-1
                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-07-876-883-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

```
GENERAL INFORMATION:
APPLICANT: PULDAM, Rebecca J.
APPLICANT: PLUIDAM, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 1; Length 39;
Pred. No. 2.4e-05;
0; Mismatches 4; Indels
                                                                                                          Score 71; DB 3; Length 17; Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08168809 Patent No. 5580852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATTORNEY/AGEWI INFORMATION:
NAME: ROLL, MICHAEL J
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
                                                                                                        ch 78.0%;
1 Similarity 76.5%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.0%;
76.5%;
                                                                                                                                                                                                                1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                         1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 39 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.0
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-962-034-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                            Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-08-168-809-16
                                                                                                                                                                                                                                                                                        RESULT 14
US-08-168-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-168-809-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: L
                                                                                                            Query Match
                                                                                                                                                                                         Ω
                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08962034
Patent No. 6015941
GENERAL INFORMATION:
APPLICANT: RAO, A. GUTURAJ
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Bell Seltzer IP Group of Alston & Bird 3605 Glenwood Ave.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21.APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 1; I Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-990
TELEFAX: 212 869-9741
TELEFAX: 6644 PENNIE
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.0
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNETH: 17 and Trops: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27622-1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3605 G1
CITY: Raleigh
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-962-034-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
```

```
APPLICANT: Butnam, Rebacca J.
APPLICANT: Butnam, Rebacca J.
TITLE OF TWANTION: DERIVATIVES OF TACHTPLESIN HAVING
TITLE OF TWANTION: DERIVATION CONTINT TOWNES PLANT PATHOGENIC FUNCI
CONFESSIONECE PLONGER: ALL SQUARES; AL
CONFESSIONECE PROBATION STATE: APPLICATION NATA: RELEASE ALLO, Version #1.25
CURRENT APPLICATION NATA: PAPLICATION NATA: RELEASE ALLO, ACTORNEY/AGENT INVORMATION:
RECISENTANTION NUMBER: 29.342
RECISENTANTION NUMBER: 29.342
RECISENTANTION NUMBER: 20.3454
TELECOMMUNICATION 1900
TELECOMMUNICATION 1900
STANDENDESS: SIGGLE
TOPOLOCIC CHARACTERISTICS:
TELECOMMUNICATION 1900
STANDENDESS: SIGGLE
TOPOLOCIC: LINGAE
TOPOLOCIC:
```

***					3
	•				
i. B		**************************************	*	· · · · · · · · · · · · · · · · · · ·	
**************************************					#
> .					
pi.			A STATE OF THE STA		
	•				
			en e		
			**************************************		***
				Mariana di Kabupatèn Barana da Kabupatèn Barana da Kabupatèn Barana da Kabupatèn Barana da Kabupatèn Barana d Kabupatèn Barana da Kabupatèn	
∳.					
			•		
er F					en en 1940 en 1945 Personale de 1945 Personale de 1945
ej.					
e E					
*					
e de la companya de l					
<u>.</u>					na n
. :			en de la companya de Mandra de la companya de la company Mandra de la companya		
in the second se					1.14
: 5.					
≱ ri :	•.	Section 1		gape and the same	

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein February 12, 2002, 12:34:40; Search time 126.85 Seconds Run on:

(without alignments)
10.209 Million cell updates/sec

1 KWSFRVSYRGISYRRSR 17 US-09-485-571-26 91 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 219241 seqs, 76174552 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	-	٠,	H	tachyplesin I prec	Ξ	tachyplesin II pre	Η		hypothetical prote	ш	hypothetical prote	hypothetical prote	C	molybdate metaboli	hypothetical prote			etical	E2A DNA	early E2A DNA-bind	outer membrane ush	protein tyrosine k	protein tyrosine k	L-JAK protein-tyro	protein-tyrosine k	hypothetical prote	hypothetical prote	probable high-affi	probable oligopept	protein F1504.37 [
SUMMARIES																														
SUMMA	1 C C C C K	420024	JX0124	A38345	JX0125	B38345	JU0124	JU0125	D86473	C82472	F84162	A84161	E86468	G75313	D42463	T02495	T22808	A72534	ERAD40	ERAD41	H82850	S48053	S43677	A55747	158401	A86205	T19179	D72485	B71130	G86476
DB	; (v	7	~	~	~	~	~	7	7	7	7	7	7	7	7	7	7	П	П	7	7	7	7	~	~	~	~	~	7
å Query Match Length	1.7	, ·	61	77	17	77	18	18	615	88	307	378	620	480	536	279	770	330	473	474	901	1099	1100	1124	1299	781	846	242	597	167
% Query Match	70.07	0 0	0.87	78.0	74.7	71.4	67.0	63.7	51.6	48.9	48.4	48.4	48.4	46.2	46.2	45.1	•	44.0	44.0	44.0	44.0	44.0	•	44.0	44.0	43.4	43.4	42.9	42.9	42.9
Score		7 ;	7.7	7.1	68	65	61	58	47	44.5	44	44	44	42	42	41	41	40	40	40	40	40	40	40	4	39.2	σ	39	39	39
Result No.	-	4 (7 (m	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

protein pl30 - rat	probable transposo	hypothetical prote	MHC HLA-DQ-beta ce	Cc protein - fruit	hypothetical prote	MHC class II histo	hypothetical prote	conserved hypothet	protein F9C16.11 [hypothetical prote	hypothetical prote	LAG1 protein - yea	pyridoxal phosphat	early E2A DNA-bind	hypothetical prote
S46992	F86403	B70918	159528	C25511	S68196	HLHU2C	A70860	D71316	E96503	H75264	T20686	S46800	E75201	ERAD12	B72752
7	7	7	7	7	7	-	7	П	~	7	7	7	~	7	7
896	1148	563	94	203	225	261	327	329	330	358	360	411	466	484	514
σ	o,	m	80	80	80	œ	00	80	œ	80	80	۵	80	80	80
42.9	42.	42.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.	41.
39	39	38.5	38	38	38	38	38	38	38	38	38	38	38	38	38
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
CiSpecies: Tachyplesin I - horseshoe crab (Tachypleus gigas)
CiSpecies: Tachypleus gigas
CiSpecies: Tachypleus gigas
CiSpecies: Tachypleus gigas
CiSpecies: A38824
Ribert: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
Ribert: Tis Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A/Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (C ssing intermediate of its precursor.
A;Reference number: JX0124; MUID:91035357
A;Accession: A38824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                  A.Experimental source: hemocyte
C;Keywords: amidated carboxyl end
F;3-16,7-12/Disulfide bonds: #status predicted
F;17/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 2; Length 17; Pred. No. 1.6e-05; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.0%;
Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-17 <MUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

ö

C;Species: Carcinoscorpius rotundicauda
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
C;Accession: JX0124
R;Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Blochem. 108, 261-266, 1990
A;Tille: Tachpplesins isolated from hemocytes of southeast Asian horseshoe crabs (C A;Tille: Tachpplesins isolated from hemocytes of southeast JX0124; MUID:91035357
A;Reference number: JX0124; MUID:91035357 tachyplesir I precursor - horseshoe crab (Carcinoscorplus rotundicauda)

A.Accession: JX0124
A.Molecule type: protein
A.Residues: 1-19 <MUT>
A.Experimental source: hemocyte
C.Keywords: amidated carboxyl end
F.1-17/Product: tachyplesin I #status experimental <MAT>
F.3-16.7-12/Disulfide bonds: #status predicted
F.3-16.7-12/Disulfide bonds: #status predicted

Length 19; Score 71; DB 2; 1 Pred. No. 1.7e-05; 78.0%; Query Match Best Local Similarity

```
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000 C;Accession: B38345; JU0123 R;Shigenaga, T.; Muta, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S. A;Dill Chem. 265, 21350-21354, 1990 A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular locally. Reference number: A38345; MUID:91065956 A;Accession: B38345 A;Accession: Basilanary A;Molecule type: MRNA A;Molecule type: MRNA A;Molecule type: MRNA A;Residues: 1-77 csHIP A;Cross-references: GB:J05689 B;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Biochem. 106, 663-669, 1989 A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesir A;Receion: Tundaria Peptides, isolated from horseshoe crab hemocytes, tachyplesir A;Receion: Tundaria A;Receion: Tundaria A;Biochem. 106, 663-669 A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesir A;Receion: Tundaria A;Biochem. 106, 663-669 A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesir A;Receion: Tundaria A;Biochem. 106 A;Title: Antimicrobial peptides, tachyplesir A;Receion: Tundaria A;Title: Antimicrobial peptides, tachyplesir A;Title: Antimicrobial peptides and A;Title: Antimicrobial peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 1-18 <MIX>
C; Comment: The peptide is one of the antimicrobial peptides in the Atlantic horsesho
C; Keywords: amidated carboxyl end
F; 4-17, 8-13/Disulfide bonds: #status experimental
F; 18/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JU0125
C,Accession: JU0125
R;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Biochen. 106, 663-668, 1989
A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Reference number: A91914; MUID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: JU0123
A,Molecule type: protein
A,Residues: 24-40 <MIV>
C;Comment: The peptide is one of the antimicrobial peptides found in the Japanese ho
C,Keywords: amidated carboxyl end
C,Seywords: amidated carboxyl end
F;40/Modified site: amidated carboxyl end (Arg) (amide in mature form from following.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A91914; MuID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyphemusin I - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Date: 31-Mar-1900 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Accession: Ju0124
E;Miyata, T; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Blochem. 106, 663-668, 1989
A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyphemusin II - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.0%; Score 61; DB 2; Length 18;
58.8%; Pred. No. 0.00074;
ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 2; Length 77;
Pred. No. 0.0007;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWCFRVCYRGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.4
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JU0125
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Tachypleus tridentatus
C;Accession: A38345; A30068
R;Shigenaga, T.; Muta, T.; Toh, Y.; Tokunaga, F.; Iwanaga, S.
J. Biol. Chem. 265, 21350-21354, 1990
A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localiza
A;Reference number: A38345; MUID:9106595
A;Accession: A38345
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7 <SHIX
A;Cross-references: GB:M57242; GB:J05689; NID:9161659; PID:9161660
A;Cross-references: GB:M57242; GB:J05689; NID:9161659; PID:9161660
A;Cross-references: GB:M57242; GB:J05689; NID:9161669
A;Cross-references: GB:M57242; GB:J05689; NID:9161669
A;Title: Tachyplesin, a class of antimicrobial peptide from the hemocytes of the horsesh
A;Reference number: A30068; MUID:89034158
A;Accession: A30068
A;Molecule type: Protein
A;Residues: 24-40 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Tachypleus gigas
Title: Tachypleus isolated from hemocytes of southeast Asian horseshoe crabs (Carcin A; Reference number: Jx0124; MUID:9103537
Airtile: Tachypleus gigas
Airtile: Tachypleus gig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tachyplesin II precursor - horseshoe crab (Tachypleus tridentatus) -C;Species: Tachypleus tridentatus
                                                                                                                                                                                                                                                                                                                                                                RESULT 3
A38345
tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 2; Length 77; Pred. No. 7.1e-05; Mismatches 4; Indels
                                                   Indels
                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 2;
Pred. No. 4.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                   Mismatches
                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.7%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.0%;
Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWCFRVCYRGICYRKCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 KWCFRVCYRGICYRRCR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                       1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Conservative
                                                                                                                                        KWSFRVSYRGISYRRSR 17
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                            g
                                                                                                                                            δ
```

07:52:22 2002

Wed Feb 13

```
| :|| | ::|:
252 KWAFRTLYEQVAYK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conserved hypothetical protein VCA0332 [imported] - Vibrio cholerae (strain N16961 serog C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Wibrio cholerae
C; Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: CB2472
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833
A; Accession: CB2472
A; Status: preliminary
A; Molecule type: DNA
A; Realdues: 1-88 cHEI>
A; Cross-references: GB:AE004372; GB:AE003853; NID:q9657741; PIDN:AAF96240.1; GSPDB:GN001
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication of the protein AAG27097.1 [imported] - Arabidopsis thaliana because the protein AAG27097.1 [imported] - Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86473
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hundrer, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; MuID:21016719
A; Reference number: B86473
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-615 <STO>A; Cross-references: GB:AE005172; NID:g11034940; PIDN:AAG27097.1; GSPDB:GN00141
C; Genetics:
A; Map position: 1
                                             CI
A;Residues: 1-18 <MIY>
C;Comment: The peptide is one of the antimicrobial peptides in the American horseshoe
C;Keywords: amidated carboxyl end
F;4-11,8-13/Disulfide bonds: #status predicted
F;4-11,8-13/Disulfide bonds: #status predicted
F;18/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 615
                                                                                                                                                                                                          63.7%; Score 58; DB 2; Length 18; 52.9%; Pred. No. 0.0023; Live 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                 1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                   2 RWCFRVCYKGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 QWRFRHSYRGTPQRHS 190
                                                                                                                                                                                                                                        Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: VCA0332
A;Map position: 2
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium species NRC-1
Cispecies: Halobacteriu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             King, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Las ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jundy, K.H.; Alam, M.; Frettas, T. Jundy, K.H.; Alam, M.; Frettas, T. Jundy, K.H.; Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M A; Reference number: Aglatobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483
                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004437; NID:g10579658; PIDN:AAG18653.1; GSPDB:GN00138 C;Genetics:
A;Gene: VNG0013C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: AE004437; NID: 910579674; PIDN: AAG18666.1; GSPDB: GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84161
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Vng0026c [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Vng0013c [imported] - Halobacterium sp. NRC-1
        Length 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 378
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2
Pred. No. 8.2;
4; Mismatches
                                                  1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB;
Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
10;
                                                                                   Mismatches
    Score 44.5;
Pred. No. 1.
                                                                                   5;
                                                                                                                                                                  2 WSFRVSYRG----ISYRRSR 17
                                                                                                                                                                                                                    58 WSGVITYRGTNIRIISVRRSR 78
Query Match 48.9%;
Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|| | ::|:
181 KWAFRTLYEQVAYK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWSFRVSYRGISYR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWSFRVSYRGISYR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Loca: Similarity
'-haa 6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-378 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <STC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: VNG 3026C
```

```
|||:|| || || :|
423 FRVNYRNGGIFYRSAR 438
                                                                                                                                                                                                                                                        Query Match 46.2
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                4 FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T19C21.1; At2g38500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||||| |||
99 AFRVSYHGIS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
A; Introns: 170/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                          Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowartz, J.R.; Shano, H.
Rer, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.J.;
C.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002046; GB:AE000513; NID:g6459901; PIDN:AAF11657.1; PID:g645990
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13

G75313

molybdate metabolism regulator-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: G75313
C;Multe, O.: Eisen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-157, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE005172; NID: 98778254; PIDN: AAF79263.1; GSPDB: GN00141
                  C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Bcv' (pinB 5' region) - Shigella boydii (fragment) C;Species: Shigella boydii (C;Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #text_change 30-Sep-1993 _C;Accession: D42463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 620;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
protein F12K21.26 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 QWRFRHNYRGTPQRHS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 WMVRVDARGVYYGHSR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 WSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Residues: 1-620 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-480 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: G75313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: F12K21.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: DR2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D42463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
hypothetical protein At2938500 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T19C21.1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02495; G84805
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A;Reference number: 214676
A;Retaus: translated from GB/EMBL/DDBJ
A;Retaus: translated from GB/EMBL, DDBJ
A;Retaus: translated from 
R;Tominaga, A.; Ikemizu, S.; Enomoto, M.
J. Bacteriol. 173, 4079-4087, 1991
A;Title: Site-specific recombinase genes in three Shigella subgroups and nucleotide A;Reference number: A42463; MUID:91286192
A;Reference number: A42463
A;Retus: preliminary
A;Molecule types
A;Residues: 1-536 ATOMA
A;Residues: 1-536 ATOMA
A;Cross-references: GB:D00660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUD:20083487
A;Accession: G84805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <STO>
A;Cross-references: GB:AE002093; NID:93786022; PIDN:AAC67368.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.1%; Score 41; DB 2; Length 279; 80.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2
Pred. No. 31;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 12, 2002, 12:34:41
Job time: 559 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.2%;
```

		W.	
er en			
			er e
			*
			.
	ong n Santagaga		
			ž i-
	· · · · · · · · · · · · · · · · · · ·		

•

P12821 homo sapien P12822 oryctolagus P09470 mus musculu P47820 rattus norv P30415 mus musculu P30414 homo sapien P46287 medicago sa P42795 arabidopsis P42796 arabidopsis P42796 arabidopsis O12556 aspergilus O14523 schizosacch

ACE_HUMAN
ACE_RABIT
ACE_MOUSE
ACE_RAT
NKCK_MOUSE
NKCK_HUJAN
RLI1_MEDSA
RLI1_ARATH
RLI1_ARATH
RLI1_ARATH
AMO1_ASPNG
IATP_SCHPO

1306 1310 1312 1313 1462 1462 181 182 182 184 671

33 33 33 34 35 36 36 36 36 36 36 36 36

34 337 337 337 44 44 45 45 45

Н

us-09-485-571-26.rsp

```
February 12, 2002, 12:39:52; Search time 67.2 Seconds (without alignments) 9.275 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         100059 segs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      sw model
                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                  US-09-485-571-26
91
1 KWSFRVSYRGISYRRSR 17
                                                                                      - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_39:*
                                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                             Run on:
```

	Description	684 ta	m	~			limulus	human ad	P11807 human adeno	Q63272 rattus norv	P52333 homo sapien	_	Q9z364 actinomyces		P24156 drosophila		P38703 saccharomyc	P04498 human adeno	Q9y227 homo sapien		-		oryza		P20282 bacillus su		Ŭ	P28667 mus musculu	P36113 saccharomyc	P22966 homo sapien	P22967 mus musculu		53	Q08047 zea mays (m
SUMMARIES	ΩΙ	TAC1_TACGI	TAC1_TACTR	TAC3_TACGI	TAC2_TACTR	PPM1_LIMPO	PPM2_LIMPO	DNB2_ADE40	DNB2_ADE41	JAK3_RAT	JAK3_HUMAN	JAK3_MOUSE	URED_ACTNA	BCA1_RAT	L2CC_DROME	HB22_HUMAN	LAG1_YEAST	DNB2_ADE12	ENP4_HUMAN	FPTA_PSEAE	MX_ANAPL	BGAL_DIACA	RL11_ORYSA	MM07_HUMAN	RS13_BACSU	MRP_HUMAN	MRP_RABIT	MRP_MOUSE	YK27_YEAST	ACET_HUMAN	ACET_MOUSE	YM11_MARPO	ACET_RABIT	GLGB_MAIZE
	DB	-	-	Н	Н	-	-	Н	Н		٦	٦	٦	٦	٦	П	П	٦	Н	7	~	-	7	-	~	-	-		Н	-	-	-	-	-
	Length	17	. 77	17	77	18	18	473	474	1100	1124	1299	271	968	203	261	411	484	616	2	721	731	182	267	120	194	198	199	551	732	732	732	737	799
	' ســــــــــــــــــــــــــــــــــــ		0.	1.7	4.	٥.	.7	0.	•	•	٠		6.	•		8.	٠	1.8	•	٠	•	•	1.2		0.7	•						0.7	0.7	0.7
dР	Query	78	78	74	71	6	63	44	44	4	4	4	4	4	4	41	4	4	7	4	4	4	4	4	4	4	4	4	4	40	4	₹	₹	4
	Score	71	71	89	65	61	28	40	40	40	40	40	39	39	38	38	38	38	38	38	38	38	37.5	•	37	37	37	37	37	37	37	37	37	37
	Result No.	н	7	ю	4	S	9	7	80	σ	10	11	12	. 13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

. 1

	phosura; phosura; seshoe	0; Gaps 0;
ALIGNMENTS	TACGI TACGI STANDARD; PRT; 17 AA. 173.64; 17.80-1991 (Rel. 20, Created) 17.80-1991 (Rel. 20, Last sequence update) 17.80-1991 (Rel. 32, Last annotation update) 17.80-1995 (Rel. 32, Last annotation update) 17.80-1991 (Rel. 32, Last annotation update) 18.80-1991 (Rel. 32, Last annotation update) 18.80-1991 (Rel. 32, Last annotation update) 18.80-1991 (Rel. 30, Last annotation update) 19.80-1991 (Rel. 30, Last annotation upda	c64; ength 17; Indels ostomata;
	111	DISULFID MOD_RES SEQUENCE SEQUENCE SUCAL 13; Atches 13; Atches 13; ATACTR P14213; O1-AN-1991 15-DEC-1998 15-DEC-1998 15-DEC-1998 15-DEC-1998 15-DEC-1998 15-DEC-1998 15-DEC-1998 15-DEC-1998 16-DEC-1998 17-DEC-1998 18-DEC-1998 18-DEC-19
	S S S S S S S S S S S S S S S S S S S	SFFF S C C C C C C C C C C C C C C C C C

Gaps

ö

Indels

4,

Mismatches

ô

Conservative

13;

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                         δ
                                                             Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation—
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93257488; Pubmed-8490053; MEDLINE-932257488; Pubmed-8490053; MEDLINE-932257488; Pubmed-8490053; Masuda M., Matsumoto A., Funakoshi S., Nakashima H., Yamamoto N., Waki M., Matsumoto A., Lancelin J.-M., Kohda D., Tate S., Inagaki F., Fujii N.; Acomparative study of the solution structures of tachyplesin I and a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin II), determined by nuclear magnetic resonance."; Biochim. Biophys. Acta 1163:209-216(1993).
                                                                                                               EQUENCE OF 24-40, AND DISULFIDE BONDS.
MEDLINE-89934158; PubMed-3141410;
Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S., Niwa M., Takao T., Shimonishi Y.;
Niwa M., Takao T., Shimonishi Y.;
Tachiyplesin, a class of antimicrobial peptide from the hemocytes of the horseshoe crab (Tachypleus tridentatus). Isolation and chemical
                                                                                                                                                                                                                                                                                                                 "Antimicrobial peptide, tachyplesin I, isolated from hemocytes of the horseshoe crab (Tachypleus tridentatus). NAR determination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 114:307-316(1993).
-i- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.

CHARACTERIZATION.

Shigenaga T., Takayenoki Y:, Kawasaki S., Seki N., Muta T., Toh Y.,

Ito A., Iwanaga S.;

Ito A., Iwanaga S.;

Separation of large and small granules from horseshoe crab

(Tachypleus tridentatus) hemocytes and characterization of their

components.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
B940CAA4A641335F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibiotic: Anidation; Cleavage on pair of basic residues; Signal. SIGNAL 24 40 TACHYPLESIN I. PROPER 41 77 DISCURID 26 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - I- SUBCELLULAR LOCATION: S-GRANULES.
- I- TISSUE SPECIFICITY: HEMOCYTES.
- I- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
   MEDLINE-91065956; PubMed=2250028; Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                       STRUCTURE BY NMR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; DB 1; Length 77;
No. 1.6e-05;
                                                                                                                                                                                                                              J. Biol. Chem. 263:16709-16713(1988).
                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 265:15365-15367(1990).
                                                                        tridentatus).";
J. Biol. Chem. 265:21350-21354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M57242; AAA63538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 24-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A30068; A30068.
PIR; A38345; A38345
                                                                                                                                                                                                                                                                                                                                                             beta-sheet structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                    structure."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
```

Score '

78.0%; 76.5%;

Query Match Best Local Similarity

```
. SEQUENCE OF 24-40.
MEDLINE-90110066; PubMed-2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                                                                                                                                                         Tachypleus gigas (Southeast Asian horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
                                                                                                                                                                                                                                                                                                                                      Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
"Tachyplesins isolated from hemocytes of Southeast Asian horseshoe crabs (Carcinoscorpius rotundicauda and Tachypleus gigas): identification of a new tachyplesin, tachyplesin III, and a processing intermedate of its precursor.";
J. Blochem. 108:261-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91065956; PubMed-2250028; Shigenaga F., Iwanaga S.; Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and bellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i - SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
E9E08CE9D2923C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 1; I
Pred. No. 1.1e-05;
.; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TACHYPLESIN III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                      17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tridentatus).";
J. Biol. Chem. 265:21350-21354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                MEDLINE=91035357; PubMed=2229025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
12
17
2241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWCFRVCYRGICYRKCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                      24 KWCFRVCYRGICYRRCR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
1 KWSFRVSYRGISYRRSR 17
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Ar
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JX0125; JX0125.
Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6853;
                                                                                                                                                                                                                                                                                NCBI_TaxID=6852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAC2_TACTR
P14214;
                                                                                                                          TAC3_TACGI
P18252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                     SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAC2_TACTR
                                                                                         RESULT 3
```

2

RREAR RAEAR RREAR REAR RREAR R

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90110066; PubMed-2514185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 17
8 13
18 18
18 AA; 2431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.7%;
52.9%;
              67.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RWCFRVCYKGFCYRKCR 18
                                                                                             2 RWCFRVCYRGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRSR 17
              Query Match 67.0
Best Local Similarity 58.8
Matches 10; Conservative
                                                                           1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR, JU0125, JU0125.
Antibiotic; Amidation.
DISULFID 4 17
DISULFID 8 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 9; Conser
                                                                                                                                                                                                                                                              POLYFHEMUSIN II.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNB2_ADE40
P11806;
                                                                                                                                                                                    PPM2_LIMPO
P14216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                     RESULT 6
PPM2_LIMPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNB2_ADE40
                                                                                                        a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.;
"Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity"

J. Blochem. 106:663-668(1989).

-I. FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                                                               GOMPONENTS.";
J. Blochem. 114:307-316(1993).
I- PUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
I- SUBCELLULAR LOCATION: S-GRANULES.
I- TISSUE SPECIFICITY: HEMOCYTES.
I- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0123; J00123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
           "Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and blological activity ".
J. Blochem. 106:663-668(1989).
                                                                                                     MEDLINE-94110249; PubMed-8282718; Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Shigenaga T., Takayenoki Y., Kawasaki S., Iwanaga S.; Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
6EBES7A4A652AEFF CRC64;
                                                                                                                                                                                                                                                                                                                         Antibiotic; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0124; JU0124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 1; Length 77;
Pred. No. 0.00017;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION.
FB3FA109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
POLYPHEMOSIN I.
                                                                                                                                                                                                                                                                                                                                                        TACHYPLESIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-90110066; Pubmed-2514185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 71.4%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KWSFRVSYRGISYRRSR 17
Takao T., Shimonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 AA;
                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPM1_LIMPO P14215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     SIGNAL
PEPTIDE
PROPEP
DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPM1_LIMPO
```

ò

```
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.;

"Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity."

J. Biochem. 106:663-668(1989).

-!- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota: Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sussenbach J.S.;
"The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41.";
adenovirus types 40 and 41.";
virology 163:1.10(1988).
-i. FUNCTION: BINDS COOPERATIVELY SINGLE-STRANDED DNA IN A SEQUENCE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenovirus type 40.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=28284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRAM-POSITIVE BACTERIA.
-!- TISSUE SPECIFICITY: HEMOCYTES.
-!- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                      ;
Score 61; DB 1; Length 10, Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 1; Length 18;
Pred. No. 0.00059;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-88160034; Pubmed-3279700;
Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
AMIDATION.
E402A109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-007-1989 (Rel. 12, Created)
01-007-1989 (Rel. 12, Last sequence update)
01-007-1994 (Rel. 30, Last annotation update)
EARLY E2A DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 AA
                                                                                                                                                                                                                                                                                                                                               18 AA
                                                                                      2; Mismatches
```

```
DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAK3_RAT
Q63272;
                                                                                                                                                                                                                                                                                                                 ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JAK3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
  SET TWANT THE SOURCE COORD TO THE TAKEN THE TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genes encoding the DNA binding protein and the 23K protease of adenovirus types 40 and 41."; Virology 163:1-10(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenovirus type 41.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
INDEPENDENT MANNER. INVOLVED IN DNA-REPLICATION, REGULATION OF MRNA FORMATION, AND HOST-RANGE SPECIFICITY. ZINC IS REQUIRED FOR DNA BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR. ACCUMULATES IN INFECTED CELLS.
                                                                  SUBCELLULAR LOCATION: NUCLEAR, ACCUMULATES IN INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%; Score 40; DB 1; Length 473; 50.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003176; Vir_DNA_binding.
Pfam; PF02236; Vir_DNA_binding; 1.
Early protein; DNA-binding; Zinc-finger; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E., Sussenbach J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
8273635BF6703A24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TAK;
MEDLINE=90272433; PubMed=2349115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88160034; PubMed=3279700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 P
53335 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLY E2A DNA-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                EMBL; M19540; AAA52196.1; -. EMBL; L19443; AAC13969.1; -. PIR; A28645; ERAD40. HSSP; P03265; IADV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-33 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 KWSSRLQYRNVA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KWSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
219
273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein.
MOD_RES 141
ZN_FING 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNB2_ADE41
P11807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luftig R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNB2_ADE41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

q

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS LEET. 342:124-128(1994).

-!- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLEUKIN-2 AND INTERLEUKIN-4 SIGNALING PATHWAY.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- SUBCELLUIAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).

-!- TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING SPLEEN, LUNG, KINDEX AND INTESTINE PROBABLY CONTAINS THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οĮ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Spleen;
MEDLINE=94192816; PubMed=8143863;
Takahashi T., Shirasawa T.;
"Molecular cloning of rat JAK3, a novel member of the JAK family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%; Score 40; DB 1; Length 474; 50.0%; Pred. No. 20;
                                                                                                                                                                                                                                                                                              EMBL; M21163; AAA42463.1; -.
EMBL; X52522; CAA36759.1; -.
PIR; D28645; ERAD4..
PIR; 310206; A10206; A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (PROBABLE).
POTENTIAL.
4350AE593088B19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53658 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein tyrosine kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| |: || ::
450 KWSTRLQYRNVA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBFAMILY
```

S

lymphoid and non-myeloid cells."

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96027605; PubMed-7559633;
Lal K.S., Jin Y., Graham D.K., Witthuhn B.A., Ihle J.N., Liu E.T.;
"A kinase-deficient splice variant of the human JAK3 is expressed in
hematopoletic and epithelial cancer cells.";
J. Biol. Chem. 270:25028-25036(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
W; 1D59CA05F4DD7EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAK3_HUMAN STANDARD; PRT; 1124 AA.
PS2333; Q13260; Q13611;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
20-AGG-2001 (Rel. 40, Last annotation update)
(L-DAR STROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of L-JAK, a Janus family protein-tyrosine kinase expressed in natural killer cells and activated leukocytes."; Proc. Natl. Acad. Sci. U.S.A. 91:6374-6378(1994).
                                                                                                                                                                                                                                      Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kawamura M., McVicar D.W., Johnston J.A., Blake T.B., Chen Y.-Q., Lal B.K., Lloyd A.R., Kelvin D.J., Staples J.E., Ortaldo J.R., O'Shea J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression of Janus kinase 3 in human endothelial and other non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verbsky J.W., Bach E.A., Fang Y.F., Yang L., Randolph D.A., Fields L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                    SH2 (ATYPICAL).
PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                  InterPro; IRR000719; BUK_DKINASE.
InterPro; IRR000719; BUK_DKINASE.
InterPro; IPR001045; Tyr_kin.
Ffam; PF00069; PKINASE. 2.
SMART; SM00295; B41; 1.
SMART; SM00295; B42; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
 send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 36-191 FROM N.A. MEDLINE=962788; Pubmed=866278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94294384; PubMed-8022790;
                                                                                                                                                                                                                                                                                                                                                                          MM.
                                                        InterPro; IPR000299; Band_4.1
                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%;
57.1%;
                            EMBL; D28508; BAA05868.1; -.
                                                                                                                                                                                                                                                                                                                                                                          122560
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | |||:|| |
878 FIVKYRGVSYGPGR 891
                                                                                                                                                                                                                                                                472
777
1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human)
                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                       Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                        Transferase;
                                                                                                                                                                                                                                                      SH2 domain;
                                                                                                                                                                                                                                                                                                                                             ACT_SITE
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                               NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
JAK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALLANTS SCID ARG-151; ILE-722 AND SER-910.

WEDLINE-20435064; PubMed=10982185;
A Schumacher R.F., Mella P., Badolato R., Fiorini M., Savoldi G., Schumacher R.F., Mella P., Badolato R., Fiorini M., Savoldi G., Galiani S., Villa A., Candotti F., Tampalini A., O'Shea J.J.,
Notarangelo L.D.;
Notarangelo L.D.;
Complete genomic organization of the human JAK3 gene and mutation of analysis in severe combined immunodeficiency by single-strand conformation polymorphism.";
Lum. Genet. 106:73-79(2000).

C. I- FINCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLEUKIN-2 AND INTERLEUKIN-2 AND PISK.

C. I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + ROCHENT TYROSINE PROSENTE TO CHECKTON TO CHECKTON TO CHECKTON TO CHECKTON THE CHECKTON TO CHECKTON THE CHECKTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i-SUBGELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).
-i-ALTERNATIVE PRODUCTS: THREE SPLICE VARIANTS WERE ISOLATED FROM DIFFERENT MANA SOURCES: BREAST (JAK3B), SPLEEN (JAK3S; SHOWN HRRE), AND ACTIVATED MONOCYTES (JAK3M), JAK3B MY BE DEFECTIVE AS IT LACK SOME PART OF THE KINASE DOMAIN.
-i-TISSUE SPECIFICITY: IN NK CELLS AND AN NK-LIKE CELL LINE BUT NOT IN RESTING T CELLS OR IN OTHER TISSUES. THE S-FORM IS MORE COMMONIX SEEN IN HEMATOPOLETIC LINES, WHERBAS THE B- AND M-FORMS ARE DETECTED IN CELLS BOTH OF HEMATOPOLETIC AND EPITHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Candotti F., Oakes S.A., Johnston J.A., Gillani S., Schumacher R.F., Mella P., Fiorini M., Ugazio A.G., Badolato R., Notarangelo L.D., Bozzi F., Macchi P., Strina D., Vezzoni P., Blaese R.M., O'Shea J.J.,
                                                                                                                                                  Macchi P., Villa A., Giliani S., Sacco M.G., Frattini A., Porta F., Ugazio A.G., Johnston J.A., Candotti F., O'Shea J.J., Vezzoni P., Notarangelo L.D.; "Mutations of Jak-3 gene in patients with autosomal severe combined immune deficiency (SCID)."; Almune deficiency (SCID).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4. DISEASE. DEFECTS IN JAKA ARE A CAUSE OF RECESSIVE T-CELL. NEGATIVE/B-CELL POSITIVE SEVERE COMBINED IMMUNODEFICIENCY (T-B+SCID), A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Structural and functional basis for JAK3-deficient severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCID), A CONDITION CHARACTERIZED BY THE ABSENCE OF CINCULATING MATURE T-LYMPHOCYTES AND NK CELLS, NORMAL TO ELEVATED NUMBERS CNONFUNCTIONAL B-LYMPHOCYTES, AND MARKED HYPOPLASIA OF LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98423994; PubMed-9753072;
Bozzi F., Lefranc G., Villa A., Badolato R., Schumacher R.F.,
Rhalil G., Loiselet J., Bresciant S., O'Shea J.J., Vezzoni P.,
Notarangelo L.D., Candotti F.;
"Molecular and biochemical characterization of JAK3 deficiency in
patient with severe combined immunodeficiency over 20 years after
bone marrow transplantation: implications for treatment.";
Br. J. Haematol. 102:1363-1366(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                               VARIANTS SCID GLY-481; LEU-586--MET-592 DEL AND ARG-759.
MEDLINE-98022793; Pubmed-9354668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                       Biol. Chem. 271:13976-13980(1996).
                                                                                                                        MEDLINE-95388142; PubMed-7659163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunodeficiency.";
Blood 90:3996-4003(1997).
                                                                                      VARIANT SCID CYS-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCID TRP-582.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFIGINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISSUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Villa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---
```

Gaps

;

Indels

5;

Mismatches

;;

8; Conservative

Matches

882 FIVKYRGVSYGPGR 895

4 FRVSYRGISYRRSR 17

ŏλ qq

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                       MISSING (IN SCID; LACK OF PHOSPHORYLATION IN RESPONSE TO CYTOKINE STIMULATION). /FITIG-VAR_010495.
                                                                                                                                                                                                                                        PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
PROSHHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                      AHPEGKHHSLSFS -> SCYSGWRDDICSMGWWPTVISRWD
LACSPCPRPLTITATTVQLPPTLHATAASVAVPNKTC (IN
                                                                                                                                                                                                                                                                                               AHPEGKHHSLSFS -> SAAGLASVSQSVDWAGVSGKPAGA
                                                                                                                                                                                                                                                                                                       (IN ISOFORM JAK3B).
HELMKLCWAPSPQDRPSFSALGPQLDMLWSGSRGCETHAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_010496.
C -> R (IN SCID; CONSTITUTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1D0FD22068E088E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_010497.

L -> S (IN SCID).

FTIG=VAR_010498.

A -> G (IN REF. 2).

MISSING (IN REF. 3).

T -> A (IN REF. 3).

A -> R (IN REF. 2).

A -> I (IN REF. 2).

M -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                P -> R (IN SCID).
/FTIG=VAR_010492.
E -> G (IN SCID).
/FTIG=VAR_01493.
R -> W (IN SCID).
                                                                                                                                                                                                                                                                                                                                               Y -> C (IN SCID).
/FTId=VAR_006284.
P -> R (IN SCID).
                                                                                                                                                                                                                                                                                                                                                                                                      FTIG=VAR_010494
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORY LATION)
                                                                                                                                                                                                                                                                                                                                        ISOFORM JAK3M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
147
1187
2212
222
610
846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               910
                                                                                                                                                                                                                                                                                                                   1124
                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                               582
                                                                                                                                                                                                                                                                                                                                                                                                               592
                                                                                                                                                                                                                                                                                                                                                                                                                                        722
                                                                                                                                                                                                                                                                                                                                                                                                                                                      759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
147
187
212
222
610
845
896
                                                                                                                                                                                                                                                                                                                                                                                                                                        722
                                                                                                                                                                                                                                                                                                                                                                                                                                                      759
                                                                                                                                                                                                                                                                                                                   1071
                                                                                                                                                                                                                                                                                                                                                                                                582
                                                                                                                                                                                                                                                                                                                                                                                                               586
                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                           NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /ARIANT
                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified an or-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                       -! - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SUBFAMILY
```

1; Length 1124;

DB 48;

Score 40; Pred. No.

44.0%;

Best Local Similarity

Query Match

```
Thie J.N.;

Thie J.N.;

This J.N.;

Throlocoment of the Jak-3 Janus kinase in signalling by interleukins

Throlocoment of the Jak-3 Janus kinase in signalling by interleukins

Throlocoment of the Jak-3 Janus kinase in signalling by interleukins

EL and 4 in lymphoid and myeloid cells.";

Nature 370:153-157(1994).

The Internation: Throsine Kinase of The Non-Receptor Type, involved in Phosphorylates Stat6, IRS1, IRS2 AND P13K.

THE INTERLEUKIN-2 AND INTERLEUKIN-4 SIGNALING PATHWAY.

PROSPINE HOSPHAPE.

TOATALYLY CATILYTY: ATP + A PROTEIN TROSINE = ADP + PROPIENT TROSINE PHOSPHAPE.

TOATALYLY CATILYTY: ATP + A PROTEIN INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BW SIMILARITY).

TROSINE LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE PRODUCED BY ALTERNATIVE SPLICING.

TESTERS SPECIFICITY: HIGHEST LEVELS FOUND IN THE THYMUS MITH SOMEWHAT LOWER LEVELS IN BONE MARROW, SPLEEN, FETAL LIVER AND ADULT CD4-CD8-THYMOCYTES. VERY LOW LEVELS IN ADULT KIDNEY, LUNG, CHESTERS BRAIN AND LIVER.

TESTERS, BRAIN AND LIVER.

TESTERS, BRAIN AND LIVER.

TESTERS, BRAIN AND LIVER.

PROBABLY CONTAINS THE CATALYTIC DOMAINS. THE SECOND ONE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR DAMAINS. THE CATALYTIC DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BALB/C;
MEDLINE-94294024;
Witthuhn B.A., Silvennoinen O., Miura O., Lai K.S., Cwik C., Liu E.T.,
                                                                                                                                                                                                                                                                                                                       "JAKS: a novel JAK kinase associated with terminal differentiation of hematopoietic cells."; oncogene 9:2415-2423(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurniak C.B., Berg L.J.; "Murine JAK3 is preferentially expressed in hematopoietic tissues and "Murine JAK3 is preferentially expressed in hematopoietic tissues and
                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4. SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBL_TaxID=10090;
                                     1299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-BALB/C X 129 F2; TISSUE-Thymus;
MEDLINE-96184772; PubMed=8605329;
                                        PRT;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=9430920; Pubmed=7518579;
Rane S.G., Reddy E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphocyte precursor cells."; 3100d 87:3151-3160(1996).
                                            STANDARD;
                                                             061746;
                                            JAK3_MOUSE S
Q62137; Q61747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
RESULT 11
JAK3_MOUSE
                                                                                                                                                                  JAK3.
```

)

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yazaki Y., Hirai H.;
"A novel signaling molecule, pl30, forms stable complexes in vivo with
v-Crk and v-Src in a tyrosine phosphorylation-dependent manner.";
EMBO J. 13:3748-3756(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                       Morou-Bermudez E., Burne R.A.; "Genetic and physiologic characterization of urease of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98030588; PubMed-9360983; Arachbana K., Urano T., Fujita H., Ohashi Y., Kamiguchi K., Iwata Hirai H., Morimoto C.; "Tyrosine phosphorylation of Crk-associated substrates by focal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     063767; 063766;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CRK-ASSOCIATED SUBSTRATE (P130CAS) (BREAST CANCER ANTI-ESTROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Mano H.,
                                                                                                  Bacteria; Firmlcutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces.NCBI_TaxID=1655;
                                                                                                                                                                                                                                                                                                                                      Infect. Immun. 67:504-512(1999).
-!- FUNCTION: PROBABLY FACILITATES NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE URED FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0042A71CC3F006B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE PHOSPHORYLATION BY FOCAL ADHESION KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%; Score 39; DB 1; 54.5%; Pred. No. 17;
30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) UREASE ACCESSORY PROTEIN URED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    968 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Fibroblast;
MEDLINE-94349922; PubMed-8070403;
                                                                                                                                                                                                                          STRAIN=WVU45;
MEDLINE=99115518; PubMed=9916052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF056321; AAD13736.1; -. EMBL; AF048781; AAD13726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 AA; 29247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002669; UreD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 54...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                         Actinomyces naeslundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01774; UreD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESISTANCE 1 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCAR1 OR CRKAS OR CAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::||| |||::
112 ::AYRGASYRQT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VSYRGISYRRS 16
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                      naes].undii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCA1_RAT
                                                                    URED.
  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM 2 AND ISOFORM 3).
ASASPTEACGSCLQLLEF -> GLSQPHRSLRELLAACWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | STATE OF A CONTROL OF A CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM 2).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
OPTCGSCR -> QAPRVGFAG (IN ISOFORM 2 AND ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-) (BY SIMILARITY) RVWSPARPTATAHGOVY -> LPCGRLPGRPYALMAKYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRDELCVAGAQLYACQDPAIF (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWSPARPTATAHGQVY -> RVVACQADRYI (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1299;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASASPTEACGSCLOLLEF -> GLSQPHR
(IN ISOFORM 2 AND ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTPHLASRVLEMSCAWRPALCLPGPRHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFE2D60B6AF3D10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat, Alternative splicing.
560 688 SH2 (ATYPICAL).
732 992 PROTEIN KINASE 1.
1032 1299 PROTEIN KINASE 2.
1038 1046 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB
Pred. No. 56;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN ISOFORM 3
                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS50001; SH2; FALSE_NEG.
                                                                                    HSSP; P11362; 1FG1.
MGD: MG1: 99928; Jak3.
InterPro: 1PR000039; Band_4.1.
InterPro: 1PR000039; Buk_pkinase.
InterPro: 1PR000039; Buk_pkinase.
InterPro: 1PR000039; But_pkinase.
Pfam; PF00069; pkinase; 3.
SWART; SM00295; But] 1.
SWART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   URED_ACTNA STANDARD; F 092364; 30-MAY-2000 (Rel. 39, Created)
                     L33768; AAA21415.1; -. L40172; AAC42085.1; -. L32955; AAA21565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 57.1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | |||:|| |
1091 FIVKYRGVSYGPGR 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282
490
550
560
607
683
706
734
750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992
1299
1046
1064
1158
1189
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683
706
734
750
750
931
1299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491
                                                                                                                                                                                                                                                                                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
```

DOMAIN DOMAIN

ö

Gaps

ö

Length 271; 1; Indels s:

RESULT 12 URED_ACTNA

q

õ

```
HB22_HUMAN
               RESULT 14
L2CC_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                RESULT
                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     1 TISSUE SPECIFICATION TESTINE CONTAINING
INTESTINE AND TESTINE
1 DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING
MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN
CONTAINING A DIVERGENT HELLX-LOOP-HELIX (HLH) MOTIF. THE SH2-
CONTAINING SITES PUTATIVELY BIND CRX, NCK AND ABL SH2 DOMAINS. THE
BINDING SITES PUTATIVELY BIND CRX, NCK AND ABL SH2 DOMAINS. THE
HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL
GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.
1- DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM
RESPONSE BLEMENT (SRE).
1- PTH: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE
YDYNHL MOTIF. THE SRC FAMILY KINASES ARE RECRITED TO THE
PHOSPHORYLATED SITES AND CAN PHOSPHORYLATE OTHER TYROSINE
RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN
MEDIATED ADHESION OF CELLS TO THE EXTRACELLURAR MATRIX.
1- DISEASE: APPEARS TO HAVE A CENTRAL FUNCTION IN TRANSFORMATION OF
SOME CELL TYPES.
1- SIMILARITY: CONTAINS 1 SH3 DOMAIN. NECESSARY FOR THE LOCALISATION
OF THE PROTEIN TO FOCAL ADHESION SAND INTERACTS WITH ONE PROLINE-
RICH REGION OF FOCAL ADHESION KINASE 1.
2 IMPLARITY: CONTAINS 1 SH3-BINDING DOMAIN. THE SH3 BINDING DOMAIN
Gaps
                                                                                                                                              ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG ISOFORM (SHOWN HERE) AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVERGENT HELIX-LOOP-HELIX MOTIF. MISSING (IN SHORT ISOFORM); E861641BFD68D377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3-binding; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-RICH.
SUBSTRATE FOR KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 61;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDS TO THE SRC SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50002; SH3; 1.
Phosphorylation; SH3 domain;
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D29766; BAA06169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D29766; BAA06170.1; -
HSSP; P29354; 1GRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer, Frontier, Program, Promise, Promise, Promoto, Smarr, Smarr, Smod326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIWWOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              <u>-</u>
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muşcomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: REQUIRED FOR LARVAL METABOLISM OR FOR THE PROGRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                         MEDLINE-86312887; PubMed=3092183;
Eveleth D.D. Jr., Marsh J.L.;
"Sequence and expression of the Cc gene, a member of the dopa
decarboxylase gene cluster of Drosophila: possible translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 1; Length 203;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22817 MW; B15D085CC0862A11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF THE LARVA INTO A PUPA. SIMILARITY: BELONGS TO THE PROHIBITIN FAMILY.
                                          21, Created)
21, Last sequence update)
34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AA.
203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 14:6169-6183(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=86055719; PubMed=2998758; Tonnelle C., Demars R., Long E.O.;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flybase; FBgn0002031; 1(2)37Cc.
InterPro; IPR001107; Band_7.
Pfam; PF01145; Band_7; 1.
SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 WSLRLIDRPRYRLTSYPRSR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 WSFRV----SYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X04228; CAA27810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; X04227; CAA27807.1; -. C25511; C25511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 50.0 nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRECURSOR (DQB1*0501).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al protein
203 AA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                          (Rel.
(Rel.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                              L(2)37CC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Developmental
                                                                                                                                                                                                                                                                                                                                                                                          regulation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HB22_HUMAN
P01919;
                                               01-MAR-1992
                                                                 01-MAR-1992
01-OCT-1996
    L2CC_DROME
P24156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-DQB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

ij

;:

á qq

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 33-261 FROM N.A.
MEDLINE-97083137; PubMed-8929711;
Yasunaga S., Kimura A., Hamaguchi K., Ronningen K.S., Sasazuki T.;
Tipliferent contribution of HLA-DR and -DQ genes in susceptibility and Teststance to insulin-dependent diabetes mellitus (IDDM).";
Tissue Antigens 47:37-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, OO (M1.1) BETA CHAIN. EXTRACELLULAR BETA-1. EXTRACELLULAR BETA-2.
                                                                                                                                                                                  MEDLINE-84031733; PubMed-6415003;
Larhammar D., Andersson G., Andersson M., Bill P., Boehme J.,
Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U.,
Widmark E., Hyldig-Ylelsen J.J., Lind P., Schenning L., Servenius B.,
Widmark E., Rask L., Peterson P.A.,
 'DO beta: a new beta chain gene in HLA-D with a distinct regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

2F5DBFDC41301BA5 CRC64;
                                                        SEQUENCE FROM N.A.
MEDLINE-88006310; Pubmed-2888727;
Turco E., Care A., Compagnone-Post P., Robinson C., Cascino I.,
                                                                                                                        "Allelic forms of the alpha- and beta-chain genes encoding DQw1-positive heterodimers.";
Immunogenetics 26:282-290(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probon, ...
SMART; SM00407; IGcl; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC II; Transmembrane; Glycoprotein; Signal.

1 32 HrA CLASS II HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interry.
Pfam: PF00047; 1g; 1.
Pfam: PF00969; MHC_II_beta; 1.
Probom: PD000328; MHC_II_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003597; Ig_c1.
InterPro; IPR000353; MHC_II_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X03068; CAA26872.1; -.
EMBL; M17564; AAA59765.1; -.
EMBL; L34101, AC41969.1; -.
PIR; A02232; HLHU2C.
PIR; C24669; C24669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 N
29748 MW;
                                                                                                                                                                                                                                                                                               their genes.";
Hum. Immunol. 8:95-103(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 604305; -.
InterPro; IPR003006; Ig_MHC.
                of expression.";
EMBO J. 4:2839-2847(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                           Prucco M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

```
Db 114 NYEVAYRGILORR 126
```

Search completed: February 12, 2002, 12:39:53 Job time: 306 sec

3 SFRVSYRGISYRR 15 :: |:|||| ||

ö

Gaps

ö

Indels

3;

41.8%; Score 38; DB 53.8%; Pred. No. 24; tive 3; Mismatches

Best Local Similarity 53.8 Matches 7; Conservative

Query Match

DB 1; Length 261;

Qy 3

```
09x5q7 streptomyce
09ybp0 aeropyrum p
085368 enterococu
043916 homo sapien
09eqc0 mus musculu
                                                                                                                                                                                  Q91nj6 arabidopsis
Q17897 caenorhabdi
Q978w0 aeropyrum p
Q96ma0 arabidopsis
Q58537 pyrococcus
Q94qe8 arabidopsis
Q92pf8 arabidopsis
Q92pf8 arabidopsis
                                                                                               O9c2kO neurospora
O9fc87 streptomyce
O9ph65 xylella fas
P97423 mus musculu
                                                                                                                                                                                                                                                                                      09c6n3 arabidopsis
005770 mycobacteri
098uh9 oryzias lat
             Q9d0k5 mus musculu
                                                                                                                                              Q9y6s2 homo sapien
Q9n4c2 caenorhabd1
Q9ad90 streptomyce
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan C., Altafi H., Bel B., Chla C., Chlou J., Chol E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lem B., Lenz C., Li J., Liu A., Huu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Troitumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC007887, AR79360.1; -.

InterPro; IPR003340; B3.

SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabicopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicaceae; Arabidopsis.
020908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                       Q9D0K5
Q9X5Q7
                                               09YBP0
085368
043316
09E0C0
09FC2K0
09PC3K0
09PK62
09PK62
09PK62
09NKC2
                                                                                                                                                                                                                                                 09L0E8
09ZPF8
099699
09C6N3
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                          3997
4111
4111
5833
7583
1081
1124
1124
767
767
767
767
11124
11148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
88.89
                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LQE3;
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                     Q9LQE3
                                                                                                                                                                                                                                                                                                                                                                                                                               Q91qe3 arabidopsis
Q967i9 arabidopsis
Q9kmK7 vibrio chol
Q9hsy4 halobacteri
Q9hsz6 halobacteri
Q9hk2 arabidopsis
Q17248 boophilus m
Q9ff24 caenorhabdi
Q47291 gallus gall
Q9rb19 burkholderi
Q53813 shigella bo
Q9rs96 deinococcus
Q9se6 deinococcus
Q9yag8 drosophila
Q9wag8 drosophila
Q9wuy9 rattus norv
Q9wag8 drosophila
Q9wuy9 rattus norv
Q9wag8 drosophila
Q9wuy9 rattus norv
Q9wag8 drosophila
                                                                                                 (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                   February 12, 2002, 12:38:40 ; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                          473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                               Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein – protein search, using sw model
                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LQE3
Q9C719
Q9KMK7
                                                                                                                                                            1 KWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                   sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
                                                                                                                              US-09-485-571-26
91
                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_mhc: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                                                                                Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                     Scoring table:
                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                           Searched:
                                                                                                                                                               Sequence:
                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
```

Gaps

ö

Score 48; DB 10; Length 570; Pred. No. 7.6; 1; Mismatches 4; Indels

52.7%; 64.3%;

Query Match Best Local Similarity 64.3°

1 KWSFRVSYRGISYR 14

ò

Q9JJU7 Q9VAQ8 Q9WUX9 P79587 Q9AJU2

042291 09RBT9 053813 09RSL6 080901

781 1106 182 318

5 6 7 8 8 110 111 113 114 116 116 116 117

Q9HSY4 Q9HSZ6 Q9LNK2 Q9C8N9 Q17248

g

```
MEDLINE-ZO406833; PubMed=10952301;
MEDLINE-ZO406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                10092 MW; B173D34A34B6A870 CRC64;
                                                                                                                                                                                                                    Mature 406:477-483(2000):
EMBL; AE004371; AAF96240.1; -.
TIGR; VCA0332; -.
                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 52.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KWAFRTLYEQVAYK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWSFRVSYRGISYR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 307 AA;
                                                                                                                                                                                                                                                                                                    88 AA;
                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9HSZ6;
Q9HSZ6;
01-MAR-2001 (
01-MAR-2001 (
                                                                                                                                                                                                        cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNG0026C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HSY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HSY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9HSZ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9HSY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DA FE
                                                                                                                                                                                                                                                                                                                                                                                                                                     ÓΫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                 RKX
RRA
RRA
RRA
RRI
RRI
RRI
DR
KW
KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

A MIDLINE-21016719; PubMed-11130712;

A Theologis A. Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

A Theologis A., Chan D., Conway A.B., Coheuk R.F., Chin C.W.,

A Chung M.K., Conway A.B., Conway A.B., Chaesy T.H., Dewar K.,

A Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Creasy T.H.,

A Chung M.K., Coldsmith A.D., Haas B., Hansen N.F., Haghes B., Huizar L.,

A Hunter J.L., Jenkins J., Johnson-Hopson C., Khay K., Lam B.,

A Hunter J.L., Mremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Hunter J.L., Miranda M., Nayyen M., Nierman W.C., Osborne B.I.,

A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Militscher J., Miranda M., Nayyen M., Nierman W.C., Osborne B.I.,

A Sakano H., Zalzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

A Sakano H., Zalzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

A Sun H., Tallon L.J., Tambunga G., Toriuni M.J., Town C.D.,

W W C., Wa G., Frasser C.M., Venter J.C., Davis R.W.;

R "Sequence and analysis of chromosome I of the plant Arabidopsis

The palaina.
                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 10; Length 615;
Pred. No. 12;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69755 MW; 817E7D03190622F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0332.
                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                     615 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
EMBL, AC069160, AAG51458.1; -
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; B3.
                                                                                                                                                                                                                            HYPOTHETICAL 69.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.6%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02309; AUX_IAA; 1.
Pfam; PF02362; B3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.6
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                     PRELIMINARY;
                     175 QWSFRHSYRGTPQR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
615 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09KMK7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCA0332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KMK7
                                                                                                                                     Q9C719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                 RESULT
Q9C7 I9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID DT DT CO OC OC OC OC OC OC
```

HID DE THE SECOND OF THE SECON

```
RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA MEDLINE-20504483; PubMed=11016950;

RA MEDLINE-20504483; PubMed=11016950;

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorson V., Sbrogna J.,

RA Swartzell S., Weil-D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.D., Omer A.D.,

RA Alam M., Lowe T.M., Liang P., Rilley M., Hood L., DasSarma S.;

RT Genome sequence of Halobacterium species NRC-1.";

RT "Genome Sequence of Sci.U.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                        ŝ
48.9%; Score 44.5; DB 2; Length 88; 52.4%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.4%; Score 44; DB 1; Length 307;
42.9%; Pred. No. 18;
tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AA; 34492 MW; AB92A26FFF80AF39 CRC64;
                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                         307 AA
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last seq)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                           PRT;
                                                        3
                                                                                                                                         || ::||| || |||| 58 WSGVITYRGTNIRIISVRRSR 78
                                                                                                            2 WSFRVSYRG----ISYRRSR 17
                                52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                           PRELIMINARY;
```

q

Qγ

DE GR DE GR

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_"TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                            Q9C8N9;
                                                                                                                                                                                                                                                                                                                                                                                                        Q9C8N9
                                                                                                                                                                                                                                                                                                                                                                    RESULT
Q9C8N9
       RA
RA
RL
DR
DR
SQ
SQ
                                                                                                                                                                                                                                                                                                        рp
                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                               MEDLINE-20504483; PubMed-11016950;
MEDLINE-20504483; PubMed-11016950;
MG W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids_II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                       Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.4%; Score 44; DB 1; Length 378; 42.9%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                        378 AA; 41710 MW; 9D3334B29435FD33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LNK2;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUS-2001 (TrEMBLrel. 17,
F12K21.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.4
Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:|| | ::|:
252 KWAFRTLYEQVAYK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWSFRVSYRGISYR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-3702;
                                                                                                 Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LNK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9LNK2
```

HID DATA BEIND BEI

ò q

```
REALINE-21016719; PubMed-11130712;

REALINE-21016719; PubMed-11130712;

REDLINE-21016719; PubMed-11130712;

RA Theologia A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Ching M.K., Conn L., Conway A.B., Hansen N.F., Hughes B., Huizar L.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Langir. Hooper S., Lee A., Lee J.M., Leaz C.A., Li J.H., Li Y.-P.,

RA Langir. Hooper S., Lu Z.A., Luros J.S., Malti R., Marziali A.,

RA Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley T., Town C.D.,

RA Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M.,

R. Tsequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N. Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL. AC023279; AAF79263.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 10; Length 620;
Pred. No. 39;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                 Score 44; DB 10; Length 620;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02309; AUX_IAA; 1.
Pfam; PF02362; B3; 1.
SEQUENCE 620 AA; 70555 MW; 88484FF185EBED3F CRC64;
                                                                                                                                                                                                 Pfam; PF02362; B3; 1.
SEQUENCE 620 AA; 70895 MW; C2FE2FAFDEC006DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUXIN RESPONSE FACTOR, PUTATIVE. F7P12.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:816-820(2000).
EMBL; ACO23913; AAG51897.1; -
InterPro; IPR003311; AUX_IAA.
InterPro; IPR003340; B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                 48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| || :||| | |
150 QWRFRHNYRGTPQRHS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KWSFRVSYRGISYRRS 16
```

Gaps

; 0

Indels

.,

41.28;

017248;

017248

RESULT Q17248

```
[1]
SEQUENCE FROM N.A.
STRAIN=YH105;
Yabannavar A., Zylstra G.J.;
Yabannavar A., Zylstra G.J.;
"Analysis of the genes for p-nitrobenzoate degradation from Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burkholderia pickettii (Pseudomonas pickettii).
Bacteria; proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | HSSF; F12931; 1FMA. |
| R INCEPTO: IPR000299; Band_4.1. |
| R INCEPTO: IPR000299; Buk_Pkinase. |
| R INCEPTO: IPR000199: SH2. |
| R INCEPTO: IPR0001245; TYL_kin. |
| R INCEPTO: IPR0001245; TYL_kin. |
| R Pfam; PF00069; Pkinase; 2. |
| R SMART; SM00295; B41; 1. |
| R SMART; SM00219; F121. |
| R SMART; SM00219; TYRK: 1. |
| R PROSITE; PS00107; PROTEIN KINASE_ATP; 1. |
| R PROSITE; PS00107; PROTEIN_KINASE_DOM; 2. |
| R PROSITE; PS00109; PROTEIN_KINASE_TYR: 1. |
| R PROSITE; PS100109; PROTEIN_KINASE_TYR: 1. |
| R PROSITE; PS10010; SH2: 1. |
| R PROSITE; PS10010; SH2: 1. |
| R PROSITE; PS10010; SH2: 1. |
| R PROSITE; PS10010; PROTEIN_KINASE_TYR: 1. |
| R PROSITE; PS10010; PROTEIN_KINASE_TYR: 1. |
| R PROSITE; PS10010; PROTEIN_KINASE_TYR: 1. |
| R PROSITE; PS10011; SH2: 1. |
| R PROSITE; PS10011; PROSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 13; Length Lippred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sofer L., Kampa D., Burnside J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034576; AAC34195.1; -.
HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
P-HYDROXYLAMINOBENZOATE LYASE.
                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AA.
                                                                                                                                                                                                                                         PRT; 1106 AA
  Pred. No. 74;
                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.38;
57.18;
                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, JANUS TYROSINE KINASE.
                                                                                                        388 KWPIPISYRDSEHRRKK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.3
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                       1 KWSFRVSYRGISYRRSR 17
Best Local Similarity 41.5
Matches 7; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | |||: | | | |
881 FIVKYRGVCYSRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09RBT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9RBT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                              042291
                                                                                                                                                                                                RESULT 10
042291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9RBT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                 δλ
                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                          Whitfeld P.L., Johnson M.C., Smith D.R.J., Snelson V.J., Clifton G.F., Brown G.S., Cairns D., Foy A.B., Irving D.O.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, U62809; AAB04998.1; -

Interpro; IPR001548; Peptidase_M2.

Pfam: PF01401; Peptidase_M2.

PROMO791; PEPDIPTASEA.

Prodom; PD004184; Peptidase_M2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                               Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sulston J.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Investigating biology...; | Science 282:2012-2018(1998). |
| EMBL; AL123876; CAB60841.1.; |
| InterPro; IPR001930; Aladiptase. |
| InterPro; IPR00130; Zn_MTpeptdse. |
| Pfam; PF01433; Peptidase_M1; 1. |
| PRINTS; PR00756; ALADIPTASE, |
| PROSTIES; PS00142; ZINC_PROTEASE; UNKNOWN_1. |
| SEQUENCE 781 AA; 91124 MW; 1E3FC20D8E071022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
6F164CF70C938E63 CRC64;
                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANGIOTENSIN-CONVERTING ENZYME-LIKE PROFEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.3%; Score 43; DB 5;
45.5%; Pred. No. 61;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         781 AA.
                                                                       660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.3%; Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 PC
660 PC
75257 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y105E8A.A.
Caenorhabditis elegans.
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|: |:|: | 488 WEYRIKYQGVS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 WSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
660 AA;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=WHOLE TICKS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y105E8A.A PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9NF24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NF24
```

6

RESULT

g ò

09NF24

ö

Gaps

ö

Length 1106;

us-09-485-571-26.rspt

ö

```
:||||| |||
99 AFRVSYHGIS 108
                                                                                                          Complete proteome. SEQUENCE 480 AA:
                                                                                                                                    480 AA;
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McLaren F.H.;
                                                                                          TIGR: DR2108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Mat.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                         080901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2933U7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0933U7
                                                                                                                                                                                                                                                                                                                                                                                                                                   080901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q9JJU7
                                                                                                                                                                                                                                                                                                                                                                                                               080901
      RT RT DR DR DR KW
                                                                                                                                                                                                                                                                                                                         ga
                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                  ö
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91286192; PubMed-2061288;
Tominaga A., Ikemizu S., Enomoto M.;
"Site-specific recombinase genes in three Shigella subgroups and nucleotide sequences of a pinB gene and an invertible B segment from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=R1;
MEDLINE-20036896; PubMed=10567266;
MEDLINE-20036896; PubMed=10567266;
Mohite O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
01-JAN-1999 (TREMBLRel. 09, Last annotation update)
BV GENE PRODUCT (FRAGMENT).
Shigella boydil.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                      2; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 318
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
picketti1 YH105.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187879; AAF0144.1; -.
                                                                                      182 AA; 20053 MW; 45FA1636CAC43E06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA; 34335 MW; 93CC950314D4E275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MOLYBDATE METABOLISM REGULATOR-RELATED PROTEIN.
                                                                                                                                                                                                  .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2
Pred. No. 41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 AA.
                                                                                                                                                 46.2%; Score 42; DB
43.8%; Pred. No. 22;
Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 173;4079-4087(1991).
EMBL; D00660; BAA00555.1; -.
NON_TER 318 318
SEQUENCE 318 AA; 34335 MW: 93C0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 FRVNYRNGGIFYRSAR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.2
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                              |: : | :|||||
63 WAANIDIEGPNYRRSR 78
                                                                                                                                                                                                                                       2 WSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus radiodurans
                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigella boydii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shigella.
NCBI_TaxID=621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Q53813
Q53813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9RSL6:
                                                                                                                                                                                                                                                                                                                                         RESULT 12
(053813
AC 053813
AC 0538133
AC 0538133
DT 01-NOV.
DT 01-JANV.
DT 01-JANV.
DY 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RSL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
Q9RSL6
      SW KE
                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Tea. 33.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Perosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thesis (2000), Laboratory of Functinnal Immunogenetics,
The Babraham Institute, Cambridge, U.K.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
IMMUNE SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. COLUMBIA;

Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,

Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC005499; AAC67368.1;

SEQUENCE 279 AA; 31775 MW; 393AAE4AE046BBB2 CRC64;
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
"Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1."; Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%; Score 41; DB 10; Length 279; 80.0%; Pred. No. 52;
                                                                                                                                                                                                                                                        Length 480;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                      52430 MW; B67C9175AAC14281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 15, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                           ;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AA
                                                                                                                                                                                                                                                           Score 42; DB
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL 31.8 KDA PROTEIN T6A23.30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN LEWIS; TISSUE-BRAIN STRIATUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                        46.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                 EMBL: AE002046; AAF11657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RT1-EL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                       234 WMVRVDARGVYYGHSR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    2 WSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norveqicus (Rat).
```

```
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN) (BY SIMILARITY).

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.

EMBL; AJ276126; CAB86228.2; -1

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR001039; MHC_1:

DR Pfam; PF00047; ig; 1.

DR Pfam; PF00047; ig; 1.

DR PROSITE; PS00290; IG_MHC_1: 1.

DR SMARY: SM00407; IGC.1: 1.
```

; 0

0; Gaps

Query Match
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 2; Indels

1 KWSFRVSYRGI 11 :||||| | : 71 EWSFRVSLRNL 81

Qy Db Search completed: February 12, 2002, 12:38:41 Job time: 754 sec

us-09-485-571-27.rag

```
February 12, 2002, 12:30:33 ; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **Singaly deneseq for feed and the feed and the feed and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522463
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                       US-09-485-571-27
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115...
116...
118...
120...
120...
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB :
Maximum DB :
                                                                                                                                                                  OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

. Description	Tachvolesin deriva	Tachyplesin deriva	Peptide which may	Antimicrobial tach	Tachyplesin analog	Antimicrobial tach	Generic tachyplesi	Tachyplesin analog	Antimicrobial tach	Antimicrobial tach	Antimicrobial tach
SUMMARIES	AAW99414	AAW99413	AAY93617	AAR75806	AAY69610	AAR75819	AAY69609	AAY69617	AAR75807	AAR75808	AAR75816
DB	20	20	21	16	21	16	21	21	16	16	16
% Query Match Length DB	17	17	17	17	17	17	17	17	17	17	21
% Query Match	100.0	7.96	96.7	83.5	83.5	79.1	79.1	79.1	78.0	78.0	78.0
Score	91	88	88	97	97	72	72	72	71	71	71
Result No.	-	7	Ю	4	S	9	7	œ	6	10	11

Antimicrobial tach New lipopolysaccha Antiviral peptide. Tachyplesin II. Li Bacterial shock tr Bacterial shock tr Tacyplesin II. Ta Tachyplesin analog Tachyplesin analog Tachyplesin analog Tachyplesin analog Tachykinins peptide t Cationic peptide t Cationic peptide t Cationic peptide T Tachyplesin analog Tachykinins peptid Antimicrobial tach Antimicrobial analog Tachyplesin analog	ALIGNMENTS 7 AA. le SM2307. antibiotic; beta-sheet; secondary structure; ribozyme; antitumour agent; antivital; sll membrane; passive transport; cytoplasm; y G, Kaczorek M; y G, Kaczorek M;
AAR75810 AAR75822 AAP91671 AAR06861 AAR06862 AAR06862 AAR38489 AAR75811 AAR75811 AAR75811 AAR75811 AAR75811 AAR75811 AAR76811 AAR768611 AAR768611 AAR768611 AAR768611 AAR768611 AAR768611 AAR768611	ALIGNMENTS AA. SM2307. Ibozyme; an l membrane; G, Kaczor G, Kaczor
AAR7 AAR7 AAR8 AAR8 AAR8 AAR8 AAR9 AAR7 AAR7 AAR7 AAR7 AAR7 AAR7 AAR7	ALI AA. tide SM2 de antib y, riboz cell me er. 7. 7. 7. 7.
01111111111111111111111111111111111111	ry) pptide a pptide a body; r rier. 1757. Grassy Grassy active
	rd; peptide; lrst entry) lvative peptidesin; peptidesin; peptidesin; peptidesin; peptidesin; peptidesin; peptidesin; periperipesin; periperipesin; peripesin; peripes
80444444444444444444444444444444444444	standard; p 99 (first in derivati achyplesin; achyplesit; achyple
	14 stan 14; -1999 teshin d teshin tachy tachy
L L D D D D D D D D D D D D D D D D D D	1 99414 99414 99414 JUN-1 JUPH JUPH JUPH JUPH JUPH JUPH JUPH JUPH
11111111111111111111111111111111111111	30D
	X P P X X P X Y P X Y P X X P X X P X Y Y X P X Y Y X P X P X P

17 AA;

```
Best Local Similarity
           Sequence
                                                   Query Match
                                                                               Matches
                                                                                                                                                                                         AAY93617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
XX
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adualphide bridge. The novel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                               ô
                      This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, fragments) and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Derivatives of antibiotic peptides lacking disulfide bridges – used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                     100.0%; Score 91; DB 20;
100.0%; Pred. No. 1.9e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tachyplesin derivative peptide SM1726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                              AAW99413 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 28; 37pp; French.
     Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                1 rwsfrvsyrgisyrrsr 17
                                                                                                                                                                                                                                                                                              1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                   17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99413;
```

g à

```
ö
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                            Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 17;
6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
DB 20; Length 17; 6e-08;
                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                   Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.7%; Score 88; DB 94.1%; Pred. No. 6e-0
                                               1; Mismatches
    Score 88;
Pred. No.
                                                                                                                                                                                                                                                  AAY93617 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-FR02939.
         96.78;
94.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                         1 RWSFRVSYRGISYRRSR 17
                                                      16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                               25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                       AAY93617;
```

AAR75806

```
Sequences AAV69610-Y69611 and AAV69617 represent tachyplesin analogues
used in an exemplification of the present invention, in which the
constine tachyplesin cysteine residues are replaced with Ala, Leu and
control tachyplesin cysteine residues are replaced with Ala, Leu and
control analogues of tachyplesin (AAV69608) is a naturally occurring
antimicrobial peptide which contains two disulphide bonds which help
control maintain its tertiary structure. The invention relates to novel
comparide analogues of tachyplesin (Y696912-AAV69614, AAV69616) in which
control methonine, phenylalanine or tyrosine, the same amino acid being
controlling fungal and viral acidyplesin analogues are functional as
intramolecular disulphide bonds, the analogues are functional as
controlling sand for controlling plant viruses. They can also be
controlling sand for controlling plant viruses. They can also be
controlling maize plants, preferably wheat, sorghum, sunflower,
controlling maize plants, preferably wheat, sorghum, sunflower,
coya or especially maize plants to provide resistance to pathogenic fungil
controlling the present sequence is not shown in the
controlling and viral activity in assistance to pathogenic fungil
controlling the present sequence is not shown in the
controlling the present sequence is not shown in the
controlling the present sequence is not shown in the
                                                                                                                                                                                                                                                                                                      New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungl; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 76; DB 21; Length 11.
Pred. No. 5.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75819 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page -; 17pp; English.
                                                                                                                                                                                  (PION-) PIONEER HI-BRED INT INC.
                                                                                                  97US-0962034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.5%;
                                                                                                                                        97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence given in column 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|:|||:|||:||
| kwafrvayrgiayrrar 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                               WPI; 2000-126327/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥,
                                                                                               31-OCT-1997;
                                                                                                                                          31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09516776-A1
                   US601.5941-A.
                                                           18-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75819;
                                                                                                                                                                                                                         Rao AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAR75819
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium praninearum, Fusarium moniforme, Sclerothina sclerotiorum, Sclerothina trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76; DB 16; Length 17
Pred. No. 5.4e-06;
5; Mismatches 0; Indels
                                                                                                                                      Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY69610 standard; peptide; 17 AA.
              AAR75806 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.5%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                   94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                          93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rachyplesin analogue, TPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|:|||:|||:|||:|
1 kwafrvayrgiayrrar 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                               19-DEC-1994;
                                                                                                                                                                                                                                                                                W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1993;
                                                                                               07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2000
                                                                                                                                                                                                                                                                                                                           22-JUN-1995
                                                                                                                                                                                                      infection.
                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY69610;
                                                       AAR75806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
```

ö

Gaps

ö

AAY69610

RESULT

ò g

Length 17;

```
WPI; 2000-126327/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6015941-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY69617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rao AG;
                                                          Rao AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY69617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC

NO SE

NO SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΩD
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---/label= Ile, Val, Met, Phe, Tyr
/note= "The molecule has the same amino acid at all four
of the above positions"
                                                                                                                                                                                                                                                                                                                   AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshee crab heamocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                             New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.1%; Score 72; DB 16; Length 17; 70.6%; Pred. No. 2.4e-05; Live 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generic tachyplesin (TP) analogue antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä.
                                                                                                                                                                                                                                                                                    Claim 1; Page 35; 45pp; English.
                                                                                        (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY69609 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0962034
                                               93US-0168809
      94WO-US14619
                                                                                                                                   Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| ||| |||| ||| ||| |
1 kwkfrvkyrgikyrrkr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                   Rao AG,
                                                                                                                                                                         WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6015941-A
                                               17-DEC-1993;
      19-DEC-1994;
                                                                                                                                     Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY69609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

ò

```
This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain list tertiary structure. The invention relates to novel to maintain list tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY69614, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the mattive the cysteine replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form antimicrobial agents. The tachyplesin analogues are functional as intramalecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medalcal applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, sorgenic fungi
                                                                                                                                                                                                   New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB 21; Length 17 pred. No. 2.4e-05; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY69617 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 23; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
(PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.1%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tachyplesin analogue, TPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
```

ö

: ;

S

ö

Gaps

ö

Length 17; 3; Indels

```
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75605) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium monificame, Sclerctinia sclerotiorum, Sclerctinia trifolorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                     AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerottinia sclerotionum, Sclerottinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide derivs. of tachyplesin – having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 16;
Pred. No. 3.5e-05;
                                                                                                                                                                                                                                                                                                                         Score 71; DB 16;
Pred. No. 3.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
    Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75808 standard; peptide; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                      78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0168809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao AG, Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AA;
                                                                                                                                                                                                                                                        17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1993;
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75808;
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animals.
                                                                                                                                                                                                                  animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR75808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                           sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala, Leu and Asp, respectively. Tachyplesin (AAY69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its teritary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAY66914, AAY69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isoleucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as intramolecular disulphide bonds, the malogues are useful for antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be corressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic funging and viruses. Note: The present sequence is not shown in the sequence given in column 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungi
                                                                                                                                                                                                                                                                                                                                                                     being
                                       New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 21;
Pred. No. 2.4e-05;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR75807 standard; peptide; 17 AA.
                                                                                                                              Example 1; Page -; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.1%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.6'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||| |||| ||| |
1 kwdfrvdyrgidyrrdr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-231570/30.
WPI; 2000-126327/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75807;
```

σ

g

ç

AAR75807 RESULT

Length 17;

Matches

11

RESULT

qq ò

AAR75816

```
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR7805) a small peptide isolated from japanese horseshoe crab haemcoytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia sclerotiorum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                                        New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71; DB 16; Length 35; Pred. No. 7.4e-05; Aismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75822 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 31; 45pp; English.
                                                                                                                                                                                                                PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%;
                                                                                                                                                       94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.68;
                                                                                                                                                                                    93US-0168809.
                                                                                                                                                                                                                                                 Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| |||:|||| ||| |
1 kwlfrvnyrgikyrrgr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rao AG,
                                                                                                                                                                                                                                                   Rao AG,
                                                                                                                                                                                                                                                                            WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1993;
                                                                                        W09516776-A1.
                                                                                                                                                      19-DEC-1994;
                                                                                                                                                                                     17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putman RJ,
                                                                                                                        22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                 Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection
                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                ö
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monificame, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                ;
0
                                                                                                                                                                                                                                                                              Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 16; Length 21;
Pred. No. 4.3e-05;
2; Mismatches 3; Indels
                Indels
                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                      Antimicrobial tachyplesin peptide derivative.
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75810 standard; peptide; 35 AA
                                                                                                                                                            AAR75816 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 34; 45pp; English.
                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| |||:|||| ||| |
1 kwlfrvnyrgikyrrgr 17
                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RWSFRVSYRGISYRRSR 17
                                                1 RWSFRVSYRGISYRRSR 17
:| |||:|||| ||| ||
1 kwlfrvtyrgikyrrgr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AA;
                                                                                                                                                                                                                                                                                                                                                                   WO9516776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1996
                                                                                                                                                                                                                          07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putman RJ,
                    12;
                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
                                                                                                                                                                                            AAR75816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              animals
```

Matches

δλ q AAR75810

XX DY XX

RESULT

ö

Gaps

ö

- .:

8 8

```
The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemocytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LBS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for tracheborachial infections, urinary tract infections, bedsores, collisis, cirrhosis, hepatic insufficiency and post-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antivirus agents of polypeptide - useful as antivirus agents for vesicular stomatitis virus or human immuno-deficiency virus
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                     Score 68; DB 10;
Pred. No. 0.00011;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 11;
Pred. No. 0.00011;
; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vesicular stomatitis virus; HIV; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 3..16 7..12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR06266 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 309; 12pp; Japanese.
                   Claim 2; Page 27; 39pp; English.
                                                                                                                                                                                                                                                                                                     74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89JP-0166811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88JP-0239051.
89JP-0166811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                            1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                     Query Match 74.7
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pachypeus tridentatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-241996/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiviral peptide.
                                                                                                                                                                                                                                                       17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP0216'230-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1988;
30-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi.
Matches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06266;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR06266
     × 0 × 0 0 0 0 0 0 0 0 0 0 0 0 × 0
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                          AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                               New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                                                                                                                                                    Score 70; DB 16; Length 17;
Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New lipo:polysaccharide- binding polypeptide(s) - useful for treating bacterial infections and immune and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New lipopolysaccharide-binding polypeptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miyazaki
                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=OTHER
/note="Arg-OH or Arg-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP91671 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Σ
                                                                                 Claim 1; Page 36; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="H-Lys"
                                                                                                                                                                                                                                                                                                                                    76.98;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label-OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88WO-JP00823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87JP-0206258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           :| ||| |||| ||| |
1 kwrfrvryrgieyrrer 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               horseshoe crab haemocytes
                                                                                                                                                                                                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iwanaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-068854/09.
WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horseshoe crab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W08901492-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1989
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP91671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAP91671
```

ö

Gaps

ö

Gaps

Search completed: February 12, 2002, 12:30:33 Job time: 366 sec

us-09-485-571-27.rag

us-09-485-571-27.rai

Sequence Sequence Sequence 1

Sequence 1 Sequence 1 Sequence 1

Sequence

Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence

ALIGNMENTS

Sequence

```
Sequence 5, Application US/08168809
Patent No. 5580852
GENERAL IPPORMATION:
GENERAL IPPORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76; DB 1; Le
Pred. No. 1.3e-06;
5; Mismatches 0;
US-08-282-030-8
PCT-US95-10219-8
US-07-856-0268-13
US-07-856-0268-14
US-08-08-18-809-11
US-07-876-883-5
US-07-876-883-5
US-07-876-0268-23
US-08-379-0392-1
US-08-356-0268-3
US-08-356-0268-3
US-08-356-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
US-07-856-0268-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELECHONE: 515.245.3595
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.5%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 83.5
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SLINSE: NO
US-08-168-809-5
  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                         US-08-168-809-5
   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1, Appl
, Appli
, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
Appli
Appli
Appli
Appli
                                                                                         (without alignments)
3.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                              Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Sequence 9, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                               212252
                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             version 4.5
- 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-168-809-18
US-08-962-034-2
US-08-168-809-6
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-07-926-965-1
US-07-976-883-2
US-07-976-883-2
US-08-168-809-4
US-08-168-809-4
US-08-168-809-16
US-08-962-034-1
US-08-168-809-16
US-08-962-034-1
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-08-168-809-2
S-08-168-809-14
S-07-876-883-3
S-08-466-550-3
S-08-168-809-12
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -08-168-809-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-10219-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-282-030-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -07-876-883-4
                                                                                                                                                                                                       212252 seqs, 22503292 residues
                                                                              February 12, 2002, 12:32:24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       protein search, using sw model
                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                1 RWSFRVSYRGISYRRSR 17
             GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                         US-09-485-571-27
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                             . . . .
                                                                                                                                                                                                                                                                                     Post-processing:
                                                                                                                                                                                                                                                    sed
                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                       OM protein
                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                 Sequence:
                                                                                                                                                                                                        Searched:
                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
```

ö

Gaps

ö

Length 17;

g

```
Sequence 6, Application US/08168809
Sequence 6, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: PUtnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI VINNERS OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION STATES

CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROTH, Michael J. 342
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 0173R US
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTER/STICS:
                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 3; Pred, No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                             PILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: SPUILI, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEPHONE: 919 420 2202
TELEPAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide US-08-962-034-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: IA
COUNTRY: USP
ZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                       APPLICANT: Putram, Rebecca J.
APPLICANT: Putram, Rebecca J.
APPLICANT: Putram, Rebecca J.
APPLICANT: Putram, Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE PLONEER Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-962-034-2
is Sequence 2, Application US/08962034
j Patent No. 6015941
j GENERAL INFORMATION:
i APPLICANT: Rao, A. GUTUTA
j TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird
STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 72; DB 1; Length 17; Pred. No. 6.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER LOSA

ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
SOFTWARE: PARCHION NATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
ALECASIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: RCALSTRATION NUMBER: 29,342
RECISTRATION NUMBER: 29,342
RECECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION THYORMATION:
THYORMATION THYORMATION THYORMATION:
THYORMATION THYORMATION THYORMATION THYORMATION T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                        RESULT 2
US-08-168-809-18
; Sequence 18, Application US/08168809
; Patent No. 5580852
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.1%;
Best Local Similarity 70.6%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 amino acids
         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 700 Capit.
CITY: Des Moines
STATE: IA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE:
US-08-168-809-18
```

δ g

```
Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
Sequence 15, Application US/08168809
Patent Mo. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATION: DERIVATION: APPLICANT:
TITLE OF INVENTION: DIRIVATION: ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71; DB 1; Le
Pred. No. 1.1e-05;
2; Mismatches 3;
                                                                                                                                                                                           ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0173R US
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCh, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173F
TELECOMMUNICATION INFORMATION:
TELEFRAX: 515-245-3595
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWLFRVNYRGIKYRRQR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPCLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                     CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: IA
COUNTRY: USA
                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                              50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50309
                                                                                                                                                                                                                                                             Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-168-809-15
                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 71; DB 1; Length 17;
Pred. No. 8.9e-06;
2; Mismatches 3; Indels
                                                                                                                                                                        Length 17;
                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
COUNTRY: USA

ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROLL, MICHAEL J.
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 0173R US
TELECOMMUNICATION NUMBER: 0173R US
TELECOMMUNICATION NUMBER: 0173R US
TELECOMMUNICATION NUMBER: 0173R US
TELECOMMUNICATION NUMBER: 0173R US
TELEPHONE: 515-245-3634
TELEPHONE: 515-245-3634
TELEPHONE: SEQ ID NO: 7:
"""RISTICS:
                                                                                                                                                                      Score 71; DB 1; I
Pred. No. 8.9e-06;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/08168809
; Patent No. 5580852
; GENERAL INFORMATION:
                                                                                                                                                                      78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.0%;
70.6%;
                                                                                                                                                                                                                                                    1 RWSFRVSYRGISYRRSR 17
:| |||:|||| || |
1 KWLFRVNYRGIKYRRQR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWLFRVTYRGIKYROR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                      Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                        TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                       ; ANTI-SENSE: NO
US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ANTI-SENSE: NO
US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-168-809-15
                                                                                                                                                                                                                                                                                                                                                                                 US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

Gaps

```
ö
                                                                               Score 70; DB 1; Length 17; Pred. No. 1.3e-05; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NAKAMURA, TAKANORI; IWANAGA, SADAAKI;
APPLICANT: OHNO, MOTONORI; MIYAZAKI, KYOSUKE
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND METHOD FOR
TITLE OF INVENTION: PREPARING THE SAME
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926,965
FILING DATE: 19920807
FILING DATE: 19920807
FILING DATE: 19-MR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/348,487
FILING DATE: 19-MR-1989
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 175U-4B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-61-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORSESHOE CRAB
TACHYPLEUS TRIDENTATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07926965; Patent No. 5416194; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                               76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 17 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-661-800
TELEFAX: 212-661-8002
                                                                                                                                                                               1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                               Ouery Match
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NE
COUNTRY:
               ; ANTI-SENSE:
US-08-168-809-21
                                                                                                                                                                                                                                                                                         RESULT 9
US-07-926-965-1
                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08168809
Sequence 21, Application US/08168809
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
APPLICANT: Raco, Araquia G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI TITLE OF SEQUENCES: 21
CORRESPONDENCE S. 22
CORRESPONDENCE ADDRESS: 21
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 71; DB 1; Length 35;
Pred. No. 1.9e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREM APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R US
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3634
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 anino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: ROth, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3595
INFORMATION FOR SEC ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.0%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RWSFRVSYRGISYRRSR 17
:| |||:|||| ||| |
1 KWLFRVNYRGIKYRRQR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.0
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IA
                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE CF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE CF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
                                                                             APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Akiyoshi
APPLICANT: Watsi, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883 FILLING DATE: 19920429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 1; I
Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pioneer Hi-Bred International 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08168809 Patent No. 5580852
                        ; Sequence 2, Application US/07876883
; Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 869-9741
TELEX: 66141 PRINIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FWCFRVCYRGICYRKCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-07-876-883-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 700 Capit
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17 amino TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                       New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IA
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UR
                                                                                                                                                                                                                                                                                                                       STATE: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                      WHEREIN CYS-3 AND CYS-16 CAN
FORM A DISULFIDE BOND, AND CYS-7 AND CYS-12 CAN FORM A DISULF
BOND: WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE AMIDATED; WHERE
OR ALL OF THE RESIDUES CAN BE PROTECTED WITH PROTECTIVE GROUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Tamamoto, Naoki
APPLICANT: Matsumoto, Naivishi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                 Score 68; DB 1; Length 17;
Pred. No. 2.8e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68; DB 1; Length 17;
Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESEE: Pennie E Edmonds
STREET: 1155 Avenue of the Americas
STREET: 1155 Avenue of the Americas
STATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 199204129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07876883
Patent No. 5449752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 7568
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.78;
70.68;
                                                                                                                                                                     74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,
; IDENTIFICATION METHOD:
; OTHER INFORMATION: WHER;
; OTHER INFORMATION: FORM;
; OTHER INFORMATION: BOND
; OTHER INFORMATION: OR A
US-07-926-965-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.7
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                         1 RWSFRVSYRGISYRKSR 17
                                                                                                                                                                                                                                                                               1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-876-883-1·
                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-07-876-883-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                 셤
```

Gaps

Gaps

```
Sequence 2, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fulli, No. 5710128utaka
APPLICANT: Vamannoto, Nacki
APPLICANT: Watsumoto, Naki
APPLICANT: Watsumoto, Naki
APPLICANT: Watsumoto, Natyoshi
APPLICANT: Wats, Michinori
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.7%; Score 68; DB 1; Length 17; 70.6%; Pred. No. 2.8e-05; Live 1; Mismatches 4; Indels
                                                                                                                                                                                    74.7%; Score 68; DB 1; Length 17; 70.6%; Pred. No. 2.8e-05; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RWCFRVCYRGICYRKCR 17
    SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                   1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                    Query Match 74.7
Best Local Similarity 70.6
Matches 12; Conservative
                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
NOLECULE TYPE: peptide
US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-426-550-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1155 A CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-426-550-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naivoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68; DB 1; Length 17;
Pred. No. 2.8e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                              0173R US
                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROTH, Michaell
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173R
TELECOMMUNICATION INFORMATION:
TELEPRAX: 515-245-3595
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 17 antino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWCFRVCYRGICYRRCR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NO COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

Gaps

Search completed: February 12, 2002, 12:32:24 Job time: 452 sec

				142
	•			
			•	
8 8				
		\$ 50.		. ***
				* <u>*</u>
			•	
				Ď
		en e		
				a a
				•
			<u>.</u>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
				* * * * * *

	4 * 4 * * * * * * * * * * * * * * * * * * *	T 12		
	en de la companya de La companya de la co			
	2) a			* 3" 3" 1"
Record 予格 関連によって、これには、これには、これには、これには、これには、これには、これには、これには				Ť
				•
		•		
				<u> </u>

١

```
hypothetical prote
MMC tla. DO beta ce
MMC class II histo
hypothetical prote
hypothetical prote
hypothetical prote
Fe(II)-pyochelin
hypothetical prote
MMC class II histo
HLA DR-beta-I - hu
MMC class II histo
hypothetical prote
integrase (phage-r
hypothetical prote
outer membrane ush
protein tyrosine k
protein tyrosine k
L-JAK protein-tyro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tachyplesin I - ho
tachyplesin I prec
tachyplesin I prec
tachyplesin II -
polyphemusin I - A
polyphemusin I -
hypothetical prote
conserved hypothet
protein F12&21.26
molybdate metaboli
                                                                                                                               February 12, 2002, 12:34:41; Search time 126.85 Seconds (without alignments) 10.209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                   219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                  219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A38824
A380125
A380124
A380125
A383455
JW00124
JW00125
JW00125
B86473
B86483
B8
                                                                                                                                                                                                                                                                                  1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                       US-09-485-571-27
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %
Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.5
                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
68
68
67
47
                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
```

30 40 44.0 1299 2 158401 31 39.5 43.4 781 2 A86205 33 39 42.9 24.2 2 D72485 34 39 42.9 767 2 G86476 36 42.9 767 2 G86476 36 42.9 767 2 G86476 39 42.9 767 2 G86476 39 42.9 148 2 F86403 37 39 42.9 148 2 F86403 38 41.8 203 2 C25511 38 41.8 203 2 C25511 38 41.8 330 2 E36503 44 3 38 41.8 330 2 E36503 44 3 38 41.8 358 2 H75264 45 38 41.8 787 2 A55034 46 38 41.8 787 2 A55034 47 38 41.8 787 2 A55034 48 41.8 787 2 A55034 49 41.8 787 2 A55034 40 38 41.8 787 2 A55034 40 38 41.8 787 2 A55034 41 38 41.8 787 2 A55034 42 38 41.8 787 2 A55034 43 38 41.8 787 2 A55034 45 38 41.8 787 2 A55034 46 52 52 52 58 58 58 58 58 58 58 58 58 58 58 58 58	protein-tyrosine k hypothetical prote probable high-affi probable agmetinas protein F1504.37 { protein p130 - rat probable transposo Cc protein - fruit hypothetical prote conserved hypothet protein F9216.11 { hypothetical prote LAG1 protein - yea pyridoxal phosphat hypothetical prote LAG1 protein - yea pyridoxal phosphat hypothetical prote Conserved phosphat pyridoxal protein	GNMENTS eus gigas) 30-Jun-1992 #text_change 11-Jul-1997 Iwanaga, S. ocytes of southeast Asian horseshoe crabs (C 57 edicted nd (Arg) #status experimental	re 68; DB 2; Length 17; d. No. 5.5e-05; Mismatches 4; Indels 0; Gaps 0;	ab (Carcinoscorpius rotundicauda) a 30-Jun-1992 #text_change ll-Jul-1997 ; Iwanaga, S. mocytes of southeast Asian horseshoe crabs (C 357 experimental <mat> redicted end (Arg) (amide in mature form from followin</mat>	3; DB 2; Length 19; 5. 6.1e-05;
30	88401 56205 22485 59168 59168 6692 66403 6564 6603 6503 6503 6503 6503 6503 6503 6503	LI DP1	Score 68; Pred. No. Mismat	crab auda ion 30 H.; I hemoc 035357 us exp s pred	Score 68; Pred. No.
30 40 44.0 1299 2 31 39.5 43.4 781 2 33 39 42.9 42.9 33 39 42.9 42.9 34 39 42.9 767 2 35 39 42.9 767 2 36 39 42.9 968 2 37 38 41.8 203 2 41 38 41.8 203 2 41 38 41.8 330 2 42 43 38 41.8 330 2 44 38 41.8 330 2 44 38 41.8 330 2 44 38 41.8 330 2 44 38 41.8 330 2 44 38 41.8 330 2 44 38 41.8 38 41.8 45 38 41.8 787 2 45 Accession: A38824 46 38 41.8 787 2 47 18 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	15 10 10 10 10 10 10 10 10 10 10 10 10 10	(Tac evis ima, fron fron D:91		shoe ndiction ima, ima, ima, ima, ima, ima, ima, ima,	
30 40 44.0 1299 31 39.5 43.4 781 32 39 42.9 242 33 39 42.9 968 34 42.9 767 38 42.9 767 38 42.9 767 38 42.9 767 38 42.9 767 38 41.8 203 40 38 41.8 329 41.8 328 41.8 328 41.8 328 41.8 328 41.8 328 42.9 318 41.8 328 42.9 328 42.9 328 43.8 41.8 328 43.8 41.8 328 43.8 41.8 328 43.8 41.8 328 44.8 38 44.8 38 44.8 38 44.8 38 44.8 38 44.8 38 44.8 38 44.8 38 44.8 38 44.8 44.8 44.8 44.8 44.8 44.8 44.8 44.		ab e_r 90 90 90 90 ed ecu MUI 1 e 1 e ca	.78 .68 e 17	G# TT GOOD LITE	. 68
30 40 44.0 31 39.5 43.4 32 39 42.9 33 39 42.9 33 39 42.9 34 42.9 35 39 42.9 36 42.9 37 42.9 38 41.8 38 41.8 41.8 42 38 41.8 43 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 44 38 41.8 45 38 41.8 47 38 41.8 41.8 41.8 41.8 41.8 41.8 41.8 41.8	1299 7819 2421 2421 11688 11688 3309 3309 3588 4111 714	hoe cr gigas equenc T.; Na fisolat its pr 0124; in hemoc arboxy bonds:	74 y 70 rvativ rrrsr 	r - ho pius r equenc T: Na 66, 19 its pr its pr in hemoc arboxy arboxy arboxi ilated	
30 40 44 31 39.5 43 32 39. 42 33 39. 42 34 39 42 34 39 42 35 39 42 36 39 42 37 39 42 38 41 38 41 40 38 41 41 38 41 42 38 41 43 38 41 44 38 41 44 38 41 44 38 41 44 38 41 44 38 41 44 38 41 44 38 41 44 38 41 44 38 41 45 38 41 46 5 48 47 116: Tachyples; prachyples; prachem: 1992 C; Accession: A38824 A; Molecule type: prachyples; pra		sesi #sc #sc 00, 00, 00, 00, 00, 00, 00, 00, 00, 00	rit nse GIS GIC	rso cor; #s, 11-2 of UT> ce: ce:	rit
30 40 31 39.5 32 39 33 39 34 39 36 39 37 38 38 38 38 38 40 38 41 38 42 38 44 38 44 38 44 38 44 38 44 38 44 38 44 38 44 38 45 39 47 12 12 12 12 12 12 12 12 12 12 12 12 12	44444444444444444444444444444444444444	hor 99999 99999 99999 9899 9899 9899 6611 6611	ila Co CSYR II	ecu 1992 1992 1992 1992 1992 1992 1992 199	ila
33 333 333 333 333 333 333 336 336 336		1 esir I - es: Tachy 30-Jun-1 sion: A38 T.; Fuji hem. 108; T.; Tachypl ntermedia ence num sion: A38 ule type: ues: 1-17 imental s ris: amid	n 1 Soc 1 1 1 Soc	esin I preses: Card 30-Jun-13 sion: JXG 17. Ful hem. 108. Tachypl ntermedlaere number sion: JXG 100 type ule type ule type ule type ule type immental sion: JXG 12/Disu filed si dified si dified si	Match Ocal
		RESULT A38824 tachypl. C;Speci,C;Acces. C;Acces. R;Muta,A;Titlec A;Titlec A;Acces. A;Acces. A;Acces. A;Acces. C;Acces. A;Acces. C;C;Acces. A;Acces.	Query Best Match Qy Db	RESULT JX0124 tachypl C;Speci C;Speci C;Acces M;Muta, J;Bioc A;Tile SSING i A;Acces A;Acces A;Acces A;Espec C;Keywo C;	Query Best

crabs (Ca

ö

Gaps

ö

δý

```
polyphemusin I - Atlantic horseshoe crab polyphemusin I - Atlantic horseshoe crab)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Accession: Ju0124
R;Miyata, T: Tokunaga, F:; Yoneya, T:; Yoshikawa, K:; Iwanaga, S:; Niwa, M.; Takao.
J: Biochem. 106, 663-668, 1989
A;Attele. Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin, A;Aterence number: A91914; MuID: 90110066
A;Accession: Ju0124
A;Accession: Ju0124
A;Accession: Ju0124
C;Comment: The peptide is one of the antimicrobial peptides in the Atlantic horseshoe C;Comment: The peptide carboxyl end
C;Kcywords: amidated carboxyl end (Arg) #status experimental
F;4-17,8-13/Disulfide bonds: #status experimental
F;4-17,8-13/Disulfide anidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyphemusin II - Atlantic horseshoe crab
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Species: Limulus polyphemus (Atlantic horseshoe crab)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C:Accession: JU0125
R;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, J. Biochen. 106, 663-669, 1989
A;Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Reference number: A91914; MUID:90110066
                                                                                                                                                                                     C; Species: Tachypleus gigas
C; Species: Tachypleus gigas
C; Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
C; Accession: JX0125
R; Muta, T.; Fujimoto, T.; Nakajima, H.; Iwanaga, S.
J. Blotchen. 108, 261-266, 1990
A; Title: Tachyplesins isolated from hemocytes of southeast Asian horseshoe c sing intermediate of its precursor.
A; Reference number: JX0124; MUID:91035357
A; Accession: JX0125
A; Accession: JX0125
A; Molecule type: protein
A; Residues: 1-17 < WUIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: hemocyte
A, Experimental source: the mocyte
C; Keywords: amidated carboxyl end
C; Keywords: amidated carboxyl end
F; 3-16,7-12/Disulfide bonds: #status predicted
F; 17/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.3%; Score 64; DB 2; Length 18; Best Local Similarity 64.7%; Pred. No. 0.00026; Matches 11; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 2; 1
Pred. No. 0.00017;
                                                                                                                                                                              - horseshoe crab (Tachypleus gigas)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.48;
64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RWCFRVCYRGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWCFRVCYRGICYRKCR 17
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
JU0125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                          qq
                                                                                                                                                                                                                                                                      tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)

(c.) Species: Tachypleus tridentatus

(c.) Species: Tachypleus tridentatus

(c.) Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 01-Dec-2000

(c.) Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 01-Dec-2000

(c.) Accession: A3845; A30068

R. Shiqenaga, T.: Muta, T.: Toh, Y.: Tokunaga, F.: Iwanaga, S.

A. Recerrence number: A38345

A. Accession: A38345

A. Accession: A38345

A. Residues: 1-77

A. Presidues: 1-77

A. Presidues: 1-77

A. Pritle: Tachyplesin, A. Canson A. Muta, T.: Iwanaga, S.: Niwa, M.: A. Reference number: A30068; MUID:89034158

A. Accession: A30068; MUID:89034158

A. Accession: A30068

A. Accession: A30068

A. Residues: 24-40 < NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Molecule type: protein A; Residues: 24-40 <MIY> A; Residues: 24-40 <MIY> C; Comment: The peptide is one of the antimicrobial peptides found in the Japanese horses C; Comment: The peptide arboxyl end C; Reyords: amidated carboxyl end F; 26-39, 30-35/pisulfide bonds: #status predicted F; 26-39, 30-35/pisulfide bonds: #status predicted F; 40/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly F; 40/Modified site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyspecies: Tachypleus tridentatus
C; Species: Tachypleus tridentatus
C; Species: Tachypleus tridentatus
C; Species: Tachypleus tridentatus
C; Species: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000
C; Accession: B38345; JU0123
R; Shigenaga, T: Muta, T: Toh, Y: Tokunaga, F.; Iwanaga, S.
R; Shigenaga, T: Muta, T: Toh, Y: Tokunaga, F.; Iwanaga, S.
A; Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization and cellular localizations and safety and procession: B38345
A; Recession: B38345
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-77 csHz.
A; Cross-references: GB:U05689
R; Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao, T.;
D; Biochem. 106, 663-668, 1989
A; Tille: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II,
A; Reference number: A91914; MUID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.7%; Score 68; DB 2; Length 77; Best Local Similarity 70.6%; Pred. No. 0.00025; Matches 12; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                         Indels
                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68;
Pred. No.
                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.7%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 KWCFRVCYRGICYRRCR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                          1 RWSFRVSYRGISYRRSR 17
                                                                                                                                        1 KWCFRVCYRGICYRCR 17
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JU0123
                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ö

Gaps

; 0

1 RWSFRVSYRGISYRRSR 17

δ

1

```
48.4%;
                                 48.9%;
ilarity 52.4%;
Conservative
                                                                                                                                                                                                                        || ::|||
58 WSGVITYRGTNIRIISVRRSR
                                                                                                                                                                            2 WSFRVSYRG----ISYRRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
3; Conserve
                                                                     Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
A, Residues: 1-620 <STO>
A, Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-480 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: G75313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: F12K21.26
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: DR2108
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyaces: In any 2000 recydence_revision 20 Augraton, R.A.; Gwinn, M.L.; Dodson, R.J.; RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F., Mature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: C82472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <HEL>
A;Cross-references: GB:AE003853; NID:g9657741; PIDN:AAF96240.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
A;Genetics: A;Genetics: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AAG27097.1 [imported] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Accession: D86473
(Stacession: D86473
(Stac
                                            C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein VCA0332 [imported] - Vibrio cholerae (strain N16961 serog
                         C.Comment: The peptide is one of the antimicrobial peptides in the American horseshoe C;Keywords: amidated carboxyl end F;4-17,8-13/Disulfide bonds: #status predicted F:18/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005172; NID:911034940; PIDN:AAG27097.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
Accession: C82472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%; Score 47; DB 2; Length 615; 56.2%; Pred. No. 5.6;
                                                                                                                                                                                                                                           67.0%; Score 61; DB 2; Length 18;
58.8%; Pred. No. 0.00082;
iive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RWCFRVCYKGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-615 <STO>
A; Residues: 1-18 <MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: D86473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; All Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
Astuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kil C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal A;Authors: Salzberg, C.M.; Venter, J.C.; Davis, R.W.
A;Aitle: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molybdate matabolism regulator-related protein - Deinococcus radiodurans (strain RI C; Species: Deinococcus radiodurans (c; Species: Deinococcus radiodurans (c; Species: Deinococcus radiodurans (c; Species: Deinococcus radiodurans (3. Dec-1999 #text_change 31-Mar-2000 (5. Accession: G75313 R; White, O.: Elsen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.; White, O.: Elsen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.; Shath, H.O.; Venter, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 A; Reference number: A75250; MUID: 20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE002046; GB:AE000513; NID:g6459901; PIDN:AAF11657.1; PID:g6
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:AE005172; NID:98778254; PIDN:AAF79263.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                            protein F12K21.26 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E86468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                        Indels
   Length
   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2;
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%; Score 42; DB 2;
50.0%; Pred. No. 29;
iive 1; Mismatches
Score 44.5; D
Pred. No. 2.1;
                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A86141; MUID:21016719
A;Accession: E86468
                                                                                                                                              17
                                                                                                                                                                                                                   78
```

g Qγ

```
A. Accession: C2468
A. Molecule type: MRNA
A. Residues: 1-261-CTON
A. Cross - references: GB:X03068; NID:932279; PIDN:CAA26872.1; PID:932280
A. Cross - references: GB:X03068; NID:932279; PIDN:CAA26872.1; PID:932280
A. Cross - references: GB:X03068; NID:932279; PIDN: Bohme, J.; Claesson, L.; De Richtshament D.; Andersson, G.; Andersson, P.A.
R. Lathamman. D.; Andersson, G.; Andersson, P.A.
H. Mill: Immunol. 8, 93-103, 1983
A. Tritle: Molecular analysis of human class II transplantation antigens and their get A. Tritle: Molecule rounder: A01743; MUID:84031733
A. Reference number: A01743; MUID:84031733
A. Residues: 33-261 CLAR>
A. Experimental Source: clone PII-beta-2
A. Experimental Source: clone PII-beta-2
A. Experimental Source: clone PII-beta-2
A. Fixperimental Source: clone FII-beta-2
A. Fixperimental Source: clone FII-beta-2
A. Fixperimental Source: clone FII-beta-3
A. Reference number: A60773; MUID:89381351
A. Reference number: A60773; MUID:89381351
A. Status: not compared with conceptual translation
A. Residues: 33-126 CARR>
A. Experimental Source: clone from DrAWIO haplotype
A. Fresidues: A3-126 CARR>
A. Residues: 33-126 CARR>
A. Residues: A3-126 CARR>
A. Residues: A3-136 CARR>
A. Residues: A3-136 CARR>
A. Residues: A3-136 CARR>
A. Residues: 33-136 CARR>
A. Residues: A3-136 CARR>
A. Residues: A3-136 CARR>
A. Residues: B4-186 A3-186 CARR>
A. Residues: 38-186 A3-186 CARR>
A. Residues: B4-186 A3-186 CARR>
A. Residues: 53-88 A3-186 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: DNA A;Nolecule type: DNA A;Residues: 53-88,'D',90-109 <HOR> A;Residues: 53-88,'D', 90-109 <HOR> A;Experimental source: allele designated DQB1*05032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 53-88, 'D', 90-109 <SC3>
A; Residues: 53-88, 'D', 90-109 <SC3>
A; Experimental source: allele designated DOB 1.3
A; Note: this allele appears to confer susceptibility to pemphigus vulgaris
A; Mote: this allele appears to confer susceptibility to pemphigus vulgaris
B; Gyllensten, U.B.; Lashkari, D.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1835-1839, 1990
A; Title: Allelic diversification at the class II DQB locus of the mammalian major h)
A; Reference number: A35054; MUID:90175391
A; Accession: A35054
A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: F33287
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A. Molecule type: DNA
A. Residues: 53-88, DNA
A. Residues: 53-88, DN, 90-109 < GYL>
A. Experimental source: allele designated DQB 1.3
A. Experimental source: allele designated DQB 1.3
B. Horn, G.T.; Bugawan, T.L.; Long, C.M.; Erlich, H.A.
B. Horn, G.T.; Bugawan, T.L.; Long, C.M.; Elich, H.A.
A. Title: Allelic sequence variation of the HLA-DQ loci: relationship to 3, A; Reference number: A35589; MUID:88320372
A. Accession: F35589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 53-88,'S',90-109 <GY3>
A; Experimental source: allele designated DQB 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: DNA
A; Residues: 53-109 <GY2>
A; Experimental source: allele designated DQB 1.1
A; Experimental source: allele designated DQB 1.1
A; Accession: B35054
A; Reference number: A91020; MUID:86055719
A; Accession: C24669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C35054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC class II histocompatibility antigen HLA-DQ beta chain (DQ5) precursor - human N,Alternate names: HLA-DC beta (5.5 pecies: Homo sapiens (man) (5.5 pecies: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Title: DO beta: a new beta chain gene in HLA-D with a distinct regulation of expressid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC HLA-DO-Deta cell surface glycoprotein - human (fragment)
MHC HLA-DO-Deta cell surface glycoprotein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: No. 199528
C;Accession: I59528
R;Sinha, A.A.; Brautbar, C.; Szafer, F.; Friedmann, A.; Tzfoni, E.; Todd, J.A.; Steinman Science 239, 1026-1029, 1988
A;Title: A newly characterized HLA DQ beta allele associated with pemphigus vulgaris.
A;Reference number: I59528; MUID:88145646
                                                                                                                                                                                                                                                                                                                                                                                                                    D42463.
D42463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:120517; OMIM:142857
A; Map position: 6p21.3-6p21.3
C; Superfamily: class II histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-94 <RES>
A;Cross-references: GB:M19239; NID:g181746; PIDN:AAA52319.1; PID:g181747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2; Length 94; pred. No. 8.2; 4; Indels 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2
Pred. No. 32;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 FRVNYRNGGIFYRSAR 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                    234 WMVRVDARGVYYGHSR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :: |:|||| ||
RHNYEVAYRGILQRR 94
                                                                                   17
                                                                                   2 WSFRVSYRGISYRRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: 159528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
```

g δý

ā

serology

qq ò

1

S

ö

Gaps

ö

Length 279; Indels

DB 2; 24;

Score 41; DB 2 Pred. No. 24; 1; Mismatches

45.1%; 80.0%;

```
A;Cross-references: GB:AE002093; NID:g3786022; PIDN:AAC67368.1; GSPDB:GN00139 C;Genetics: T19C21.1; At2g38500 A;Gene: T19C21.1; At2g38500 A;Introns: 170/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 12, 2002, 12:34:41 Job time: 559 sec
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :11111 | 111
99 AFRVSYHGIS 108
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                      A:Title: A. Title: A. Titl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, August 1998
A: Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A: Reference number: 214676
A: Accession: T02495
A: Status: translated from GB/EMBL/DDBJ
A: Accession: T02495
A: Status: translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-279
A: Molecule type: DNA
A: Residues: 1-279
A: Rounslated source: Cultivar Columbia
A: Resperimental source: cultivar Columbia
B: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
             R;Turco, E.; Care, A.; Compagnone-Post, P.; Robinson, C.; Cascino, I.; Trucco, M.
Immunogenetics 26, 282-290, 1987
A;Title: Allelic forms of the alpha- and beta-chain genes encoding DOWI-positive heterod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Species: Arabidopsis thaliana (mouse-ear cress)
:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
:Accession: T02495; G84805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2938500 [imported] - Arabidopsis thaliana N:Alternate names: hypothetical protein T19C21.1 C;Specias: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change IC;Accession: T02495; G84805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.1%; Score 41; DB 1; Length 261; 53.3%; Pred. No. 23; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 RHNYEVAYRGILQRR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

P22968 oryctolagus P12821 homo sapien P12822 oryctolagus P09470 mus musculu P47820 rattus norv P30415 mus musculu P30414 homo sapien P95070 mycobacteri P52767 pinus thunb P17353 spinacia ol Q55143 synechocyst

ACET_RABIT
ACE_HUNAN
ACE_RAIT
ACE_MOUSE
ACE_RAT
NKCR_MOUSE
NKCR_MOUSE
KL30_MYCTU
KL30_MYCTU
KR130_MYCTU
KR146_FINTH
KR16_FINTH
KR16_FINTH
KR16_FINTH

737 1306 1310 1312 1462 1462 65 71 134 135

440.7 440.7 440.7 440.7 740.7 339.6 339.6 339.6

37 337 337 336 336 336 336 336

ALIGNMENTS

```
February 12, 2002, 12:39:53 ; Search time 67.2 Seconds
(without alignments)
9.275 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                  100059
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       100059 segs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                            1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                             US-09-485-571-27
                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_39:*
                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB :
Maximum DB :
                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                         Run on:
```

	Description	23684	P14213 tachypleus	4	~	215	5 limulus	σ	~	'n	Q63272 rattus norv	P52333 homo sapien	_	Q9z364 actinomyces	042887 schizosacch	Q63767 rattus norv	P24156 drosophila		Q9y227 homo sapien	-		~	2 baci.	P03992 homo sapien	uns u	P30009 rattus norv	P10260 mouse mamma	P11806 human adeno	P11807 human adeno		Q9pjb1 chlamydia m	238 anas	229	P22967 mus musculu
SUMMARIES	DI	TAC1_TACGI	TAC1_TACTR	TAC2_TACTR	TAC3_TACGI	PPM1_LIMPO	PPM2_LIMPO	HB22_HUMAN	FPTA_PSEAE	YM11_MARPO	JAK3_RAT	JAK3_HUMAN	JAK3_MOUSE	URED_ACTNA	SPEC_SCHPO	BCA1_RAT	L2CC_DROME	LAG1_YEAST	ENP4_HUMAN	K6PF_DROME	PLD1_RAT	VP30_EBOZM	RS13_BACSU	HB25_HUMAN	MACS_MOUSE	MACS_RAT	PR73_MMTVB	DNB2_ADE40	DNB2_ADE41	Y632_CHLTR	Y921_CHLMU	MX_ANAPL	- 1	ACET_MOUSE
	Length DB				17 1		18 1		720 1		1100 1			271 1	413 1	968 1	203 1	411 1	616 1	787 1	1075 1	288 1	120 1	261 1			320 1	73		529 1	529 1	721 1	732 1	732 1
æ	Query		4	74.7	Н	0		S	5	44.0	4	44.0				42.9	41.8		41.8		-	ч.	0	40.7	0	0	0	0	0	40.7	40.7	40.7	40.7	40.7
	Score	69	68	68	65	64	61	41	41			40	40	39	39	39	38	38	38	38	m	37.5	. 37	37	37	37	37	37	37	37	37	37	37	37
	Result No.	П	7	m	4	ហ	9	7	Φ.	0	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

SEQUENCE FROM N.A.

RP

	crab). ; Xiphosura;	norseshoe : a wMLY.	0; Gaps		X1phosura;
		otundicauda; -229025; -229025; kajima H., Iwanaga S.; rom hemocytes of Southeast Asian horseshoe cromplesin tachyplesis gigas): tachyplesin III, and a of its precursor."; 1990):	CRC64; Length 17; ; Indels		Signification (Rel. 13, Created) (Rel. 13, Created) (Rel. 37, Last sequence update) (Rel. 37, Last annotation update) I PRECURSOR. II PRECURSOR. Active the properties of the properties o
17 AA.	UI-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update) TACHYPLESIN I. Tachypleus gigas (Southeast Asian horseshoe crab), and Carcinoscorpius rotundicauda (Southeast Asian horseshoe Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata Limulidae; Tachypleus.	axID=6852, 6848; CE. S-T.gigas, and C.rotundicauda; E-9103537; Pubmed-229025; Pulimoto T., Nakajima H., Iwanaga S.; plesins isolated from hemocytes of Southeast As. (Carcinoscorplus rotundicauda and Tachypleus gification of a new tachyplesin, tachyplesin III, sing intermediate of its precursor."; chem. 108:261-266(1990). MILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUS: 388244; A38824.	2923C94 DB 1; T1.1e-05	, , , , , , , , , , , , , , , , , , ,	(Rel. 13, Created) (Rel. 20, Last sequence update) (Rel. 37, Last annotation update) I PRECURSOR. tridentatus (Japanese horseshoe crab) Merazoa; Arthropoda; Chelicerata; Mer. Tachypleus.
PRT;	Created) Last sequence update) Last annotation update) Lheast Asian horseshoe c licauda (Southeast Asian thropoda; Chelicerata;	C Girdy, d		Q	Created) Created) Last sequence update) Last annotation update) R. (Japanese horseshoe cr
ANDAR	(Rel. 20, Creat (Rel. 20, Last (Rel. 32, Last II. gigas (Southeast pius rotundicaud Metazoa; Arthrop	NCBL_TaxID=6852, 6848; SEQUENCE. SPECIES—T.gigas, and C.rotundicaud. MarbinNe—91035357; pubmed—2229025; Muta T., Fujimoto T., Nakajima H., "Tachyplesins isolated from hemocycrabs (Carcinoscorplus rotundicaud. identification of a new tachyplesipocessing intermediate of its prediction. 1. Biochem. 108:261-266(1990) SIMILARITY: BELONGS TO THE TACIPIER: A38824; A38824.	4. ion. 16 12 17 2269 74. 70.	ISYRRSR 17 ICYRRCR 17	SIGNUAND; (Rel. 13, Creat, (Rel. 20, Last, (Rel. 37, Last, I PRECURSOR. Lidentatus (Jag Metazoa, Arthrop
£		NCBL_TaxID=6852, 6848; [1] SEQUENCE. SPECIES=T.gigas, and C.r. MEDLINE-9103357; PubMed MATELINE-9103357; PubMed MATELINE-9103537; PubMed MATELINE-9103507; Na "Tachyplesins isolated f crabs (Carcinoscorpius r identification of a new processing intermediate J. Biochem. 108:261-266 -1 - SIMILARITY: BELONGS PIR, A38824,	124; ic; 1 1 1 Simi 2;	SYRG	TACLINGIN P14213; 01-JAN-1990 (Rel. 01-NOV-1991 (Rel. 15-DEC 1998 (Rel. TACHYPLESIN I PREC TACHYPLESIN I PREC EUKARYOTE, METAZOG LIMULIGAE; TACHYPL
30E	_	RN (1) SEQUENCE RC SPECIES* RX MEDLINE* RX MEDLINE* RY Tachypl. RT crabs (CRT crabs (CRT processii RT jentifi. RT processii RT jentifi. RT processii RC 1- Bioch CC 1- Bioch CC 1- SIMI	DB PIR: JXO KW Antibiot KT DISULFID FT DISULFID FT MOD_RES SQ SEQUENCE Query Match Best Loca:	Oy 1 R Db 1 K RESULT 2 TACI_TACT R	-

Gaps

;

Indels

4;

Mismatches

;;

Conservative

12;

17

1 RWSFRVSYRGISYRRSR

```
Matches
                                                            δŏ
                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 24-40.

STRUCTURE 93257488; PubMed-8490053;

Tamamura H., Kuroda M., Masuda M., Otaka A., Funakoshi S.,

Tamamura H., Kuroda M., Maki M., Matsumoto A., Lancelin J.-M.,

Nakashima H., Yamamura H., Fuyli N.;

Kohda D., Tate S., Inagaki F., Fuyli N.;

A comparative study of the solution structures of tachyplesin I and
a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemiusin

III), determined by nuclear magnetic resonance.";

Hiochim. Biophys. Acta 1163:209-216(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacohen. 114:307-316(1993).

J. Biochen. 114:307-316(1993).

GRAM-POSITIVE BACTERIA.

SUBCELLUAR LOCATION: SGRANULES.

SUBCELLUAR LOCATION: SPECIFICITY: HEMOCYTES.

SUBCELLIAR LOCATION: OF THE TACHYPLESIN/POLYPHEMUSIN FAMILY.

SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                 MEDIINE-99034158; PubMed-3141410; Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Tokunaka H. Hemocytes of Miya M., Takao T., Shimonishi Y.; and T. Tokunaka H. Takao T., Takao T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Ikanaga S., Separation of large and small granules from horseshoe crab "Separation of large and characterization of their (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
B940CAA4A641335F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibiotic; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial period, tachyplesin I, isolated from hemocytes of horseshee rab (Tachypleus tridentatus). NMR determination of the beta-sheet structure. ;
J. Biol. Chem. 265:15365-15367(1990).
                                   Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NWR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                              SEQUENCE OF 24-40, AND DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 263:16709-16713(1988).
                                                                                                                                                                  Biol. Chem. 265:21350-21354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
MEDLINE=94110249; Pubmed=8282718;
                      MEDLINE=91065956; PubMed=2250028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M57242; AAA63538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
40
77
39
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A30068; A30068.
PIR; A38345; A38345.
                                                                                                                                               tridentatus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-90110066; PubMed-2514185; MEDINE-90110066; PubMed-2514185; Minka M., Miyata T., Tokunaga F., Yonga T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Takao T., Shimonishi I., and polyphemusins I and II: Chemical structures and biological activity.; J. Biochem. 106:663-668(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (radurprises of the components.")
J. Biochem. 114:307-316(1993).
J. Biochem. 114:307-316(1993).
J. Biochem. 114:307-316(1993).
J. Biochem. 114:307-316(1993).
J. BIOCHELOUS SEGNETIA.
J. SUBCELLULAR LOCATION: S-GRANULES.
J. TISSUE SPECIFICITY: HEWOCYTES.
J. SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; B38345; B38345.
PIR; JU0123; JU0123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE=94110249; PubMed=8282718; Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Shigenaga T., Takayenoki Y., Kawasaki S., Iwanaga S.; "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                 Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota: Metazoa: Arthropoda: Chelicerata; Merostomata: Xiphosura;
Limulidae: Tachypleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.

BY SIMILARITY.

AMIDATION (G-1 PROVIDE AMIDE GROUP).

ASP/GIUG-RICH (ACIDIC).

6EBES7A4A652AEFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibiotic; Amidation; Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDLINE-91065956; PubMed=2250028;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
"Antimicrobial tachyplesin peptide precursor. cDNA cloning and callular localization in the horseshoe crab (Tachypleus tridentatus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68; DB 1;
Pred. No. 5.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACHYPLESIN II.
                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                           77 AA
                                                                                                                                                                                                                                                                                                                                                          identatus).";
Biol. Chem. 265:21350-21354(1990).
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.78;
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ж
Ж
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ||| ||| ||| ||| ||| || || 24 RWCFRVCYRGICYRKCR 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9335
TACHYPLESIN II PRECURSOR.
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 24-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                          NCBI_TaxID=6853;
                                                                                             TAC2_TACTR
P14214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                 RESULT 3
                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
```

RESULT

Score 68; DB 1; Length 77; Pred. No. 5.1e-05;

74.78; 70.68;

Best Local Similarity

m ∳

Query Match

```
HB22_HUMAN
P01919;
                                                                                                    PPM2_LIMPO
P14216;
                                                                                                                                                                                                                                                                                                                                                      MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     DISULFID
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-DQB1
                                                                                   RESULT 6
PPM2_LIMPO
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HB22_HUMAN
                                     ò
                                                      qq
                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.;
"Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and J. Bloohem. 106:663-668(1989).
--- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                              Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
NCBI_TaxID=6852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -t- TISSUE SPECIFICTTY: HEWOCYTES.
-t- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR; JU0124; JU0124.
Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                      Score 65; DB 1; Length 17;
Pred. No. 3.5e-05;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                  AMIDATION.
E9E08CE9D2923C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION.
FB3FA109D2923504 CRC64;
                                                      Tachypleus gigas (Southeast Asian horseshoe crab).
                01-NoV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
701-NOV-1995 (Rel. 11.
                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
POLYPHEMUSIN I.
17 AA.
                                                                                                                                                                                                                                                                                                                                                                                           18 AA.
                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-90110066; Pubmed-2514185;
                                                                                                  SEQUENCE.
MEDLINE=91035357; Pubmed=2229025;
                                                                                                                                                                                                                                                                                      71.48;
64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2459 MW;
                                                                                                                                                                                                                                                           2241 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAM-POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                          1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                     1 KWCFRVCYRGICYRKCR 17
                                                                                                                                                                                                                                                                                      Query Match 71.4
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
STANDARD;
                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                        PPM1_LIMPO
P14215;
TACGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                 PPM1_LIMPO
δ
                                                                                                                                                                                                                                                                                                                                            g
```

```
Mydata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Yonega T., Yoshikawa K., Iwanaga S., Niwa M., Takao T., Shimonishi Y.; Yonega T., Shimonishi Y.; Yonega T., Yonega
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_FaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tonnelle C., Demars R., Long E.O.; "DO beta: a new beta chain gene in HLA-D with a distinct regulation of expression."; EMBO J. 4:2839-2847(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bustrycha: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA CHAIN
PRECURSOR (DQB1*0501).
Score 64; DB 1; Length 10; Pred. No. 5.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 1; Length 18;
Pred. No. 0.00018;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
E402A109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN'1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CTT-1994 (Rel. 30, Last annotation update)
POLYPHEMUSIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
MEDLINE-90110066; PubMed-2514185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86055719; PubMed-2998758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.0%;
58.8%;
                            70.3%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AA; 2431 MW;
                                                                                                                                                                                                             2 RWCFRVCYRGFCYRKCR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RWCFRVCYKGFCYRKCR 18
                                                                                                                                                                  1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWSFRVSYRGISYRRSR 17
                                                             Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
```

```
RESULT 8
FPTA_PSEAE
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                    MEDIINE=97083137; PubMed=8929711; MEDIINE=97083137; PubMed=8929711; Yasunaga S., Kimura A., Hamaguchi K., Ronningen K.S., Sasazuki T.; "Different contribution of HiA-DR and -DQ genes in susceptibility and resistance to insulin-dependent diabetes mellitus (IDDM)."; Tissue Antigens 47:37-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
                                                                                                       Larhanmar D., Andersson G., Andersson M., Bill P., Boehme J., Claesson L., Denaro M., Emmoth E., Gustafsson K., Hammarling U., Heldin E., Hyldig-Nielsen J.J., Lind P., Schenning L., Servenius B., Widmark E., Rask L., Peterson P.A.; "Molecular analysis of human class II transplantation antigens and their genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (POTENTIAL).
2F5D8FDC413D1BA5 CRC64;
                             , Care A., Compagnone-Post P., Robinson C., Cascino I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 261; Pred. No. 7.3;
                                                   Allelic forms of the alpha- and beta-chain genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DQ(W1.1) BETA CHAIN.
EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
CONNECTING PEPTIDE.
                                                                                             SEQUENCE OF 33-261 FROM N.A. (CLONE PII-BETA-2). MEDLINE-84031733; PubMed=6415003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SW00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
MHC II; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1.
Pfam; PF00069; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGG1; 1.
                                                                  DQw1-positive heterodimers.";
Immunogenetics 26:282-290(1987).
                         MEDLINE=88006310; PubMed=2888727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%;
                                                                                                                                                                                                                                                                                                                                                   EMBL; X03068; CAA26872.1; -.
EMBL; M17564; AAA59765.1; -.
EMBL; L34101; AAC41969.1; -.
                                                                                                                                                                              Hum. Immunol. 8:95-103(1983).
                                                                                                                                                                                                  SEQUENCE OF 33-261 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.1
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
261
111
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                  Prucco M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                        Turco E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                           EMBL;
```

```
this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 15692 / PAO1;

STRAIN=ATCC 15692 / PAO1;

XX MEDLINE=2043737; Pubmed=10984043;

XA BLINE=20437377; Pubmed=10984043;

XA Stover C.K., Pham X.-Q.T., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Erinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Hickey M.J., Erinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Brody L.L., Coulter S.N., Folger K.R. Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer Geomes sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000)

"TRANSFORT OF FELIII) PYCCHELIN.

"TRANSFORT OF FELIII) PYCCHELIN.

"TRANSFORT OF FELIII) PYCCHELIN.

"SUBCELIGIAR LOCATION: OUTER MEMBRANE.

"I SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ankenbauer R.G., Quan H.N.;
"Fpt.A, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate siderophore receptor homologous to hydroxamate siderophore receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U03161; AAC43213.1; -.
EMBL, AE004839; AAG07609.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2: 1.
Outer membrane; Iron transport; Transport; Signal; Receptor;
                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 720;
Pred. No. 21;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 38 FE(III)-PYOCHELIN RECEPTOR. 73 720 TONB C-TERMINAL BOX. 720 AA; 79992 MW; DA796313116EOCC2 CRC64;
                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FPTA OR PA4211.
720 AA.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 39-51.
STRAIN-PAO / IA602;
MEDLINE-94117363; PubMed-8288523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db . 637 RWSVGGGLQAQSDYSVDYRGVSMRQ 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWS-----FRVSYRGISYRR 15
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 176:307-319(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%;
ilarity 36.0%;
Conservative
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                    Pseudomonas
          FPTA_PSEAE
P42512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
```

RESULT 9

..

Gaps

0;

4; Indels

Mismatches

3;

| :: |:|||| || 112 RHNYEVAYRGILQRR 126 1 RWSFRVSYRGISYRR 15

ò

.ي ź

```
945
976
1100
                                                                                                                                DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID DIT OF OCCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                      01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 35, Last annotation update)
HYPOTHETICAL 83.1 KDA PROTEIN IN COB-ATPA INTERGENIC REGION (ORF 732).
                                                                                                  micoloniation.
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Marchantiophyta;
Marchantiales; Marchantiaceae; Marchantia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi T., Shirasawa T.;
"Molecular cloning of rat JAK3, a novel member of the JAK family of
protein tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 342:124-128(1994).
                                                                                                                                                                            Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N., Asashi K., Kanegaer T., Ogura Y., Kohchi T., Ohyama K.; Masashi K., Kanegaer T., Ogura Y., Kohchi T., Ohyama K.; Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial genome."; mitochondrial genome."; J. Mol. Biol. 223:17(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%; Score 40; DB 1; Length 732; 47.1%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion; Hypothetical protein.
SEQUENCE 732 AA; 83092 MW; 936CF036E9D06442 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1100 AA.
732 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Mendel; 2082; MARPO:ymfll;1.
InterPro: IPR000442; Intron_maturse2.
InterPro: IPR000477; RVTse.
Pfam: PF01348; Intron_maturas2; 1.
 PRT;
                                                                                 Marchantia polymorpha (Liverwort)
                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-92114051; Pubmed-1731062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Spleen;
MEDLINE=94192816; PubMed=8143863;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; M68929; AAC09442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 RLDFRMGQRAFSYERQR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=3197;
                                                                                             Mitochondrion Mitoch
YM11_MARPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JAK3_RAT
063272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.
-!-CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE = ADP + PROSINE PHOSPHATE.
-!-SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).
-!-TISSUE SPECIFICITY: TRANSCRIBED IN A VARIETY OF TISSUES INCLUDING SPLEEN, LUNG, KIDNEY AND INTESTINE.
-!-DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORILARITY.

HOSPHORILARIDON (AUTO-) (BY SIMILARITY).

WH. 1D59CA05F4DD7EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAK3_HUMAN STANDARD;
PE2333; (1324).
PE2333; (1325), (1326), (1311;
D1-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AdG-2001 (Rel. 40, Last annotation update)
20-AdG-2001 (Rel. 40, Last annotation update)
(LEUKOCYTE JANUS KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                             FIGURE TYPE: THE STATE OF THE TYPE TO TL-2 AND IL-4 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2 (ATYPICAL).
PROTEIN KINASE 1.
PROTEIN KINASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000299; Band_4.1.
InterPro; IPR000299; Buk_pkinase.
InterPro; IPR000390; SH2.
InterPro; IPR000309; SH2.
InterPro; IPR000245; Tyr_kin.
Pfam; PF00069; pkinase; 2.
SWART; SW00295; B41; 1.
SWART; SW00295; B42; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00117; PROTEIN_KINASE_DOW; 2.
PROSITE; PS00011; PROTEIN_KINASE_DOW; 2.
PROSITE; PS00011; PROTEIN_KINASE_DOW; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.08;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D28508; BAA05868.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           777
1091
832
851
945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | | |||:|| |
878 FIVKYRGVSYGPGR 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2 domain; Repeat.
DOMAIN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
```

```
Candotti F., Oakes S.A., Johnston J.A., Giliani S., Schumacher R.F., Mella P., Fiorini M., Vagazio A.G., Badolato R., Notarangelo L.D., Bozzi F., Macchi P., Strina D., Vezzoni P., Blaese R.M., O'Shea J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic organization of the human JAK3 gene and mutation analysis in severe combined immunodeficiency by single-strand conformation polymorphism.";

Hum. Genet. 106:73-79(2000).

"Hum. Genet. 106:73-79(2000).

"THE INTERLENTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN THE INTERLENTION. TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED IN PHOSPHORYLATES STAT6, IRS1, IRS2 AND PI3K.

"HOSPHORYLATIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

"SUBGELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE ASSOCIATED (BY SIMILARITY).

ASSOCIATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96027605; PubMed-7559633; Lai K.S., Jin P., Liu E.T.; Lai K.S., Jin Y., Graham D.K., Witthuhn B.A., Ihle J.N., Liu E.T.; "A kinase-deficient splice variant of the human JAK3 is expressed in hematopoletic and epithelial cancer cells."; J. Blol. Chem. 270:25028-25036(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=55388142; Pubmed=7659163; Macchin L., Frattini A., Porta F., Macchin A., Villa A., Giliani S., Sacco M.G., Frattini A., Porta F., Mazchin A.G., Johnston J.A., Candotti F., O'Shea J.J., Vezzoni P., Notarangelo L.D.; Mutations of Jak-3 gene in patients with autosomal severe combined immune deficiency (SCID)."; Mature 377:65-68(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94294384; PubMed-8022790; MEDLINE-94294384; PubMed-8022790; MEDLINE-94294384; PubMed-8022790; Medline -94294384; PubMed-8027, Johnston J.A., Blake T.B., Chen Y.-Q., Lal B.K., Lloyd A.R., Kelvin D.J., Staples J.E., Ortaldo J.R., O'Shea J.J.; O'Shea J.J.; Andlecular cloning of L-JAK, a Janus family protein-tyrosine kinase expressed in natural killer cells and activated leukocytes."; Proc. Natl. Acad. Sci. U.S.A. 91:6374-6378(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98423994; PubMed-9753072;
Bozzi F., Lefranc G., Villa A., Badolato R., Schumacher R.F.,
Khalil G., Loiselet J., Bresciani S., O'Shea J.J., Vezzoni P.,
Notarangelo L.D., Candotti F.;
Molecular and biochemical characterization of JAK3 deficiency in
Patient with severe combined immunodeficiency over 20 years after
bone marrow transplantation: implications for treatment.";
Br. J. Haematol. 102:1363-1366(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression of Janus kinase 3 in human endothelial and other non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Savoldi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS SCID ARG-151; ILE-722 AND SER-910.
MEDLINE-20435064; PubMed-10982185;
Schumacher R.F., Mella P., Badolato R., Fiorini M., Savoldi G.
Gillani S., Villa A., Candotti F., Tampalini A., O'Shea J.J.,
Notarangelo L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 36-191 FROM N.A.
MEDLINE-96278845; PubMed-8662778;
Verbsky J.W., Bach E.A., Fang Y.F., Yang L., Randolph D.A.,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS SCID GLY-481; LEU-586--MET-592 DEL AND ARG-759.
MEDLINE-98022793; PubMed-9354668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphoid and non-myeloid cells.";
J. Biol. Chem. 271:13976-13980(1996).
                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fields L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Villa A.;
                                   Mammalia;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR EMBL; 090607; AAA19626.1; ...

DR EMBL; 031601; AAC50226.1; ...

DR EMBL; 031602; AAC50226.1; ...

DR EMBL; 031602; AAC50227.1; ...

DR HUSSP; P11362; 1FGI.

DR MIM; 600802; ...

DR MIM; 600802; ...

DR MIM; 600802; ...

DR INTERPO: IPR000719; EUK_PKinase.

DR INTERPO: IPR000719; EUK_PKinase.

DR INTERPO: IPR000719; EUK_PKinase.

DR INTERPO: IPR000719; EUK_PKinase; Z.

DR SMART; SM00225; B41; 1.

DR SMART; SM00225; B41; 1.

DR SMART; SM00219; TYKC; 1.

SMART; SM00219; TYKC; 1.

SMART; SM00119; PKOTEIN_KINASE_DOM; Z.

DR ROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE, ATP-binding; Disease mutation; SCID.

W SH2 domain; Repeat; Alternative splicing; Disease mutation; SCID.

TOWAIN S21 781 PROTEIN KINASE 1.

PROMIN S21 781 PROTEIN KINASE 1.

PROMIN S21 781 PROTEIN KINASE 1.

PROMIN S21 111 PROTEIN KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN ISOFORM JAKABB)
HELMKLCWAPSPORPSFSALGPOLDMLWSGSRGCETHAFT
HELMKLCWAPSPORPSFSALGPOLDMLWSGSRGCETHAFT
AHPEGKHISLSFS -> SCYSGWRDDICSMGWWPTVISRWD
LACSPCPRPLTITATTVQLPPTLHATAASVAVPNKTC (IN
ISOFORM JAKABM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
PHOSPHORYLARION (AUTO-) (BY SIMILARITY).
HELMKLCWAPSPQDRPSFSALGPQLDMLWSGSRGCETHAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHPEGKHHSLSFS -> SAAGLASVSQSVDWAGVSGKPAGA
                                                                                                                                                                               DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
DIFFERENT MRNA SOURCES: BREAST (JAK3B), SPLEEN (JAK3S; SHOWN HERE), AND ACTIVATED MONOCYTES (JAK3M). JAK3B MAY BE DEFECTIVE AS IT LACK SOME PART OF THE KINASE DOMAIN.
TISSUE SPECIFICITY: IN NK CELLS AND AN NK-LIKE CELL LINE BUT NOT IN RESTING T CELLS OR IN OTHER TISSUES. THE S-FORM IS MORE COMMONLY SEEN IN HEMATOPOIETIC LINES, WHEREAS THE B- AND M-FORMS ARE DETECTED IN CELLS BOTH OF HEMATOPOIETIC AND EPITHELIAL
                                                                                                                                                                                                                                                                                                                                                            OF
                                                                                                                                                                                                                                                                   PTM: TRACSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4.
DISEASE: DEPECTS IN JAK3 ARE A CAUSE OF RECESSIVE T-CELL
DISEASE: DEPECTS IN JAK3 ARE COMBINED IMMUNODEFICIENCY (T-B+
NEGATIVE/B-CELL POSITIVE SEVERE COMBINED IMMUNODEFICIENCY (T-B+
SCID). A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING
SCID). A CONDITION CHARACTERIZED BY THE ABSENCE OF CIRCULATING
MATURE T-LYMPHOCYTES AND NK CELLS, NORMAL TO ELEVATED NUMBERS OF
NONFUNCTIONAL B-LYMPHOCYTES, AND MARKED HYPOPLASIA OF LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE 1.
PROTEIN KINASE 2.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y -> C (IN SCID).

FTTd=VAR_0065284.

P -> R (IN SCID).

FTId=VAR_010492.

FTG=VAR_010493.

/FTId=VAR_010493.

R -> W (IN SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
MOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                      <u>:</u>.
```

```
ö
                           PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-94309920; PubMed-7518579;
Rane S.G., Reddy E.P.;
"JAK3: a novel JAK kinase associated with terminal differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94294024; PubMed-8022486;
Witthuhn B.A., Silvennoinen O., Miura O., Lai K.S., Cwik C., Liu E.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gurniak C.B., Berg L.J.;
"Murine JAK3 is preferentially expressed in hematopoietic tissues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JAK3_MOUSE STANDARD; PRT; 1299 AA.
062137; 061747; 061746;
01-NOV-1997 (Rel. 35, Created)
20-NUC-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TYROSINE-PROTEIN KINASE JAK3 (EC 2.7.1.112) (JANUS KINASE 3) (JAK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Involvement of the Jak-3 Janus kinase in signalling by interleukins 2 and 4 in lymphoid and myeloid cells."; Nature 370:153-157(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΝŢ
                      MISSING (IN SCID; LACK OF PHOSPHORYLAIN RESPONSE TO CYTOKINE STIMULATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- FUNCTION: TYROSINE KINASE OF THE NON-RECEPTOR TYPE, INVOLVED THE INTERLEDKIN-2 AND INTERLEDKIN-4 SIGNALING PATHWAY. PHOSPHORYLATES STATE, IRS1, IRS2 AND PI3K.
-I- CATALYICA ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 1124;
                                                                                                                    /FTId=VAR_010496.
C -> R (IN SCID; CONSTITUTIVE PHOSPHORYLATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1D0FD22068E088E4 CRC64;
                                                                                                                                                                                         /FTIG=VAR_010497.
L -> S (IN SCID).
/FTIG=VAR_010498.
A -> G (IN REF. 2).
MISSING (IN REF. 3).
T -> A (IN REF. 2).
A -> R (IN REF. 2).
P -> R (IN REF. 2).
M -> I (IN REF. 2).
A +> G (IN REF. 2).
A -> G (IN REF. 2).
  /FTId-VAR_010494.
                                                  /FTIG=VAR_010495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-BALB/C x 129 F2; TISSUE-Thymus;
MEDLINE-96184772; PubMed-8605329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ymphocyte precursor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.0%;
illarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hematopoletic cells.";
Oncogene 9:2415-2423(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lood 87:3151-3160(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882 FIVKYRGVSYGPGR 895
                         592
                                                                                                722
                                                                                                                                           759
                                                                                                                                                                                                                                                                     34
147
187
212
222
610
846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥;
                                                                                                                                                                                                                                                                  34
147
187
212
222
610
845
896
                         586
                                                                                             722
                                                                                                                                              759
                                                                                                                                                                                                                     910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thle J.N.;
                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                     VARIANT
                         VARIANT
                                                                                                VARIANT
                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JAK3_MOUSE
JOAK3_MOUSE
JOAK3_MOUSE
JOAK3_MOUSE
DT 10-NOV-
DT 10-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
õ
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM 2 AND ISOFORM 3).
ASASPTEACGSCLQLLEF -> GLSQPHRSLRELLAACWNS
(IN ISOFORM 2 AND ISOFORM 3).
QTPHLASRVLEMSCAWRPALCLPGPRHI -> SDPTPGIPS
                                                                                               TESTES, BRIN AND LIVER.
DOMAIN: POSSESSES TWO PHOSPHOTRANSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
       ASSOCIATED (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
FISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN THE THYMUS WITH SOMEWHAT LOWER LEVELS IN BONE MARROW, SPLEEN, FETAL LIVER AND ADULT CD4-CD8-THYMOCYTES. VERY LOW LEVELS IN ADULT KIDNEY, LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat: Alternative splicing.
550
688
SH2 (ATYPICAL).
732
992
PROTEIN KINASE 1.
1032
1299
RATP (BY SIMILARITY).
1064
ATP (BY SIMILARITY).
1158
BY SIMILARITY).
1189
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
222
238
RVWSPARPTATAHGOVY -> LPCGRLPGRPYALMAKXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM 2 AND ISOFORM 3).
QPTCGSGR -> QAPRVGPAG (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRDELCVAGAQLYACQDPAIF (IN ISOFORM 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM 3).
SKTTGOPOSAP -> EPHDRPAFATLSPQLDPLWRGRPG
SKTTGOPOSAP 2 AND ISOFORM 3).
L-NR: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                           FTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-2 AND IL-4. SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. JAK
SUBCELLULAR LOCATION: WHOLLY INTRACELLULAR, POSSIBLY MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN ISOFORM 3).
VWSPARPTATAHGQVY -> RVVACQADRYI (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> G (IN REF. 2).
S -> P (IN REF. 3).
G -> N (IN REF. 3).
MISSING (IN REF. 3).
K -> N (IN REF. 3).
A -> P (IN REF. 2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                            MGD: MGI:99928; Jak3.
InterPro: IPR000299; Band_4.1.
InterPro: IPR000199; Buk_pkinase.
InterPro: IPR000199; Buk_pkinase.
InterPro: IPR001245; Tyr_kin.
Pfam; PF00069; pkinase; 3.
SMART; SM00295; B41; 1.
SMART; SM00295; B41; 1.
SMART; SM00219; Tyrkc; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00119; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 2.
PROSITE; PS00011; SH2; FALSE_DOM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM 2)
                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; L33768; AAA21415.1; -.
EMBL; L40172; AAC42085.1; -.
EMBL; L32955; AAA21565.1; -.
HSSP; P11362; IFGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1066
62
276
280
282
282
490
550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568
656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1066
62
276
280
282
282
490
550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
491
                                                                                                                                                                                                          SUBFAMILY
                                                                                                                                                              COMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH2 domain;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CINIB AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                           <del>:</del>
```

```
09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCA1_RAT

11D BCA1,

BCA1,

BCA1,

BCA1,

BDT 30-M

DT 30-M

DD CRK-

CR CRC-

CR RATH

CO BUKA

CO BUKA

CO MAINTON

CO MAINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morou-Bermudez E., Burne R.A.; "Genetic and physiologic characterization of urease of Actinomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Actinomycetaceae; Actinomyces.NCBI_TaxID=1655;
                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 271;
                                                                                                                                                                                    Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
EL -> DV (IN REF. 3).
A -> G (IN REF. 2 AND 3).
N -> Y (IN REF. 3).
T -> N (IN REF. 3).
G -> EW (IN REF. 2 AND 3).
R -> S (IN REF. 3).
SG -> OR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 67:504-512(1999).
-!- FUNCTION: PROBABLY FACTLITATES NICKEL INCORPORATION.
-!- SIMILARITY: BELONGS TO THE URED FAMILY.
                                                                                                               -> OR (IN REF. 3)
EFE2D60B6AF3D10C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0042A71CC3F006B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
17;
                                                                                                                                                                                      Score 40; DB 1;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99115518; PubMed=9916052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF056321; AAD13736.1; ... EMBL; AF048781; AAD13726.1; ... InterPro; IPR002669; UreD. Pfam; PF01774; UreD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
SPEC_SCHPO
ID SPEC_SCHPO STANDARD; B
50 04287;
DT 20-AUG-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29247 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last see
30-MAY-2000 (Rel. 39, Last and
UREASE ACCESSORY PROTEIN URED
                                                                                                                                                                                            44.0%;
57.1%;
                                                                                                                                      144314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                44.0
Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                    1091 FIVKYRGVSYGPGR 1104
               560
607
683
706
734
750
                                                                                                                                                                                                                                                                     4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::||| |||::
112 IAYRGASYRQT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 AA;
                                                                                                                                        1299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
               559
607
683
706
734
750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=WVU45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       naeslundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nickel.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  URED_ACTNA
Q92364;
               CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                   URED_ACTNA
                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                           ŏ
                     FT
FT
FT
FT
FT
SQ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licensee(asb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11. Hydrolase; Manganese; Signal; Multigene family.
22 PUTATIVE AGMATINASE 2.
32 MANGANESE I (BY SIMILARITY).
33 MANGANESE I AND 2 (BY SIMILARITY).
34 MANGANESE I AND 2 (BY SIMILARITY).
35 MANGANESE I (BY SIMILARITY).
36 MANGANESE I (BY SIMILARITY).
37 MANGANESE I (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE AGMATINASE 2 PRECURSOR (EC 3.5.3.11) (AGMATINE UREOHYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCAL RAT STANDARD; PRT; 968 AA.
063767; 063766;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SESSTRANCE I PROTEIN).
BCARISTRANCE I PROTEIN).
                                                                                                                                                                                                                                                                                                           Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                         Score 39; DB 1; Length 413;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                        -i - SIMILARITY: BELONGS TO THE ARGINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AL021815; CAA16996.1; -.
HSSP, P53608; 2CEV.
Interpro, IPR000287; Arginase.
Pfam: PF00491; arginase; 2.
PROSITE; PS00147; ARGINASE_1: FALSE_NEG-PROSITE; PS00148; ARGINASE_2: 1.
PROSITE; PS01053; ARGINASE_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fibroblast;
MEDLINE=94349922; PubMed=8070403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 58.3
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
206
229
231
233
331
413 AA;
                                                                                                                                                                                                    Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RWSFRVSYRGIS
                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                            SPBC8E4.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
```

σ

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for a license arrows.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bainformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                       A Tachibana K., Urano T., Fujita H., Ohashi Y., Kamiguchi K., Iwata S., Hirai H., Morimoto C.;

A Hirai H., Morimoto C.;

A Hirai H., Morimoto C.;

AT "Tyosine phosphorylation of Crk-associated substrates by focal adhesion kinase. A putative mechanism for the integrin-mediated tyrosine phosphorylation of Crk-associated substrates.";

J Biol. Chem. 272:29081-22090(1997).

A Biol. Chem. 272:29081-22090(1997).

IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY).

CHORD TYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION.

IMPLICATED IN INDUCTION OF CELL MIGRATION (BY SIMILARITY).

ADAPTER PROTEIN CRKL AND LYN KINASE.

CHARDELULAR LOCATION: FOCAL ADHESIONS AND STRESS FIBERS.

UNPHOSPHORYLATED FORM LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO THE MEMBRANE UPON TYROSINE PHOSPHORYLATION.

CHARD TRODUCTS: 2 ISOSORMS; A LONG ISOSOPOM (SHOWN HERE)

AND A SHORT ISOFORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.

LATESINE SPECIFICITY: WIDELY EXPRESSED. HIGHER EXPRESSION IN LUNG, INFERENT AND METERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING MULTPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN CONTAINING A DIVERSERNT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-BINDING SITES PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS. THE HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF PSEUDOHYPHAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION WITH CASL.
                                           "A novel signaling molecule, pl30, forms stable complexes in vivo with v-Crk and v-Src in a tyrosine phosphorylation-dependent manner."; EMBO J. 13:3748-3756(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN, NECESSARY FOR THE LOCALISATION OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-RICH REGION OF FOCAL ADHESION KINASE 1.
-1- SIMILARITY: CONTAINS 1 SH3-BINDING DOMAIN. THE SH3 BINDING DOMAIN.
BINDS TO THE SRC SH3 DOMAIN.
-1- SIMILARITY: BELONGS TO THE CAS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED TO THE PHOSPHORIAME OTHER TYROSINE PHOSPHORIAME OTHER TYROSINE RESIDUES. TYROSINE PHOSPHORIAMION IS TRIGGERED BY INTEGRIN MEDIAMED ADHESION OF CELLS TO THE EXTRACELLUIAR MATRIX. DISEASE: APPEARS TO HAVE A CENTRAL FUNCTION IN TRANSFORMATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM RESPONSE ELEMENT (SRE).

PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE
., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Mano H.,
f., Hirai H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO-RICH.
SUBSTRATE FOR KINASES.
SER-RICH.
SH3-BINDING (POTENTIAL).
DIVERGENT HELIX-LOOP-HELIX MOTIF.
MISSING (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfan: PF00018; SH3; 1.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 1.
PROSTE: PS50002; SH3; 1.
PROSTPORYLATION; SH3 domain; SH3-binding; Cell adhesion; Alternative splicing.
                                                                                                                                       TYROSINE PHOSPHORYLATION BY FOCAL ADHESION KINASE.
                                                                                                                                                         MEDLINE=98030588; PubMed=9360983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D29766; BAA06169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA06170.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTESTINE AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOME CELL TYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D29766; BAA06
P29354; IGRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
```

```
SQ SEQUENCE 968 AA; 104262 MW; E861641BFD68D377 CRC64;

Query Match 42.9%; Score 39; DB 1; Length 968;

Best Local Similarity 56.2%; Pred. No. 62;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps

Qy 2 WSFRVSYRGISYRRSR 17
```

ö

Search completed: February 12, 2002, 12:39:53 Job time: 806 sec

23 WGPRVSRRPQSYRAAR

q

```
030202 homo sapten
09476 homo sapten
009035 homo sapten
009035 homo sapten
030084 homo sapten
030084 homo sapten
030093 homo sapten
029884 homo sapten
099bp0 aeropyrum p
09ybv0 aeropyrum p
09ywxy fattus norv
09ybv0 aeropyrum p
                                                                                                                                                                                                                          Q9c2kO neurospora
Q9fc87 streptomyce
Q9nf24 caenorhabdi
Q9zs31 solanum tub
                                                chlamydia p
homo sapien
homo sapien
                             arabidopsis
         streptomyce
caenorhabd1
                                       heterodera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Chol E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J.: Lenz C., Li J., Liu A., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveria A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, Ac007881; ARF79360.1; -.
InterPro; IPR00340; B3.
Fiam; PF02362; B3: 1.
SEQUENCE 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                            09m9x1
                                      Q9gpul | Q9mbu4 | Q98201 |
                                                                    029883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker J.R.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F1504.42.
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                             030202
09TQ76
009035
009035
029877
030084
019764
019764
029884
0293093
029884
029884
029884
        Q9AJU2
Q20908
Q9M9X1
Q9GPU1
                                                                                                                                                                                                                                                         092531
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                 Q9K722
                                                                                                                                                                                                                           29C2K0
                                                  09MBU4
                                                                    029883
                                                                                                                                                                                                                                      29FC87
                                                                                                                                                                                                                                               09NF24
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                               52
89
90
106
1106
1108
1229
2229
2229
2239
334
336
3336
53336
53336
53336
53336
53336
53336
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                  09L0E3
                                                                                                                                                                                                                                                                                                                    RESULT
Q9LQE3
Q91qe3 arabidopsis
Q9c7i9 arabidopsis
Q9kmk7 vibrio chol
                                                                              (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                   February 12, 2002, 12:38:41; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LQE3
Q9C719
Q9KMK7
                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                               RWSFRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                     sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ü
                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                           sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
                                                                                                       US-09-485-571-27
91
                                                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
                                                                                                                                                                                                                                                                                                                               sp_fund1:*
                                                                                                                                                                                                                                                                                                SPTREMBL 17:*
                                                                                                                                                                                                                                                                                                                                                                     sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                        Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                           Title:
Perfect score:
                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                Database:
                                                                                                                                                                                  Searched:
                                                                                                                                Sequence:
                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ.
```

Gaps

ö

Score 48; DB 10; Length 570; Pred. No. 8.2; 1; Mismatches 4; Indels

52.7%; 64.3%;

Query Match
Best Local Similarity 64.3
Matches 9; Conservative

Q91nk2 arabidopsis Q926m9 arabidopsis Q9220 gallus m Q4229 gallus gall Q97bt9 burkholderi Q53813 shigella bo Q97s16 deinococcus Q91rr7 homo sapien Q30079 homo sapien Q30097 homo sapien Q30091 arabidopsis Q9hsy4 halobacteri Q9vaq8 drosophila

Q53813 Q9RSL6 Q9TNR7 Q29785 Q30079

Q9RBT9

88 620 620 620 1106 182 318 480

080901 Q9HSY4 Q9VAQ8

Q9LNK2 Q9C8N9 Q17248 O42291 1 RWSFRVSYRGISYR

ò

g

```
VCA0332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.R.
                                                                                                                                                  Complete | SEQUENCE
                                                                                                        cholerae.
                                                                                                                                                                                                                                                                                                                    Q9LNK2
                                                                                                                                                                                                                                                                                               4
                                                                                                                                         TIGE;
                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                          Q9LNK2
                                                                                                                                                                                                                                                                                                                      δλ
ö
                                                                                                                                                                                                                      CSTRAIN=CV. COLUMBIA:

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Chao O., Chen H., Cheuk R.F., Chin C.W.,

A Buehler E., Chan A., Coro D., Chen H., Cheasy T.H., Dewar K.,

A Buehler E., Chan A., Coro D., Chen H., Cheasy T.H., Dewar K.,

A Chung M.K., Conn L., Coroway A.B., Croavay T.H., Dewar K.,

A Lin P., Etgu P., Feldblyum T.V., Feng J.-D., Frong B., Fujii C.Y.,

A Lin P., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A Lin C.J., Xroo H.L., Kreementskaia I., Krurtz D.B., Kwan A., Lam B.,

A Lin C.J., Xroo H.L., Kreementskaia I., Martz D.B., Kwan A., Lin S.A.

A Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Lin S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

A Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Fallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

B Gylence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69755 MW; 817E7D03190622F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PROTEIN VCA0332.
                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB 10;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                     615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AC069160; AAG51458.1; -. InterPro; IPR003311; AUX_IAA. InterPro; IPR003340; B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.6%;
56.2%;
                                                                                                                           HYPOTHETICAL 69.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 408:816-820(2000)
                                                                       PRELIMINARY;
     Query Match
Best Local Similarity
Local 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09KMK7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9KMK7
                                                                        Q9C719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Q9KMK7
                                                   RESULT
09C719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                         δλ
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Altafi H., Bel B., Chin C., Chiou J., Chol E., Chan S., Kim C., Altafi H., Bel B., Chin C., Chiou J., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Gonn L., Conway A., Gonzalez A., Liu A., Liu S., Wukharsky N., Lee J., Lenc C., Li J., Liu S., Wukharsky N., Lee J., Lenc E., Pham P., Sakano H., Schwartz J., Southwick A., Thaveni A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome
STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406633; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Frase C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                               UNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theologis A., Ecker J.; Submitted (JUV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AC032279; AAF79263.1; Interpro; IPR003340; B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AA; 10092 MW; B173D34A34B6A870 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F12K21.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.5; DB Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 WSFRVSYRG----ISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 WSGVITYRGTNIRIISVRRSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.9%;
                                                                                                                                                                                                                                                                                                                                                                          Mature 406:477-483(2000).
EMBL; AE004371; AAF96240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
```

Page

SEQUENCE

S

-JUN-2001 01-JUN-2001 01-JUN-2001

09C8N9; Q9C8N9

RESULT Q9C8N9

ò g

```
TISSUE-WHOLE TICKS;
Whitfeld P.L., Johnson M.C., Smith D.R.J., Snelson V.J., Clifton G.F.,
Whitfeld P.L., Johnson M.C., Smith D.R.J., Snelson V.J., Clifton G.F.,
Brown G.S., Calirs D., Foy A.B., Irving D.O.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U62809; AAB04998.1;
InterProv. IPRO01548;
Pam: PF01401; Peptidase_M2.
Pfam: PF01401; Peptidase_M2.
PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                 Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acarl;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 13; Length 1106;
Pred. No. 1.1e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sofer L., Mampa D., Burnside J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF034576; AAC34195.1; -.
HSSP; P12931; IFMK.
InterPro; IPR000299; Band_4.1.
InterPro; IPR000299; Euk_Pkinase.
InterPro; IPR001996; SH2.
InterPro; IPR001245; Tyr_kin.
Pfam; PF00069; pkinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase, Tyrosine-protein kinase.
106 AA; 124750 MW; 004F75F851A282B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
6F164CF70C938E63 CRC64;
     ANGIOTENSIN-CONVERTING ENZYME-LIKE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 5;
Pred. No. 65;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00295; B41; 1.
SMART; SM00252; SH2; 1.
SMART; SM00219; TyrKc; 1.
PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 2.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD004184; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TEMBLrel. 05, La. 01-JUN-2001 (TEMBLrel. 17, Las. JANUS TYROSINE KINASE. JAK. Galling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 Po
75257 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.3%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.3
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 WEYRIKYQGVS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 WSFRVSYRGIS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=SPLEEN;
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                        NCBI_TaxID=6941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
SEQUENCE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 042291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04229:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            042291
     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATHDOOR NAME OF THE PARTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RC STRAIN—CV. COLUMBIA.

RX MEDLINE—21016719; PubMed=11130712;

RA THOLOGIS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA THOLOGIS A., Cane J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Ching M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fulii C.Y.,

RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

RA Langin Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin Hooper S., Lie A., Lu Z.A., Luros J.S., Maiti R., Marziali A.,

Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Millischer J., Miranda M., Nguyen M., Ngoney T., Rowley D.,

RA Sun H., Tallon L.J., Tambunga G., Torlumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RY "Sequence and analysis of chromosome 1 of the plant Arabidopsis

RY InterPro; IPR003311; AA651897.1; -.

BR InterPro; IPR003311; AA651897.1; -.

BR InterPro; IPR003311; ANY. IAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 620;
                                                                                   Length 620;
                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF02362; B3; 1.
INCE 620 AA; 70555 MW; 88484FF185EBED3F CRC64;
  70895 MW; C2FE2FAFDEC006DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 9
                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              660 AA
                                                                                                                                                                                                                                                                                                                                                                                 620 AA
                                                                                Score 44; DB
Pred. No. 42;
                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last
AUXIN RESPONSE FACTOR, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   017248 PRELIMINARY;
017248;
01.NOV-1996 (TrEMBLrel. 01, Cr
01.NOV-1996 (TrEMBLrel. 01, La
01.JUN-2001 (TrEMBLrel. 17, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.4%;
50.0%;
                                                                                48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02309; AUX_IAA; 1.
                                                    Ouery Match
Best Local Similarity 50.v.
There is a Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 50.00
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| || :||| | |
187 QWRFRHNYRGTPQRHS 202
                                                                                                                                                                                                                        1 RWSFRVSYRGISYRRS 16
                                                                                                                                                                                       1 RWSFRVSYRGISYRRS 16
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
620 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
```

SEQUENCE

9

RESULT Q17248

25222

g

ð

ö

Gaps

ö

ö

Gaps

480 AA.

RESULT

g

```
ATRAIN=R1;
MEDILINE=20036896; PubMed=10567266;
Medicine=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Law D., Medicine M.C., Richardson D.L.,
Modfat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makartova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Metchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       Bacteria: Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the radioresistant bacterium Deinococcus radiodurans \mathrm{Rl}\,.\,"\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                52430 MW; B67C9175AAC14281 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HLA-DQB1*0501 BETA CHAIN-MHC CLASS II ANTIGEN.
                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-UUN-2001 (TrEMBLrel. 17, Last annotation update) MOLYBDATE METABOLISM REGULATOR FELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2
Pred. No. 68;
1; Mismatches
                                                       Created)
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                       Science 286:1571-1577(1999).
EMBL: AE002046; AAF11657.1; -
TIGR; DR2108; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                     01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 WMVRVDARGVYYGHSR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WSFRVSYRGISYRRSR 17
                                                                                                                                  Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. SEQUENCE 480 AA;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                     Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9TNR7
             Q9RSL6
ID Q9RSL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
09TNR7
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-91286192; PubMed-2061288; MEDLINE-91286192; PubMed-2061288; Tominaga A., Ikemizu S., Enomoto M.; Tominaga A., Ikemizu S., Enomoto M.; Since specific recombinase genes in three Shigella subgroups and mucleotide sequences of a pinB gene and an invertible B segment from Shigella boydii.";
                                                                                                                                                                                                                                                                                                                           Yabannavar A., Zylstra G.J.;
Yabannavar A., Zylstra G.J.;
"Analysis of the genes for p-nitrobenzoate degradation from Ralstonia pickettii YH105."
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187879; AAF01444.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
BY GENE PRODUCT (FRAGMENT).
Shigella boydil.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                       Burkholderia pickettii (Pseudomonas pickettii).
Bacteria: Proteobacteria: beta subdivision; Raistonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA; 34335 MW; 93CC950314D4E275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        182 AA; 20053 MW; 45FA1636CAC43E06 CRC64;
                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
P-HYDROXXLAMINOBENZOATE LYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%; Score 42; DB 2;
43.8%; Pred. No. 24;
Live 3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                       182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 173;4079-4087(1991).
EMBL: D00660; BAA00555.1; -.
NON_TER 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRVNYRNGGIFYRSAR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRVSYR--GISYRRSR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : | :|||||
|63 WAANIDIEGPNYRRSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 WSFRVSYRGISYRRSR 17
                                                                                                                        PRELIMINARY;
                                   4 FRVSYRGISYRRSR 17
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=YH105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=621;
                                                                                                                                                                                                                                                                                NCBI_TaxID=329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                   Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q53813
Q53813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
                                                                                                                                            09RBT9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                             Q9RBT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q53813
```

q õ

δy

ó

Gaps

; 0

Length 480;

2;

93 AA.

PRT;

ഗ

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q30080
Q30080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               030080
                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97083137; PubMed=8929711;
Yasunaga S., Kimura A., Hamaquchi K., Ronningen K.S., Sasazuki T.;
"Different contribution of HLA-DR and -DO genes in susceptibility and resistance to insulin-dependent diabetes mellitus (IDDM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS II HLA-DQ-BETA-I FIRST DOMAIN MRNA (DRW6,DQM1.9), PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88145646; PubMed-2894075;
Sinha A., Braulbar C., Szafer F., Friedmann A., Tzfoni E.,
Todd J.A., Steinman L., McDevitt H.O.;
"A newly characterized HLA DO beta allele associated with pemphigus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 239:1026-1029(1988).

-!- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).

-!- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN,
BETA-1 DOMAIN INTERPRO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 94;
                  Length 93;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 AA; 11169 MW; 65EBB6D0400BED61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                  Score 41; DB 7;
Pred. No. 17;
3; Mismatches
                                                                                                                                                                                                                                         94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M19239; AAA52319.1; -.
InterPro; IPR000353; MHC_II_beta.
Pfam; PF000969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC; MHC_II]; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                         PRT;
                  45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01,
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                1 RWSFRVSYRGISYRR 15
                                                                                                                   1 :: |:||| ||
79 RHNYEVAYRGILQRR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: |:|||| ||
80 RHNYEVAYRGILORR
Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      CDS (FRAGMENT).
HLA-DQB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA-DQB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                  Q29785
Q29785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 030079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
030079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930079
                                                                                                                                                                                             | CONTROL | CONT
                                                                                                ò
                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yasunaya S., Kimura A., Hanguchi K., Ronningen K.S., Sasazuki T.;
Yasunaya S., Kimura A., Hanguchi K., Ronningen K.S., Sasazuki T.;
"Different contribution of HLA-DR and -DO genes in susceptibility and
resistence to insulin-dependent diabetes mellitus (IDDM).";
Tissue Antigens 47:37-48 (1996).
-!- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DONAIN.
Tissue Antigens 47:37-48(1996).
-!- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SINILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN, BETA L DOMAIN INTERPRO FAMILY.

EMBL; L.4103; AAC41971.1; -.

HSSP; F06343; IIAK.
                                                                                                                                        -!- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN, BETA-1 DOMAIN INTERPRO FAMILY.

EMBL; L34102; AAC41970.1; -.

HSSP; P06343; 11A2.

Interpro; IPR003597; Ig_c1.

Interpro; IPR000353; MHC_II_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26337 MW; B494C32F3D782F08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AA; 26318 MW; 64A5452E72F4BD45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLASS II HLA-DQ-BETA-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ore 41; DB 7
ed. No. 44;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC; 1.
Glycoprotein; MHC; MHC II; Transmembrane.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 1g; 1.

Pfam; PF00969; MHC_II_beta; 1.

Probom; PD000328; MHC_II_beta; 1.

SMART: SMO407; IGcl, 1.

PROSITE; PS00290; IGc_MHC; 1.

Glycoprotein; MHC; MHC II; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINZ-97083137; Pubmed-8929711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 19; 1.
Pfam; PF00069; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
SWART; SM00407; IGG1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000353; MHC_IL_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 RHNYEVAYRGILORR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
```

Length 229;

DB 7;

45.1%; Score 41;

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative splicing; Glycoprotein; MHC; MHC II; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.1%; Score 41; DB 7; Length 237; Best Local Similarity 53.3%; Pred. No. 46; Matches 8; Conservative 3; Mismatches 4; Indels
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER 1 1
SEQUENCE 237 AA; 27038 MW; 460B63ABCA7BC8EA CRC64;
                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MHC CLSS II HLA-DQ-BETA-1 (FRAGMENT).
                              4;
                                                                                                                                                                                                                                                                                        237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 12, 2002, 12:38:42 Job time: 755 sec
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: |:|||| ||
80 RHNYEVAYRGILORR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RWSFRVSYRGISYRR 15
                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                        1 RWSFRVSYRGISYRR 15
                                                                                                                               | :: |:|||| ||
80 RHNYEVAYRGILQRR 94
                                                                                                                                                                                                                                       RESULT 15
030097
AC 030097
DT 01-NOV-
DT 01-
                                                                                                                                                                                                                                                                                                 030097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                        ΩD
                                                                                                    δ
```

```
1
                                                                                                                          February 12, 2002, 12:30:33 ; Search time 242.57 Seconds
(without alignments)
5.191 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                            522463
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                        1 RSRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                     US-09-485-571-30
91
                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14:
15:
16:
                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                         OM protein
                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	DB ID Description	7 20 AAW99415 Tachyplesin deriva	18 AAW23770 Tachytegrin and/or	18 AAW23769 Tachytegrin and/or	21 AAG48001	21 AAG48000	22 AAB86197	21 AAB41819	22 AAM39298	22 AAM39299	22 AAB94096	700
	Query Match Length DB ID	17 20	19 18	19 18	66 21						734 22	
de	Query Match L	100.0	48.4	48.4	46.2	46.2	45.6	45.1	45.1	45.1	45.1	
	Score	91	44	44	42	42	41.5	41	41	41	41	,
	Result No.		7	m	4	2	9	7	æ	6	10	

10488 11029 11129 11129 1183 3398 41129 4217 4217 4217 4217 4217 1198 1198 1198 1198 1198 1198 1198 11	Human polypeptide	ALIGNMENTS de; 17 AA. y) eptide SM2310. tide antibiotic; beta-sheet; secondary structure; ody; ribozyme; antitumour agent; antiviral; l; cell membrane; passive transport; cytoplasm; rier. 757. 297. Grassy G, Kaczorek M;
A A A A A A A A A A A A A A A A A A A	41 45.1 1048 41 45.1 1048 41 45.1 11029 40 44.0 44.0 18 40 44.0 398 40 44.0 427 40 44.0 427 40 44.0 855 38 41.8 254 38 41.8 268	AAW99415 standard; pept AAW99415; 08-JUN-1999 (first ent Tachyplesin derivative Linear; tachyplesin; pe alisulphide bridge; anti anti-inflammatory; mann anti-inflammatory; mann anti-inflammatory; mann anti-inflammatory; mann AO9907728-A2. 18-FEB-1999. 06-AUG-1998; 98WO-FRC 12-AUG-1997; 97FR-001 (SYNT-) SYNT:EM SA. Calas B, Chavanieu A,

```
AAW23769;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
×555555555555555
                                                                                                                                                                                                                                                                                                                                                                                0;
                             This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antibudur agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cpds. based on protegrin(s) and tachyplesin(s) - designated tachytegrin(s) and parevin(s), useful as antimicrobial and antiviral agents, e.g. for treatment of sexually transmitted diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protegrin; tachyplesin; antimicrobial; antiviral; oral mucositis; sexually transmitted disease; endotoxin; HIV; Staphylococcus aureus; Pseudomonas; H. pylori; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; Trichomonas vaginalis; Herpes simplex type 2; animal; plant.
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 91; DB 20; 100.0%; Pred. No. 1e-07;
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Optionally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachytegrin and/or parevin compound peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page 44; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23770 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Optional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label = MeGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= MeGly
          Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US11323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0000898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 rsrrysigrysvrfswk 17
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-108914/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gu CL,
                                                                                                                                                                                                                                                                                             17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9702287-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW23770;
                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A NO DE SAN CONTRA CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                 \mathbb{Z}_{\times}^{\times}
```

```
The present sequence represents a peptide sequence found in compounds based on protegrins and tachyplesins, designated tachytegrins and parevins. The present sequence is from a tachytegrin as the peptide has correctly residues at positions a parevins have Cys residues at positions 5 and 16. Both compounds can be used as preservatives (e.g. positions 5 and 16. Both compounds can be used as preservatives (e.g. in foodstuffs, cosmetics or medicaments) or in treatment of viral or microbial infection in animals or plants. They are useful, e.g. in microbial infection in animals or plants. Taphylococcus aureus, treatment of oral mucositis, infection by Staphylococcus aureus, those caused by Chlamydia trachomentis, Treponema pallidum, Neisseria, gonorrhoeae, Trichomonas vaginalis, Herpes simplex type 2 and HIV. DNA encoding the compounds can also be expressed in situ, in animals or plants, to combat infections. The compounds can also be used as standards in antimicrobial assays and in binding endotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a peptide sequence found in compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cpds. based on protegrin(s) and tachyplesin(s) - designated tachytegrin(s) and parevin(s), useful as antimicrobial and antiviral agents, e.g. for treatment of sexually transmitted diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protegrin; tachyplesin; antimicrobial; antiviral; oral mucositis; sexually transmitted disease; endotoxin; HIV; Staphylococcus aureus; Pseudomonas; H. pylori; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; Trichomonas vaginalis; Herpes simplex type 2; animal; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 18; Length 19;
Pred. No. 2;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Optionally amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachytegrin and/or parevin compound peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
4..17
/label= Optional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW23769 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang CC, Gu CL, Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US11323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :||: |||
ryxvgrfxvrf 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
```

```
99US-0139454.
99US-0139455.
99US-0139456.
                                                                                                                                                                                                                                                                                                                                                                 99US-0139763.
99US-0139817.
99US-0139899.
                                                                                        99US-0136392
99US-0136782
                                                                                                                                                                      99US-0138540
99US-0138847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0143542
99US-0143624
                     99US-0134768
                                            99US-0135124
99US-0135353
                                                                  99US-0135629
99US-0136021
                                                                                                               99US-0137222
                                                                                                                          99US-0137528
                                                                                                                                                 99US-0137724
                                                                                                                                                          99US-0138094
                                                                                                                                                                                             99US-0139119
                                                                                                                                                                                                       99US-0139452
                                                                                                                                                                                                                    99US-0139453
                                                                                                                                                                                                                              99US-0139492
                                                                                                                                                                                                                                                                                     99US-0139458
                                                                                                                                                                                                                                                                                                 99US-0139459
                                                                                                                                                                                                                                                                                                           99US-0139460
                                                                                                                                                                                                                                                                                                                                           99US-0139463
99US-0139750
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0140354
                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0140695
99US-0140823
                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0140991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0141842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0144325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0144814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0145086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0145085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0145276
                                                                                                                                      99US-0137502
                                                                                                                                                                                                                                                                                                                                                                                                   99US-0140353
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0141287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0145224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99us-01
         14 - MAY - 1999)

18 - MAY - 1999)

20 - MAY - 1999)

21 - MAY - 1999)

22 - MAY - 1999)

25 - MAY - 1999)

26 - MAY - 1999)

27 - MAY - 1999)

28 - MAY - 1999)

30 - JUN - 1999)

30 - JUN - 1999)

31 - JUN - 1999)
                                                                                                                                                                                                                                     18 - JUN - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999;
16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                           18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999;
21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .9-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-1999,
23-JUL-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                          24 - JUN - 1
                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
        parevins. The present sequence is from a tachytegin as the peptide has Cys residues at positions 4 and 17, where parevins have Cys residues at positions 5 and 16. Both compounds can be used as preservatives (e.g. in foodstuffs, cosmetics or medicaments) or in treatment of viral or microbial infection in animals or plants. They are useful, e.g. in freatment of oral mucositis, infection by Staphylococcus aureus, Pseudomonas or H. pylori, or sexuelly transmitted diseases, including those caused by Chlamydia trachomatis, Treponema pallidum, Neisseria gonorrhoeae, Trichomonas vaginalis, Herpes simplex type 2 and HIV. DNA encoding the compounds can also be expressed in situ, in animals or plants, to combat infections. The compounds can also be used as standards in antimicrobial assays and in binding endotoxins.
                                                                                                                                                                                                                    Gaps
based on protegrins and tachyplesins, designated tachytegrins and
                                                                                                                                                                                                                  ;
                                                                                                                                                                                          Score 44; DB 18; Length 19; Pred. No. 2;
                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 60568.
                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                     AAG48001 standard; Protein; 66 AA
                                                                                                                                                                                             48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0128234.
99US-0128714.
99US-0129845.
99US-0130077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0130449.
99US-0130510.
99US-0130891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0126785
99US-0127462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0131449
99US-0132048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0132407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0132486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132863
99US-0134256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0134218
99US-0134219
                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                                           Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                       4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                     || :||: |||
6 rykvgrfkvrf 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1999
                                                                                                                                                                                                                                                                                                                                           AAG48001;
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                             RESULT
AAG48001
ID AAG4
                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                             g
```

```
PR 27-JUL-1999; 99US-0145918.
PR 72-JUL-1999; 99US-0145918.
PR 72-JUL-1999; 99US-0145918.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146386.
PR 04-AUG-1999; 99US-0147302.
PR 06-AUG-1999; 99US-0147302.
PR 13-AUG-1999; 99US-0147302.
PR 13-AUG-1999; 99US-0147302.
PR 13-AUG-1999; 99US-014743.
PR 13-AUG-1999; 99US-014473.
PR 13-AUG-1999; 99US-014473.
PR 13-AUG-1999; 99US-0144726.
PR 13-AUG-1999; 99US-0149723.
PR 13-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151070.
PR 13-AUG-1999; 99US-0153758.
PR 23-SEP-1999; 99US-0153758.
PR 23-SEP-1999; 99US-0153758.
PR 23-SEP-1999; 99US-0153758.
PR 23-SEP-1999; 99US-0153729.
PR 13-CCT-1999; 99US-0155753.
PR 14-CCT-1999; 99US-0155753.
PR 14-CCT-1999; 99US-0155753.
PR 14-CCT-1999; 99US-0155753.
PR 14-CCT-1999; 99US-0155753.
PR 13-CCT-1999; 99US-01557753.
PR 13-CCT-1999; 99US-01557753.
PR 14-CCT-1999; 99US-01557779.
PR 13-CCT-1999; 99US-01557779.
PR 13-CCT-199
```

```
ö
                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                 Gaps
                                                                                                 ö
                                                                                 21; Length 66;
                                                                                                  4; Indels
                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 60567.
                                                                                 Score 42; DB;
Pred. No. 14;
3; Mismatches
                                                                                                                                                                           AAG48000 standard; Protein; 87 AA.
                                                                                                                                                                                                                                                                                                                                              990s-0121825.
990s-0123180.
990s-012548.
990s-012664.
990s-0126785.
990s-0126785.
990s-0128714.
990s-0128714.
990s-0130077.
990s-0130077.
990s-0130891.
990s-0131891.
990s-0131891.
990s-0131891.
990s-0131881.
990s-0132485.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132486.
990s-0132487.
990s-0134788.
99US-0161405.
99US-0161359.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161361.
99US-0161992.
99US-0161993.
                                                                                    46.28;
                                                                                                                                                                                                                                                                                                                               2000EP-0301439
                                                                                                                                                                                                               (first entry)
                                                                                                  6; Conservative
                                                                                                                               :|:||| : |||
37 fslgryfislpwk 49
                                                                                                                     5 YSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 - APR - 1999;
30 - APR - 1999;
30 - ARR - 1999;
05 - MAX - 1999;
06 - MAX - 1999;
06 - MAX - 1999;
11 - MAX - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                 EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999
                                                                                                                                                                                                               18-OCT-2000
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                              AAG48000;
                                                                                                                                                               Ŋ
                                                                                                                                                               RESULT
AAG48000
                                                                                                                                                                                        g
                                                                                                                        ŏλ
     PR
PR
PR
PR
PR
PR
```

·	
9905-0147038 9905-0147302. 9905-0147302. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147303. 9905-0147311. 9905-0148341. 9905-0148341. 9905-0148341. 9905-0148341. 9905-0148341. 9905-0148341. 9905-0148341. 9905-014836. 9905-0149368. 9905-0149368. 9905-0149368. 9905-0151065. 9905-0159231. 9905-0159231. 9905-0159231. 9905-0159231. 9905-0159231. 9905-0159231. 9905-0159231. 9905-0159231.	99US-0161406. 99US-0161359. 99US-0161360. 99US-0161361. 99US-0161992.
03 AUG-1999 04 AUG-1999 05 AUG-1999 06 AUG-1999 06 AUG-1999 06 AUG-1999 07 AUG-1999 08 AUG-1999 09 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 AUG-1999 16 AUG-1999 17 AUG-1999 18 AUG-1999 19 AUG-1999 10 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 SEP-1999 16 SEP-1999 17 AUG-1999 18 AUG-1999 19 AUG-1999 10 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 SEP-1999 16 AUG-1999 17 AUG-1999 18 AUG-1999 19 AUG-1999 10 AUG-1999 11 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 SEP-1999 16 AUG-1999 17 AUG-1999 18 AUG-1999 18 AUG-1999 19 AUG-1999 19 AUG-1999 10 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 AUG-1999 16 AUG-1999 17 AUG-1999 18 AUG-1999 18 AUG-1999 18 AUG-1999 19 AUG-1999 19 AUG-1999 10 AUG-1999 10 AUG-1999 11 AUG-1999 12 AUG-1999 13 AUG-1999 14 AUG-1999 15 AUG-1999 16 AUG-1999 17 AUG-1999 18 AU	25-OCT-1999; 26-OCT-1999; 26-OCT-1999; 26-OCT-1999; 28-OCT-1999;
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	ች የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ የ
990S - 0136021 990S - 0136392 990S - 0136392 990S - 0137222 990S - 0137222 990S - 0137222 990S - 0137222 990S - 0137528 990S - 0137528 990S - 0137528 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139455 990S - 0139452 990S - 0139455 990S - 0140353 990S - 0140353 990S - 0144332 990S - 0144335 990S - 01445085 990S - 0145085 990S - 0145085 990S - 0145085 990S - 0145085 990S - 0145085	99US-0145919 99US-0145919 99US-0146386 99US-0146388 99US-0146389

22-MAY - 1999 23-MAY - 1999 24-MAY - 1999 01-JUN - 1999 03-JUN - 1999 04-JUN - 1999 07-JUN - 1999 16-JUN - 1999 16-JUN - 1999 18-JUN - 1999 19-JUL - 1999 22-JUL - 1999 19-JUL - 1999 23-JUL - 1999 24-JUL - 1999 25-JUL - 1999 26-JUL - 1999 27-JUL - 1999 28-JUL - 1999 28-JUL

ï

Gaps

1;

28-OCT-1999; 29-OCT-1999;

9

Matches

```
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

which represent the human ORFX open reading frames 1 to 3161. The ORFX
continoses have activities such as: cytostatic; hepatotropic; vulnerary;
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipostiatic; antipostiatis antiathritic; immunosuppressant;
costeopathic; anticonvulsant; antiathritic; immunosuppressant;
contidiabetic; hypotensive; dermatological; immunosuppressive;
antidiabetic; hypotensive; dermatological; immunosuppressive;
antithyroid; and antianaemic. The sequences can be used for determining
antithyroid; and antianaemic. The sequences can be used for determining
the presence of or predisposition to, or preventing or treating
the presence of or predisposition to, or preventing or treating
pathological conditions associated with an ORFX-associated disorder. The
public acids can be used to express ORFX proteins in gene therapy
conclierative disorders, neurodegenerative disorders, osteoarthritis,
confiderative disorders, neurodegenerative disorders mellitus,
cardiovascular disease, diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppessant; cardiant; minunosuptant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitinacterial; antifungul; antirheumatic; antithyroid; antitinacterial; antifungul; antirheumatic; antithyroid; cancin; encuodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; StDD; cardiovascular disease; diabetes mellitus; hypothyroidism; StDD; severe combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombolic; contrareactive; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
Indels
                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF1583 polypeptide sequence SEQ ID NO:3166.
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 2383-2384; 5507pp; English.
  Mismatches
                                                                                                                                                                                                           AAB41819 standard; Protein; 717 AA.
    4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127607.
99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thrombosis; contraceptive.
                                               1 RSRRYSIGR-YSVRFSWK 17
                                                                                                                                                                                                                                                                                                         08-FEB-2001 (first entry)
    Conservative
                                                                                 :| |||| | : : :||
607 qsyrysisrtytcghnwk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC76028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-ocr-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1999;
         ..
6
                                                                                                                                                                                                                                                                  AAB41819;
              Matches
                                                                                                                                                                                               AAB41819
                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the immunodeficiency virus type 1 subtype C/B' which can be used for the induction of specific humoral and cellular immune responses. (I) and induction of specific humoral subtype control of the statement of prevention of human immune deficiency virus-1 (HIV-1) infections, also for rational of human immune deficiency virus-1 (HIV-1) infections, also for rational continuant of test or therapeutic reagents, or gene therapy vectors.

The polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence crepresents a protein encoded by the HIV-1 subtype C genome described in the method of the invention.
                                                                                                                                   ö
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection; diagnosis; human; humoral immune response; antiviral; cellular immune response; vaccine; treatment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41.5; DB 22; Length 3025; Pred. No. 8.1e+02;
                                                                                                                                        ö
                                                                                      DB 21; Length 87;
19;
                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Xaa represents a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHAO/) SHAO Y.
(GENE-) GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
                                                                                                                    pred. No. 19;
3; Mismatches
                                                                                                Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wagner R, Wolf H, Shao Y, Graf M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1 subtype C protein fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..3025
/label= Xaa
                                                                                                                                                                                                                                                                                                                                                      AAB86197 standard; Protein; 3025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6%;
50.0%;
                                                                                                46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-2000; 2000DE-1056747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99DE-1055089
                      99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                               Conservative
                                                                                                                                                                                                                            :|:||| : |||
58 fslgryfislpwk 70
                                                                                                                                                                                            5 YSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-336417/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3025 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                     Query Match
Best Local Similarity
```

Misc-difference

21-AUG-2001

AAB86197;

9

RESULT AAB86197

a ò

DE10056747-A1

31-MAY-2001.

16-NOV-1999;

infection

Sednence

Query Match

```
555555555555
                                                                                                                                                                                                               QQ
                                                                                                                                                                                                                                                                              ò
                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F, W
Zhang J;
                                                                                                                              ö
                                                                                                        Length 717;
                                                                                                       Score 41; DB 21; Length 71
Pred. No. 2.3e+02;
; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ten R, Ma Y, (
tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 2443; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, us such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    χα c,
                                                                                                                                                                                                                        AAM39298 standard; Protein; 717 AA
                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 2443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                              .,
S
                                                                                                         45.18;
37.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000us-0488725.
2000us-0552317.
2000us-059842.
2000us-0620312.
2000us-0653450.
2000us-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0727344
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                             :||:| |:: | |:
420 arrfsaggwearrgwr 435
                                                                                                                              6; Conservative
                                                                                                                                                 2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                         717 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI58454
                                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000;
                                                                                                                                                                                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
Wang J, W
Zhao QA,
                                                                          Seguence
                                                                                                                                                                                                                                             AAM39298
                                                                                                                              Matches
                                                                                                                                                                                                                AAM39298
                                                                                                                                                                                                     RESULT
  88888888
                                                                                                                                                   ò
                                                                                                                                                                     g
```

```
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treating disorders
localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
;
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F,
Zhang J
                                                                                                                                                                                                                                                                                                         Score 41; DB 22; Length 717;
Pred. No. 2.3e+02;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ten R, Ma Y, (
tu C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 2444; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.3e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and polypeptides, us
such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM39299 standard; Protein; 734 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                                                                                                             45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0488725
2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         :||:| |:: | |:
420 arrfsagqwearrgwr 435
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-442253/47.
                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                          717 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu C,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI58455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                               specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O.
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM39299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΥΤ',
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03 - AUG ..
                                                                                                                                                                            Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM39299
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonclectide complementary trand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonuclectide comprises at least 15 nucleotides; or (b) a combination
immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous that a coalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thiombolytic activity, chemoclactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                     C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K, Yamamoto J;
Otsuki T;
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                           Score 41; DB 22; Length 734;
Pred. No. 2.38+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; SEQ ID 14312; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T, Hayashi K, Si
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:14312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB94096 standard; Protein; 734 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11.-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                      45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   437 arrfsaggwearrgwr 452
                                                                                                                                                                                                                                                                                                         2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota T, Isogai T, Nisl
Ishii S, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                         734 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB94096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB94096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                       8
```

```
complementary strand of a polynucleotide which comprises a 5 -end complementary strand of a polynucleotide which comprises a 5 -end comprised and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3 -end sequence, where the polynucleotide which comprises a 3 -end sequence, where the compination of oligonucleotide which comprises a 1 -east 15 nucleotides and the compination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for the particularly full-length conwas. The primers are also useful for the checking and/or diagnosis of the abnormality of the proteins encoded by the full-length conwas. The primers allow obtaining of the full-length conwas assily without any specialised methods. AnH03166 to AAH13632 AAH13633 represent human amino acid sequences; and AAH13632 to AAH13632.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F,
                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                      Score 41; DB 22; Length 734;
Pred. No. 2.3e+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R, Ma Y, C
, Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM41084 standard; Protein; 738 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 6015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0652191.
19-CT-2000; 2000US-0633036.
29-NOV-2000; 2000US-0737344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       :||:| |:: | |:
437 arrfsagqwearrgwr 452
                                                                                                                                                                                                                                                                                                                                                                                                              2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                  of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI60240
                                                                                                                                                                                                                                                                                                     734 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang J, W
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM41084;
                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM41084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                      δλ
```

```
99US-0130510
99US-0130891
  2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                    N-PSDB; AAI60241
                                                                                                                                                                                                                                                                                                                                                                                                                       C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG42154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG42154
    80 X C C C C C C C C C C C C X S X F F X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F R X F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                      The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity and Shy-Drager Syndrome other uses include the Activinibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                         C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ren F, W.
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 22; Length 73:
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen R, Ma Y,
Xu C, Xue AJ,
                                       Example 2; SEQ ID NO 6015; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM41085 standard; Protein; 738 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 6016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||:| |:: | |:
437 arrfsagqwearrgwr 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, P
Wang 2, V
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM41085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 8
9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
ò
```

```
in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinolibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, concer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 22; Length 738;
Pred. No. 2.3e+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 52535.
                                                                                                          Example 2; SEQ ID NO 6016; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG42154 standard; Protein; 1048 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0127462.
99US-0128234.
99US-0128714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0123180
99US-0123548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0125788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0126264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0126785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0130077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||:| |:: | |:
437 arrfsaggwearrgwr 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
```

99US - 0131449 99US - 0132404 99US - 0132404 99US - 0132484 99US - 013248 99US - 013286 99US - 013286 99US - 013428 99US - 013428 99US - 013428 99US - 013428	99US-013553. 99US-013529. 99US-013629. 99US-013621. 99US-0136321. 99US-013722. 99US-013722. 99US-013722. 99US-0137528. 99US-0137528. 99US-0138640. 99US-0138452. 99US-0138452. 99US-0139452. 99US-0139452. 99US-0139453. 99US-0139456. 99US-0139456. 99US-0139459. 99US-0139458. 99US-0139459. 99US-0139459. 99US-0139463. 99US-0139463. 99US-0139463. 99US-013963. 99US-013963. 99US-013963. 99US-013963. 99US-013963. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354. 99US-0140354.	99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144 99US-0144
8-APR-1999; 80-APR-1999; 80-APR-1999; 90-APR-1999; 90-MAY-1999; 90-MAY-1999; 90-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999; 91-MAY-1999;	22-MAY-1999; 24-MAY-1999; 28-MAY-1999; 28-MAY-1999; 01-UUN-1999; 04-UUN-1999; 04-UUN-1999; 06-UUN-1999; 16-UUN-1999; 16-UUN-1999; 16-UUN-1999; 18-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 19-UUN-1999; 118-UUN-1999; 118-UUN-1999; 118-UUN-1999; 118-UUN-1999; 118-UUN-1999; 118-UUN-1999; 118-UUN-1999;	10-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999;
	2	

99US-0144814 99US-0145086 99US-0145088 99US-0145087 99US-0145087 99US-0145145 99US-0145145 99US-0145214 99US-0145218	990S-0146886. 990S-0146888. 990S-0146888. 990S-0147204. 990S-0147204. 990S-0147192. 990S-0147460. 990S-0147463. 990S-0147463. 990S-0147463. 990S-0147463. 990S-0147463. 990S-0147463. 990S-0147766. 990S-014884. 990S-014992. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0150866. 990S-0150866. 990S-0150866. 990S-0150866. 990S-0151889.	990s-0150 990s-01540 990s-01540 990s-01554 990s-01554 990s-0156 990s-01570 990s-01570 990s-01580 990s-0159 990s-0159 990s-0159 990s-0159 990s-0159 990s-0159
21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999;	28-001-1999; 02-A0G-1999; 02-A0G-1999; 04-A0G-1999; 04-A0G-1999; 06-A0G-1999; 06-A0G-1999; 06-A0G-1999; 06-A0G-1999; 11-A0G-1999; 11-A0G-1999; 11-A0G-1999; 11-A0G-1999; 11-A0G-1999; 20-A0G-1999; 20-A0G-1999; 20-A0G-1999; 20-A0G-1999; 21-A0G-1999; 22-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 23-A0G-1999; 25-A0G-1999; 25-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 27-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999; 28-A0G-1999;	13-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 24-SEP-1999; 28-SEP-1999; 06-OCT-1999; 06-OCT-1999; 07-OCT-1999; 12-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999;
	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	

```
990S-013724
990S-0138094
990S-0138847
990S-0138847
990S-0139119
990S-0139452
990S-0139452
990S-0139455
990S-0139455
                                                          990S-0134941.
990S-0135124.
990S-0135353.
990S-0135629.
990S-0136021.
990S-0136782.
                                                                                                                                                                                                                                               99US-0139458.
99US-0139459.
99US-0139460.
                                                                                                                                                                                                                                                                                                                                                                          990S-0141287.
990S-0141842.
990S-0142154.
990S-0142055.
                                                                                                                    99US-0137222.
99US-0137528.
99US-0137502.
                                                                                                                                                                                                                                                                                        99US-0139463.
99US-0139750.
99US-0139763.
                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0142803.
99US-0142920.
99US-0142977.
99US-0143542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0143624.
99US-0144005.
99US-0144085.
99US-0144086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0144325.
99US-0144331.
99US-0144332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0144884.
99US-0144814.
99US-0145086.
                                                                                                                                                                                                                                                                         99US-0139461
99US-0139462
                                                                                                                                                                                                                                                                                                                  99US-0139817
99US-0139899
                                                                                                                                                                                                                                                                                                                                  99US-0140353
99US-0140354
                                                                                                                                                                                                                                                                                                                                                  99US-0140695
                                                                                                                                                                                                                                                                                                                                                          99US-0140823
99US-0140991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144333
99US-0144334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144335
99US-0144352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0145089
99US-0145192
   99US-0132863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0144632
 11 KAY - 1999;
14 KAY - 1999;
14 WAY - 1999;
14 WAY - 1999;
14 WAY - 1999;
16 WAY - 1999;
17 WAY - 1999;
18 WAY - 1999;
18 WAY - 1999;
19 WAY - 1999;
10 WAY - 1999;
11 WAY - 1999;
11 WAY - 1999;
11 WAY - 1999;
12 WAY - 1999;
13 WAY - 1999;
14 WAY - 1999;
15 WAY - 1999;
16 WAY - 1999;
17 WAY - 1999;
18 WAY - 1999;
                                                                                                                                                                                                                                                                                                                 21 - JUN - 1999;
22 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
30 - JUN - 1999;
                                                                                                                                                                                                                                                       18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999;
20-JUL-1999;
                                                                                                                                                                                                                                        18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1999;
   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                              Gaps
                                                                                                                                                                                              ά;
                                                                                                                                                                            Score 41; DB 21; Length 1048;
Pred. No. 3.3e+02;
Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 52534.
                                                                                                                                                                                                                                                                       AAG42153 standard; Protein; 1129 AA
                                                                                                                                                                                                                        |:|| |:|
| 419 rkyssgkyqdhptgyrpvrvewk 441
                                                                                                                                                                                                              RRYSIGRYS-----VRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0121825.
990S-0123180.
99US-0123748.
99US-012624.
99US-012624.
99US-0128234.
99US-0128714.
99US-0130745.
99US-0130745.
99US-013074.
99US-013074.
99US-013089.
99US-0132407.
990S-0159584.
990S-0160741.
99US-0160767.
99US-0160767.
99US-0160814.
99US-0160814.
99US-0160914.
99US-0160981.
99US-0160981.
99US-0161360.
99US-0161360.
99US-0161360.
99US-0161360.
99US-0161360.
99US-0161360.
99US-0161360.
                                                                                                                                                                             / Match
Local Similarity 39.1%;
hes 9; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                           2000EP-0301439
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          25 - FEB - 1999;

05 - MAR - 1999;

23 - MAR - 1999;

25 - MAR - 1999;

26 - MAR - 1999;

01 - APR - 1999;

06 - APR - 1999;

19 - APR - 1999;

21 - APR - 1999;

23 - APR - 1999;

30 - APR - 1999;

06 - MAY - 1999;

06 - MAY - 1999;

06 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                          EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000;
                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                             Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                        AAG42153;
                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                               AAG42153
                                                                                                                                                                                                                             g
  ò
```

99US-0160980

```
990S-0145145.
99US-0145218.
99US-0145218.
99US-0145218.
99US-0145913.
99US-0145913.
99US-0145918.
99US-0145918.
99US-0145951.
99US-0145951.
99US-0147302.
99US-0147302.
99US-0147302.
99US-0147303.
99US-0147303.
99US-0147303.
99US-0147303.
99US-0147303.
99US-0147303.
99US-0147303.
99US-0147303.
99US-014936.
99US-014936.
99US-014936.
99US-014936.
99US-014936.
99US-014936.
99US-014930.
99US-014930.
99US-014930.
99US-014930.
99US-014930.
99US-014932.
99US-0151080.
99US-014930.
99US-0151080.
99US-0159293.
99US-0159293.
99US-0159330.
99US-0159330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990S-0160741.
990S-0160767.
990S-0160768.
990S-0160770.
990S-0160814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0159584
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1999;
20-SEP-1999;
20-SEP-1999;
24-SEP-1999;
24-SEP-1999;
24-SEP-1999;
26-CT-1999;
06-CT-1999;
06-CT-1999;
13-CT-1999;
13-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
14-CT-1999;
18-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
21-CT-1999;
  23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
04-AUG-1999;
04-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
11-AUG-1999;
11-AUG-1999;
11-AUG-1999;
11-AUG-1999;
11-AUG-1999;
11-AUG-1999;
11-AUG-1999;
13-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
21-AUG-1999;
                                                                                                                                                                                                                                                                                                                           25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1999;
10-SEP-1999;
```

```
Ή,
                                                                                                                                                                                                                                                                                 protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                   Gaps
                                                                                                                                    ..
60
                                                                                                                 Score 41; DB 21; Length 1129;
pred. No. 3.6e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                   Arabidopsis thallana protein fragment SEQ ID NO: 52533.
                                                                                                                                                                                                                 AAG42152 standard; Protein; 1193 AA.
                                                                                                                                                                    |:|| |:|
500 rkyssgkygdhptgyrpvrvewk 522
                                                                                                                                                       3 RRYSIGRYS-----VRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                           990S-0121825.
990S-012348.
990S-0125788.
990S-012664.
990S-0126785.
990S-012874.
990S-012874.
990S-0128714.
990S-0130077.
990S-0130077.
990S-01300891.
990S-0130891.
990S-0131449.
990S-0132486.
                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-0301439.
                                                                                                                      45.1%;
       99US-0160981.
99US-0160989.
99US-0161404.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161361.
99US-0161992.
99US-0161992.
                                                                                                                                                                                                                                                        18-OCT-2000 (first entry)
                                                                                                                                 Local Similarity 39.1 es 9; Conservative
                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR 1999;

06-APR 1999;

10-APR 1999;

11-APR 1999;

21-APR 1999;

23-APR 1999;

23-APR 1999;

23-APR 1999;

30-APR 1999;

30-APR 1999;

05-MAY 1999;

06-MAY 1999;

11-MAY 1999;

14-MAY 1999;

14-MAY 1999;

14-MAY 1999;

14-MAY 1999;

14-MAY 1999;
                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                             EP1033405-A2.
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                        AAG42152;
                                                                                                                          Query Match
                                                                                                                                                                                                       RESULT 15
                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                               q
                                                                                                                                                               δ
    PR
PR
PR
PR
PR
PR
PR
```

99US-0145951. 99US-0146386. 99US-0146388. 99US-0146389. 99US-0147308. 99US-0147302.	990S-0147203 990S-0147303 990S-0147493 990S-0147493 990S-0140171 990S-0148319 990S-0148341 990S-0148841 990S-0148865 990S-0148664 990S-0149568	990S-0149929 990S-0149902 990S-0149930 990S-0150566 990S-0150884 990S-0151065 990S-0151089 990S-0151080 990S-0151303 990S-0151303 990S-0151303	990S-0154018 990S-0154039 990S-0155139 990S-015568 990S-015685 990S-015685 990S-015685 990S-015685 990S-015775 990S-015785 990S-015885 990S-015829 990S-015829 990S-015829	99US-0159330. 99US-015931. 99US-0159631. 99US-015968. 99US-016074. 99US-0160776. 99US-0160776. 99US-0160814. 99US-0160815. 99US-0160981. 99US-0160981.
			15-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 28-SEP-1999; 28-SEP-1999; 29-SEP-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999;	
			* * * * * * * * * * * * * * * * * * *	
	·			
	\$\d\dagge\da			0.00 0.00
99US - 013494 99US - 013512 99US - 013535 99US - 013602 99US - 013602 99US - 013678	9990S-013750 9990S-0137750 9990S-013805- 9990S-013805- 990S-013984- 9990S-013945- 9990S-013945- 9990S-013945- 9990S-013945- 9990S-013945- 9990S-013945-	99908 - 01394 6 9 99908 - 01394 6 9 9908 - 01394 6 9 9908 - 01394 6 6 9 9908 - 01394 8 6 9 9908 - 0139811 9 9908 - 014038 9 9908 - 014088 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	99US-0141287. 99US-0141284. 99US-0142154. 99US-0142055. 99US-0142390. 99US-01422030. 99US-014334.	990S-014433 990S-014443 990S-014488 990S-014488 990S-014508 990S-014508 990S-014508 990S-014508 990S-014519 990S-014519 990S-014519 990S-014519

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

```
February 12, 2002, 12:32:24 ; Search time 106.12 Seconds (without alignments) 3.605 Million cell updates/sec
OM protein - protein search, using sw model
                                                      Run on:
```

US-09-485-571-30 91 1 RSRRYSIGRXSVRFSWK 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

212252 seqs, 22503292 residues Searched:

212252 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo	82,		182,	93,	26,	79,	85,	177,	184,	18,	20,	21,		81,		10,	10,	7, 4		291		24,	24, Appl	2, 1	4	26, Appl
Description	Sednence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sednence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
GI	US-09-128-344A-82	US-U9-128-344A-83 US-09-128-344A-181	US-09-128-344A-182	US-08-679-493A-93	US-08-679-493A-26	US-09-128-344A-79	US-09-128-344A-85	US-09-128-344A-177	US-09-128-344A-184	US-09-521-668B-18	US-09-521-668B-20	US-09-193-104-21	US-09-461-697-391	US-09-128-344A-81	US-09-128-344A-180	US-08-473-981A-10	US-08-474-087-10	US-09-240-915-7	US-09-591-435-7	US-09-188-930-291	۰	US-08-867-941-24	º	US-08-760-489-2	US-08-760-489-4	US-09-193-104-26
h DB	4.	2 O 4 4	4	90 4	1 4	æ :	4	8	8	7 4	7 4	4	4	4	4	2	2	4	4	8	0	4	4	7 2	7 2	4
Lengt			1	6	101		-	-	_	42	427	15	7	1	~	125	125	25	254	268	90	944	944	1487	1487	15
% Query Match Length	4.8.4	4 8 4 8 . 4 4 9 . 4	48.4	44.5	44.5	44.0	44.0	44.0	44.0	44.0	44.0	42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.2
Score	44	7 7 7	44	40.5	40.5	40	40	40	40	40	40	39	38	38	38	38	38	38	38	38	38	38	38	38	38	37.5
Result No.	н с	7 E	4	S	9 1	^	œ (σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

	°°
8, APP11 2, APP11 11, APP11 64, APP1 10, APP1 35, APP1 207, APP1 207, APP1 207, APP1 207, APP1 20, APP	Gaps1
sedneuce sed	; •
bes Sed in Sed i	თ
	gth 1 Indel
	e e
10 20	;; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
US-07-894-212A-8 US-07-894-212A-2 US-07-893-928A-1 PCT-US96-03916-63 US-08-890-865A-10 US-08-93-35-95-35 US-08-73-35-95-35 US-08-685-589A-207 US-08-08-58-589A-207 US-08-08-125-758A-4 US-08-225-758A-2 US-08-238-699A-5 US-08-238-699A-5 US-08-238-699A-5 US-08-33-311-17 US-08-463-288A-17 US-08-33-311-17 US-08-463-288A-17 US-08-463-288A-17	N S S S S S S S S S S S S S S S S S S S
212 222 928 928 928 928 928 93 93 93 93 93 93 93 93 93 93 93 93 93	LIGNMENTS TACHYTEGRINS 128,344A 47,622 000,898 re 44; DB 4 ac. No. 0.56; Mismatches Mismatches TACHYTEGRINS
28994-	ALIGNMENT 28344A L. L. (99/128,344A 08/647,622 60/000,898 Version 4.0 Version 4.0 2; Mismatch 28344A L. L. L.
207-108-0-10	ALIC 19/128 (9/128 (1/647) (1/906) 11/906 (1/128) 11/128
US-100 US	ALIGNME 28344A L. L. AND TACHYT 709/128,34 08/647,622 60/000,898 60/000,898 iversion 4 polypeptid polypeptid polypeptid polypeptid polypeptid L. L. L. L. AND TACHYT 709/128,34
111224283144171772	A-82 A-82 Application US/09128344 6307016 CORMATION: Lehrer, Robert I. Harwig, Sylvia S. L. Chang, Conway C. Gu, Chee L. Chang, Conway C. Gu, Chee L. Chang, Conway C. Gu, Chee L. Chang, Conway C. Chang, Conway C. Surverion: Parevins and T PELCATION NUMBER: US/09/1 LCATION NUMBER: US 60/00 NG DATE: 1996-07-03 LACATION NUMBER: US 60/00 NG DATE: 1995-07-06 SEQ ID NOS: 201 FastSEQ for Windows Vers CORMATION: Synthetic polyp A-82 A-82 AA-83 A-83 A-83 A-83 A-83 A-83 A-83 A-8
6647 6647 6623 6623 6623 6623 6623 6623 6623 673 773 773 774 774 774 774 774 774 774 7	Separt 1.
<u> </u>	tion tion tion tion (199
555550066666111777222	plicat follo
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	A-82 Gu Applicat 6307016 Charer, Harwig, Chang, Cha
	344A-82 182, Applica (b. 63070lb) INT: Lehrer, NT: Lehrer, NT: Lehrer, NT: Harwig, NT: Harwig, NT: Harwig, NT: Harwig, NT: Harwig, NT: Gu, Che (b. 1820) INT: Gu, Che (b. 1820) INFORMATION: SM: Artifici (b. 1820) INFORMATION: SM: Applica (b. 1820) INFORMATION: Lehrer, NT: Gu, Che (b. 63070lb) INFORMATION: Lehrer, NT: Lehrer, Lehrer, NT: Lehrer, NT: Lehrer, Lehrer, NT: Lehrer, NT: Lehrer, NT: Lehrer, Lehrer, Lehrer, NT: Lehrer,
	CANT:
\$\$010K4K97\$\$010K4K	RE ELLIARIS OF TREAPENSYRKE ELLILARIS OF THE ANGLE AND THE STATES OF THE ANGLE AND THE ANGLE ANGLE AND THE ANGLE ANGLE AND THE ANGLE AND THE ANGLE ANGLE AND THE ANGLE AND THE ANGLE ANGLE ANGLE ANGLE AND THE ANGLE ANGLE ANGLE AND THE ANGLE A
GGWWWWWWWWWWWWWA444444	RESULT Sequee PERENA Sequee PERENA APPL APPL PITTL FITTL FILE CURR CURR CURR CURR PRIOD PR
	S O S S S S S S S S S S S S S S S S S S

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INCRAFILOR. Ethan W.

TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
TITLE REPERENCE: 55-95
FILE REPERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR PILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-07-14
PRIOR PILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SEQ ID NOS: 216
SEQ ID NO 93
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 19;
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PARENTINS AND TACHYTEGRINS
FILE REFERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1996-08-03
PRIOR APPLICATION NUMBER: US 60/000,898
PRIOR FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 182
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 4;
Pred. No. 0.56;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human immunodeficiency virus type 1 US-08-679-493A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40.5; DE
Pred. No. 10;
3; Mismatches
                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/08679493A Patent No. 6303295 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-679-493A-93
US-08-679-493A-93
Sequence 93, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.5%;
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MOD_RES
LOCATION: 8,13
COTHER INFORMATION: Xaa = MeGly
NAME/KEY: DISULFID
LOCATION: (4)...(17)
US-09-128-344A-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSRRYSI-GRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :||: |||
6 RYXVGRFXVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-679-493A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 4; Length 19; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 4; Length 19; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Chang, Sylvia S. L.
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
TILE REFERENCE: 8060-0053-999
CURRENT APPLICATION NUMBER: US/09/128,34A
CURRENT FILING DATE: 1996-00-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-06
NUMBER: OF SEQ ID NOS: 201
SOFTWARE: FESTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic polypeptide NAME/KEY: DISULFID ; LOCATION: (4)...(17) US-09-128-344A-181
                            PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/000,898
PRIOR FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 201
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 80
                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic polypeptide NAME/KEY: MOD_RES LOCATION: 8,13 OTHER INFORMATION: Xaa = MeGly US-09-128-344A-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4

So-09-123-44A-182
Sequence 182, Application US/09128344A
Patent No. 6307016
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
; APPLICANT: Harwig, Sylvia S. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 181, Application US/09128344A Patent No. 6307016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           48.48;
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || :||: |||
6 RYKVGREKVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :||: |||
6 RYXVGRFXVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-128-344A-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 181
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             á
```

ij

```
Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                       APPLICANT: Chang, Conway C.
APPLICANT: Chang, Colway C.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REFERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 60/000,898
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-06
NUMBER: OF SEQ. ID NOS: 201
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 85
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lebrer, Robert I.
APPLICANT: Chang, Sylvia S. L.
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
TITLE OF INVEWTION: PAREVINS AND TACHYTEGRINS
FILE REFRENCE: 8067-0053-999
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR APPLICATION NUMBER: US 08/647,622
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1996-07-06
NUMBER OF SEQ ID NOS: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 4;
Pred. No. 2.3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 4;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic polypeptide; NAME/KEY: DISULFID; LOCATION: (4)...(17)
US-09-128-344A-177
                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHEE INFORMATION: Synthetic polypeptide US-09-128-344A-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 177, Application US/09128344A parent No. 6307016 General INFORMATION: APPLICANT: Lehrer, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 134, Application US/09128344A
           Harwig, Sylvia S. L. Chang, Conway C.
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.۰۰
احد 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RYSIGRYSVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||::||::||
6 RYAVGRFAVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RYSIGRYSVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||::||::||
6 RYAVGRFAVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-128-344A-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-128-344A-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT FILING DATE: 1996-07-12 PRIOR APPLICATION NUMBER: 60/001203 PRIOR APPLICATION NUMBER: 60/003,112 PRIOR APPLICATION NUMBER: 60/003,112 PRIOR FILING DATE: 1995-09-01 NUMBER OF SEQ ID NOS: 216 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 26 LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.5%; Score 40.5; DB 4; Length 101; 52.9%; Pred. No. 11; Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 4; Length 18; Pred. No. 2.3; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 79, Application US/09128344A
Patent No. 6307016
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
FAPLICANT: Chang, Colway C.
APPLICANT: Chang, Colway C.
APPLICANT: Gu, Chee, U.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS
FILE REPERENCE: 8067-0053-999
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1996-03
FRIOR APPLICATION NUMBER: US 08/647,622
FRIOR APPLICATION NUMBER: US 06/000,898
FRIOR FILING DATE: 1996-07-03
FRIOR FILING DATE: 1996-07-03
FRIOR APPLICATION NUMBER: US 60/000,898
FRIOR FILING DATE: 1996-07-03
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 201
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 79
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-128-344A-79
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT

CCATION: (1)..(101)

COTHER INFORMATION: X is selenocysteine.

US-08-679-493A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-128-344A-85; Sequence 85, Application US/09128344A; Sequence No. 6307016; GENERAL INFORMATION; APPLICANT: Lehrer, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SRRYSIGR-YSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 44.0
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RYSIGRYSVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-344A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Gaps

; 0

ö

Gaps

ó

```
## PAPERIC NO. 6303383

| GENERAL INFORMATION:
| AAPLICANT: NARMURA, JUN
| AAPLICANT: KANNO, SCHEI
| AAPLICANT: KANNO, SCHEI
| AAPLICANT: KANNO, SCHEI
| AAPLICANT: MARMATSU, TSUTGSHI
| AAPLICANT: MARMATSU, TSUTGSHI
| TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA
| TITLE OF INVENTION: TEMPERATURE OF 1999-6
| PRIOR APPLICATION NUMBER: JP 11-69896
| PRIOR PLING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-16
| NUMBER OF SED ID NOS: 20
| SEQ ID NO 20
| LENGTH: 427
| TYPE: DRT
| TYPE: RT
| T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-103-104-21
i Sequence 21, Application US/09193104A
Fatent No. 6172193
GENERAL INFORMATION
APPLICANT: Fiordalisi, Glanfranco
APPLICANT: Fordalisi, Glanfranco
APPLICANT: Fordalisi, Glanfranco
APPLICANT: Fordalisi, Glanfranco
TITLE OF INVENTION: Escape Mutant of the Surface Antigen of Hepatitis B
TITLE OF INVENTION: Virus
FILE REPERENCE: SBD1004US
CURRENT APPLICATION NUMBER: US/09/193,104A
CURRENT APPLICATION NUMBER: US/09/193,104A
CURRENT PILING DATE: 1997-12-01
SARLIER PILING DATE: 1997-12-01
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 4; Length 154; Pred. No. 30; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 4; Length 427;
Pred. No. 61;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Hepatitis B virus US-09-193-104-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.5.
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 KYLWERASVRFSW 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US SEQUENCE 18, Application US/09521668B

SEQUENCE 1NO. 630383

GENERAL INFORMATION:
APPLICANT: NARMON, SOHEI

APPLICANT: KANNO, SOHEI

APPLICANT: KANNO, SOHEI

APPLICANT: MAKAMATON
APPLICANT: MAKAMATON

APPLICANT: MAKAMATON

APPLICANT: MAKAMATON

APPLICANT: MAKAMATON

APPLICANT: MAKAMATON

TITLE OF INVENTON: TEMPERATURE SENSITIVE PLASMID FOR CORYNEFORM BACTERIA

FILE REFERENCE: 0010-1093-0

CURRENT APPLICATION NUMBER: US/09/521,668B

CORRENT FILING DATE: 2000-03-08

PRIOR PILING DATE: 2000-03-08

NUMBER OF SEQ ID NOS: 20

SEQ ID NO 18

LENGTH: PALENT NOS: 20

SEQ ID NO 18

LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.0%; Score 40; DB 4; Length 427;
43.8%; Pred. No. 61;
tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 4; Length 18;
Pred. No. 2.3;
4; Mismatches 0; Indels
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Chang, Conway C.
APPLICANT: Glang, Conway C.
APPLICANT: Glang, Conway C.
APPLICANT: Glang, Conway C.
TITLE OF INVENTION: PAREVINS AND TACHYTEGRINS FILE REFERENCE: 8067-0053-999
CURRENT FILING DATE: 1998-08-03
FRIOR APPLICATION NUMBER: US 09/647,622
PRIOR PAPLICATION NUMBER: US 09/647,622
PRIOR PAPLICATION NUMBER: US 09/647,622
PRIOR FILING DATE: 1995-07-03
SOFTWARE FEASTESQ FOR WINDOWS VERSION 4.0
SEQ ID NO. 184
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Synthetic polypeptide NAME/KEY: DISULFID ILCATION: (4)...(17) US-09-128-344A-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Brevibacterium lactofermentum US-09-521-668B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-521-668B-20
; Sequence 20, Application US/09521668B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | :| ::| ||
276 RWREYEVGSKNLRSSW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RYSIGRYSVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RYAVGREAVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-09-521-668B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

;

ö

; 0

```
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Praramam, Kasturi
; APPLICANT: RAIL Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SCO ID NO 391
; LENGTH: 14
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-461-697-391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%; Score 38; DB 4; Length 14; 70.0%; Pred. No. 3.6; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.8%; Score 38; DB 4; Length 19; 54.5%; Pred. No. 4.9; tive 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
UG-09-128-344A-81
Sequence 81, Application US/09128344A
Patent No. 6307016
GENERAL INFORMATION:
APPLICANT: Lefrer, Robert I.
APPLICANT: Chang, Conway C.
APPLICANT: Chang, Conway C.
APPLICANT: GLOOP PAREVINS BUSINES FILE REFERENCE: 8067-0053-99
CURRENT APPLICATION NUMBER: US/09/128,344A
CURRENT FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
PRIOR FILING DATE: 1996-07-03
PRIOR FILING DATE: 1995-07-06
SPRIOR FILING DATE: 1995-07-06
SPRIOR FILING DATE: 1995-07-06
SOFTWARE: FLANG DATE: 1995-07-06
SEQ ID NOS: 201
SEG ID NOS: 201
SEG ID NOS: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-128-344A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 YSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 | |:|| ||
5 YSSGKYSYRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: February 12, 2002, 12:32:24 Job time: 452 sec

||::|::||| 6 RYTVPRFTVRF 16

g

					4
	en e				
		v		d m	
				:	
			•		*
				•	
					· ·
en e					
					** *
*					
					9
				en de la companya de La companya de la co	
en e					
		And Control of			
•					
,	\$ ************************************		and the Market of the Salah Salah Salah Salah Sa		
			en de la companya de La companya de la co		
f'	-	**		the state of the s	Maria Ma

```
February 12, 2002, 12:34:41; Search time 126.85 Seconds (without alignments) 10:209 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

    protein search, using sw model

                                                                                                                                                                                                                        1 RSRRYSIGRYSVRFSWK 17
                                                                                                                                                                                   US-09-485-571-30
91
                                                                                                                                                                                   Title:
Perfect score:
                                                                        OM protein
                                                                                                                                                                                                                          Sequence:
                                                                                                           Run on:
```

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha-mannosidase-	hypothetical prote	conserved hypothet	hypothetical prote	magnesium-protopor	probable membrane	ribonucleotide red	hypothetical prote	major surface anti	major surface ant1	surface antigen -	surface antigen -	small surface prot	surface antigen -	surface antigen -
H72278	E02027 H84639	A82583	T24541	T50729 .	S54520	T43215	T29227	JQ1579	JQ1580	JQ2119	JQ2120	JQ2225	JQ2121	JQ2122
2.0	7 7	7	~	~	~	~	7	7	Н	~	7	~	~	7
832	899	928	1151	1193	1656	1740	2049	226	226	226	226	226	226	226
41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.2	41.2	41.2	41.2	41.2	41.2	41.2
38	38	38	38	38	38	38	38	37.5	37.5	37.5	37.5	37.5	37.5	37.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

ve,

14-000 hvnotherival protein E187,15-30 - brahidoneis thaliana
C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000 .
R.Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenav
SUGMITTEGA TO THE FIOTEIN Sequence Database, NOVEMBET 1999 A-Reference number: 223010
A; Accession: T45688
A;Status: preliminary
A MOLECULE TYPE: UNA A: Restfiles: 1-124 CCHO>
A:Experimental source: cultivar Columbia; BAC clone F18L15
Z Genetics:
A; Note: F13L15.30
Oliery March 48 4%. Goore 44. DR 2. Iendth 124.
Similarity 50.0%; Pred. No. 3.2; 8; Conservative 4; Mismatches 4
Qy 2 SRRYSIGRYSVRFSWK 17
: : :
RESULT 2 146641
rearranged T-cell receptor delta-chain/ Vdelta4-Ddeltas-Jdelta4 - pig (fragmen
C;Species: Sus scroia domestica (domestic pig) C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text change 23-Jul-1999
C; Accession: 146641
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
O . minimular. 1307, 1307, 1307. A:Title: Diversity of T cell receptor delta-chain cDNA in the thymns of a one-m
A; Reference number: 146623; MUID:95363165
A;Accession: 146641 A:Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-130 (YAN)
A;CLOSS TETERIEUCES: DE:L49202; NIL)GLUGHIOO; FILD:BANOOS20:1; FID:GLUGHIO) C:SLOBFFamily: immunoqlobulin V region: immunoqlobulin homology
C:Keywords: T-cell receptor
Query Match 47.3%; Score 43; DB 2; Length 130;
Similarity 64.3%; Pred. No. 5;
varive

mont

ö

£

```
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001
C;Accession: A86193
C;Accession: A86193
C;Accession: A86193
C;Accession: A86194
C;Accession: A86194
C;Accession: A86194
C;Accession: A86195
C;Accession: A86195
C;Accession: A86195
C;Accession: A86195
C;Accession: A86195
C;Accession: A86193
C;Accession: A86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHWWWE
VHWWE
VHWWE
C. YEAUCULTAL polyprotein - western equine encephalomyelitis virus (strain BF51703)
C. Species: western equine encephalomyelitis virus
C. Date: 31-Mar-1991 #sequenec_revision 31-Mar-1991 #text_change 16-Jul-1999
C. Accession: A55587
R. Hahn, C. S.: Lustig, S.; Strauss, E.G.; Strauss, J.H.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant virus.
A7Tille: Western equine encephalitis virus is a recombinant encephalitis virus predicted 
A7TILIS A7TILLE: Western equine encephalitis virus predicted 
C. Superfamily: togavirus structural polyprotein E3 #status predicted 
C. Superfamily: togavirus estatus predicted 
C. Superfamily: togavirus estatus predicted 
F736-737/Product: membrane estatus predicted 
F737-737/Promain: transmembrane #status predicted 
F737-737/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F737-737/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F737-737/Promain: transmembrane #status predicted 
F736-727/Promain: transmembrane #status predicted 
F737-737/Promain: transmembrane #status predicted 
F737-737/Promain: transmembrane #status predicted 
F737-737/Promain: transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1;
Pred. No. 1e+02;
I; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB Pred. No. 99; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|| |:|
564 RKYSSGKYQDHPTGYRPVRVEWK 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RRYSIGRYS-----VRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.1
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 SRNFSVGREGLEYVW 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
140335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ľ
                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T51920
R; Schile, U; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, August 2000
A; Reference number: Z25858
A; Accession: T51920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T4619
R; Beran, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Isubmitted to the Protein Sequence Database, April 2000
A; Reference number: 224493
A; Reference number: 224493
A; Reference number: 224493
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-540 GBEN>
A; Cross-references: EMBL:DB
A; Experimental source: cultivar Columbia; BAC clone F18022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Map position: 6
A:Introns: 66/2: 1311/3
G:Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-2S] homology
C:Reywords: 2Fe-2S; metalloprotein
F:68,73,76,98/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                   probable xanthine dehydrogenase [imported] - Neurospora crassa
A.Altendate names: protein B3111.320
C;Species: Neurospora crassa
C;Date: 20-0ct-2000 #sequence_revision 20-0ct-2000 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tRNA synthase-like protein - Arabidopsis thaliana
NALeranate names: protein F18022.250
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Motecule type: DNA
A;Rosidues: 1-1364 «SCH>
A;Cross-references: EMBE:AL391572; GSPDB:GN00116; NCSP:B23111.320
A;Cross-references: EMBC:AL391572; GSPDB:GN00116; NCSP:B23111.320
Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
A: Introver: 331/1; 349/3; 377/2; 403/3; 440/3; 477/2; 505/2; 518/1
A; Note: F18022.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2; Length 1364;
Pred. No. 53;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 540;
Pred. No. 30;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A86193
hypothetical protein [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 RRDSIGEYSANDAWE 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 RRYSIGRYSVRFSWK 17
                                                            ::|| | ||||| |
63 QNRRNSEGRYSVEF 76
                    1 RSRRYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: NCSP:B23111.320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               рp
                    δ
                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

Wgd Feb 13 07:52:31 2002

A; Introns: 69/2; 97/2; 242/3

ö

Gaps

ö

Indels

Length 331;

5

DB (

```
external glycoprotein, transmembrane protein(external glycoprotein, EGP, transmembr
C;Species: feline immunodeficiency virus
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: F45557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Maki, N.; Miyazawa, T.; Fukasawa, M.; Hasegawa, A.; Hayami, M.; Miki, K.; Mikami, Arch. Virol. 123, 29-45, 1992
A;Title: Molecular characterization and heterogeneity of feline immunodeficiency vi A;Reference number: A45557; MUID:92198230
A;Reference T. F45557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: protein Tile managers characters of the NiAlternate names: protein Tile names: protein Sequence Database, March 2000

A: Reference number: 224463

A: Accession: Tile names: protein Tile n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: sequence extracted from NCBI backbone (NCBIN:89826, NCBIP:89854)
C;Superfamily: feline immunodeficiency virus env polyprotein
C;Reywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL138656
A;Experimental source: cultivar Columbia; BAC clone T14E10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter-like protein · Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2;
Pred. No. 88;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2;
Pred. No. 1e+02;
5; Mismatches
                                                                                                                          Score 40; DB 2
Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-855 <MAK>
A;Experimental source: strain TM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%;
                                                                                                                          44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.0%;
57.1%;
                                                                                   Ouery Match
Best Local Similarity 50.0.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|:|:| |: | | 449 KSKRHSEARFRIRCKW 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.0
Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                    :: [| ||:| |:|
122 KFDIGEYSLRTSFK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSRRYSIGRYSVRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-723 <OBE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 3
A; Note: T14E10.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
T40144
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ay1871

hypothetical protein jhp0933 - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori

A;Variety: strain J99

C;Species: Helicobacter pylori

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Accession: A/1871

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A/1800; MUID:99120557

A;Accession: A/1871

A;Accession: A/1871

A;Accession: A/1871

A;Clost comparison of two unrelated isolates of the human gastric path A;Reference number: A/1800; MUID:99120557

A;Residues: 1-267 caRN>

A;Clost comparison of two unrelated isolates of the human gastric path A;Residues: 1-267 caRN>

A;Cross-references: GB:AE001522; GB:AE001439; NID:94155505; PIDN:AAD06511.1; PID:9415551

A;Experimental source: strain J99

C;Genetics:
A;Gene: Jhp0933
hypothetical protein 1 - Corynebacterium glutamicum
C:Species: Corynebacterium glutamicum
C:Species: Corynebacterium glutamicum
C:Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999
C:Accession: 140335
R:Yamaguchi, R.; Terabe, M.; Miwa, K.; Tsuchiya, M.; Takagi, H.; Morinaga, Y.; Nakamori, Agric. Biol. Chem. 50, 2771-2778, 1986
A:Title: Determination of the complete nucleotide sequence of Brevibacterium lactofermen A:Reference number: 140334
A:Accession: 140335
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-240 <RES>
A:Cross-references: GB:D00038; NID:9216381; PIDN:BAA00026.1; PID:9216383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A'250c

A'250c

A'250c

C'Species: Caenorhabditis elegans

C'Species: Caenorhabditis elegans

C'Species: Caenorhabditis elegans

C'Species: Caenorhabditis elegans

C'Accession: T22968

R'Mortimore, B.

Submitted to the EMBL Data Library, November 1996

A'Reference number: 21964

A'Reference number: 21964

A'Status: preliminary; translated from GB/EMBL/DDBJ

A'Molecule type: DNA

A'Rolacule type: DNA

A'Residues: 1-331 
A'Residues: EMBL:281557; PIDN:CAB04537.1; GSPDB:GN00023; CESP:F59A1.9

A'Experimental source: clone F59A1

C;Genetics: CESP:F59A1.9

A'Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB;
Pred. No. 29;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 32;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | ::| ||
89 RWREYEVGSKNLRSSW 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.0
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 44.0
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||| ||::|
91 SVGRYMVRYATK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 SIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ö

Gaps

.. 0

Indels

Length 723;

ö

Gaps

ö

5; Indels

Length 855;

1;

Gaps

4;

Indels

Length 191;

```
A; Molecule type: DNA
A; Residues: 1-191 - KRAN>
A; Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30275.1; PID:d1031218; PID:g3.
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBI
C; Genetics:
A; Gene: PH1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein AT4907440 [imported] - Arabidopsis thaliana hypothetical protein AT4907440 [imported] - Arabidopsis thaliana (mouse-ear cress)

C; Species: Arabidopsis thaliana (mouse-ear cress)

C; Species: Beb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C; Accession: F85072

A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A; Reference number: A85001; MUID: 20083488.

A; Accession: F85072

A; Accession: F85072

A; Accession: F85072

A; Reference speciminary

A; Molecule type: DNA

A; Residues: 1-261 <STO>
A; Cross-references: GB:NC_001268; NID: 97267340; PIDN: CAB81114.1; GSPDB: GN00140

C; Genetics:
A; Genetics:
A; Approximation Approximation Approximation A; Approxim
                                                                                                                                                                                                                                                                Score 39; DB 2;
Pred. No. 34;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2
Pred. No. 46;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: February 12, 2002, 12:34:42
ne: 560 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.9%;
                                                                                                                                                                                                                                                                          42.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 RRYFYSWSVKRVPVRFEW 151
                                                                                                                                                                                                                                                                                                                                                                                                    3 RRY----SIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| || |: ::| |:
87 RYSSFRFHIKFIWE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
9
                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search com
Job time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypotherical protein PHI175 - Pyrococcus horikoshii
hypotherical protein PHI175 - Pyrococcus horikoshii
C:Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: A71060
C:Accession: A71060
C:Accession: A71060
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
N.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
N.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
A; A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A; Reference number: A71000; MuID:98344137
A; Accession: A71060
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60s ribosomal protein 116-c - fission yeast (Schizosaccharomyces pombe)
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C; Accession: T40144
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.
A; Recence number: 221842
A; Accession: T4014
A; Stetus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-197 *WOO>
A; Coss-references: EMBL:AL022103; PIDN:CAA17885.1; GSPDB:GN00067; SPDB:SPBC2G2.05
A; Experimental source: strain 972h-; cosmid c2G2
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Aintrons: 14/2
C; Superfamily: Escherichia coli ribosomal protein L13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AE002093; NID:94006823; PIDN:AAC95165.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39.5; DB 2;
Pred. No. 29;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pred. No. 30;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.4%;
nilarity 52.9%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 SRKYCTIGRLSSEVGWK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SRRY-SIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 RYSSFRFHIKFIWE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-171 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-171 <STC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: E84472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: At2g05880
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

ö

Gaps

.; 0

4; Indels

Length 261;

; ;

us-09-485-571-30.rpr

4.			
*.			
en e	en e	3 3	
	• • • • • • • • • • • • • • • • • • •		
			•
en e			
100 m s			Jan 1
			e e e e e e e e e e e e e e e e e e e
		av .	
			, and
	of the second se		
			ä
Arriva Santan			
			. 43
			·
		and the second s	
A MARK A A S			
			, in the second

Page

4

```
February 12, 2002, 12:39:53 ; Search time 67.2 Seconds
(without alignments)
9.275 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                   US-09-485-571-30
91
1 RSRRYSIGRXSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SwissProt_39:*
                                                                                                                                                                                                                          Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф			SUMMAKIES	
Result No.	Score	Query	Length	DB	QI.	Description
						1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
7	44	48.4	794	Ч	CDB6_HUMAN	Q9y5e3 homo sapien
~	41	45.1	1236	7	POLS_WEEV	weste
ო	40	44.0	855	-	ENV_FIVT2	2 feline i
4	39.5	43.4	197	-	R16C_SCHPO	043004 schizosacch
ഗ	39	42.9	1194	7	BCHH_RHOCA	P26162 rhodobacter
9	38.5	42.3	662	7	VG63_HSV11	Q00159 ictalurid h
7	38	41.8	102	٦	UL65_HCMVA	P17148 human cytom
80	38	41.8	275	П	ICA2_HUMAN	P13598 homo sapien
σ	38	41.8	368	П	YCZ2_YEAST	
10	38	41.8	888	-	YGCB_ECOLI	P38036 escherichia
11	38	41.8	006	-	AXN1_HUMAN	O15169 homo sapien
12	38	41.8	1193	-	BCHH_RHOSH	
13	38	41.8	1656	_	ATC8_YEAST	Q12674 saccharomyc
14	37.5	41.2	400	7	VMSA_HPBVT	
12	37.5	41.2	648	-	AMYA_PYRFU	_
16	37.5	41.2	1309	-	ST16_SCHPO	Q09743 schizosacch
17	37	40.7	118	П	LHG2_RHOCA	
18	37	40.7	123	-	YC65_MESVI	
19	37	40.7	142	П	RL17_CHLPN	0927s9 chlamydia p
20	37	40.7	308	Н	ER25_CANAL	m
21	37	40.7	339	П	TRPD_BACST	
22	37	40.7		Н	EXUT_BACSU	034456 bacillus su
23	37	40.7		Н	ENO_AERPE	Q9y927 aeropyrum p
24	37	40.7		-	LEU1_SALTY .	P15875 salmonella
25	37	40.7		Н	FIB1_ADE40	P18047 human adeno
56	37	40.7		٦	UVRA_VITST	Q08518 vitreoscill
27	37	40.7		-	CCMF_RHIME	
28	37	40.7		7	SM4G_HUMAN	Q9ntn9 homo sapien
59	37	40.7	841	Н	AXN_CHICK	042400 gallus gall
30	m	40.7	950	~	UVRA_NEIGO	
31	36.5	40.1	802	7	PAC_ARTVI	arthrobact
32	36	39.6	141	-	RL17_CHLTR	P47760 chlamydia t
33	36	39.6	142	-	RL17_CHLMU	O9pin5 chlamydia m

P39135 bacillus su O64262 mycobacteri O926m6 rickettaia P53045 saccharomyc P30615 saccharomyc P30897 mus musculu P3478 rattus norv Q40153 lithospermu Q12499 saccharomyc P10335 staphylococ O02466 branchiosto	SINIS	794 AA.	<pre>, Created) , Last sequence update) , Last annotation update) PRECURSOR (PCDH-BETA6).</pre>	Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.	SEQUENCE FROM N.A. MEDLINE-99308636; PubMed-10380929; MEDLINE-99308636; PubMed-10380929; MAINTALIS TO MAINTALIS TO A Large family of human neural cadherin- "A straiking organization of a large family of human neural cadherin- "The cell adhesion genes.";	DENT CELL-ADHESION PROTEIN. RANE PROTEIN (BY SIMILARITY). MAINS.	is produced through a collaboration formatics and the EMBL outstation. There are no restrictions on its long as its content is in no way moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/)).		protein; Signal; Repeat;	HERIN BETA 6. JULAR (POTENTIAL).	FT DOMAIN 34 132 CADHERIN 1. FT DOMAIN 246 345 CADHERIN 2. FT DOMAIN 350 449 CADHERIN 3. FT DOMAIN 454 559 CADHERIN 6. FT DOMAIN 454 669 CADHERIN 6. FT CARBOHYD 46 46 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 183 183 N.LINKED (GLCNAC) (POTENTIAL). FT CARBOHYD 416 416 N.LINKED (GLCNAC) (POTENTIAL).
ACSU BPMD2 RICPR YEAST YEAST MOUSE RAT SOLTU LITER LITER LITER	ALIGNMENT		ce up tion CDH-E	niate arrhí	je fe	EPENI MEMBI	t. It loind tute as] t rem ment ib.c]		1ycol	NTIAL OCADI ACELI NTIAL PLASI	ERIN ERIN ERIN ERIN ERIN NKED NKED
SFP_BACSU VG69_BPMDS Y301_RICPR ER25_YEAST YK67_YEAST TA2R_MOUSE TA2R_RAT ELS_SOLTU EL14B_LTTER NOP5_YEAST LIP_STAAU	AL.	PRT	Created) Last sequence up Last annotation PRECURSOR (PCDH-	Crai	0929	UM-DI	righ of B nsti lons s no green sb-s	, ,	5. 5. n; G.	POTE PROT EXTR POTE CYTO	CADH CADH CADH CADH N-LI
			eated it se it an	lata; ites;	1038 of a	ALCI TYF 6 CA	copy tute cs l titut ent l	1; 5.	[N_1; [N_2; nesic fami		
224 269 269 309 314 341 341 341 690				~ ·	PubMed= ;; ization n genes.	ENTIAL COCATION:	ntry is s Instit nformati it inst stateme a licen to licen	AD43760. J. 26; Cadh dherin; CADHERIN	A; %. CADHERI CADHERI Cell adi	27 794 688 709 794	132 241 241 449 559 669 669 1183
$\begin{array}{c} \mathbf{x} \mathbf{x} \mathbf{x} \mathbf{x} \mathbf{x} \mathbf{x} \mathbf{x} x$		ST	(Rel. (Rel. (Rel. N BET	s (Human) Metazoa; utheria; 9606;	M N.A 8636; tis T organ hesio	LAR L	ROT e Swiss Bioi Bioi - prof	99; A 99; A 1NC 1R0021 8; Ca 1205;	12; (0232; 0268; (ing;	1 28 28 689 710	34 137 246 350 454 566 183 416
334 335 337 337 337 338 336 44 44 336 336 336 336 336 336 336		RESULT 1. CDB6_HUMAN ID CDB6_HUMAN AC Q9Y5E3;	20-AUG-2001 (Rel. 40 20-AUG-2001 (Rel. 40 20-AUG-2001 (Rel. 40 PROTOCADHERIN BETA 6 PCDHB6.	apien ota; ia; E axID=	SEQUENCE FRO MEDLINE=9930 Wu Q., Mania "A striking like cell ad	-!- FUNCTION -!- SUBCELLU -!- SÎMILARI	This SWISS-P between the the Buropean use by non modified and entities req or send an e	EMBL; AF1524 HSSP; P15116 InterPro; IP Pfam; PF0002 PRINTS; PR00	SMAKI; SMOOT PROSITE; PSO PROSITE; PSS Calcium-bind Transmembran	SIGNAL CHAIN DOMAIN TRANSMEM DOMAIN	DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN CARBOHYD CARBOHYD
তাতা এটা এটা কৰা কৰা কৰা		80 86		80008	R R R R R R R R R R R R R R R R R R R	28888	388888888	388888	X X D D X	FT FT FT	

```
684
719
758
777
1206
270
515
637
936
1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                            ENV_FIVT2
Q02282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                 TRANSMEM
TRANSMEM
                                                                         TRANSMEM
                                                                                                                                                    CARBOHYD
                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                     SEQUENCE
                                                                                                                                CARBOHYD
                                                           TRANSMEM
                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          ENV_FIVT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                       δŏ
     FT
FT
FT
FT
FT
FT
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULS_WEEV STANDARD; PRT; 1236 AA.
PDLS_WEEV SCAROOS; Q88699; Q88700;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C (EC 3.4.21.-)
CAPSID PROTEIN (P130) [CONTAINS: COAT PROTEIN E2;
(CAPSID PROTEIN C): SPIRE GLYCOPROTEIN E3; SPIRE GLYCOPROTEIN E2;
Western equine encephalitis virus.
VIRUSES: SSRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; Serine protease.
         565 565 N-LINKED (GLCNAC. . .) (POTENTIAL).
794 AA; 87349 MW; A4E84E17896C16BD CRC64;
                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.
                                                                                    Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPIKE GLYCOPROTEIN E3.
SPIKE GLYCOPROTEIN E2.
6 KDA PEPTIDE.
SPIKE GLYCOPROTEIN E1.
CHARGE RELAX SYSTEM (BY S
CHARGE RELAX SYSTEM (BY S
CHARGE RELAY SYSTEM (BY S
                                                                                  Score 44; DB 1;
Pred. No. 6.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COAT PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MENUS; DYROUS548; Alpha_El_glycop. InterPro; IPR002548; Alpha_E2_glycop. InterPro; IPR002533; Alpha_E3_glycop. InterPro; IPR001836; Alpha_core. InterPro; IPR001836; Alpha_core. InterPro; IPR001836; Alpha_core; 1. Pfam; PF00184; Alpha_core; 1. Pfam; PF001843; Alpha_E2_glycop; 1. Pfam; PF01583; Alpha_E2_glycop; 1. Pfam; PF01583; Alpha_E3_glycop; 1. Pfam; PF01583; Alpha_E3_glycop; 1. PRINTS; PR00798; TOGANIRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J03854; AAA42999.1; -.
PIR; A35587; VHWVWE.
                                                                                          48.4%;
                                                                                              Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                         HSSP; P03316; 1WYK.
                                                                                                                                                                   1 RSRRYSIGRYSV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEMAGGLUTININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=11039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S03.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphavirus
                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                RESULT 2
POLS_WEEV 1
DOL JAB9
DATE POLS_WEEV 1
DOT 01-JAB9
DE EADA
DOT 01-JAB9
DE (CAPS)
DE (CAP
                                                                                                                                                                                                           a
                                                                                                                                                                           ò
                           SO
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENV POLYPROTEIN PRECURSOR (GPL50 POLYPROTEIN) [CONTAINS: GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of feline immunodeficiency virus rev gene activity."; J. Virol. 65:4539-4542(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-92198230; PubMed-1312825;
Maki N., Miyazawa T., Fukasawa M., Hasegawa A., Hayami M., Miki K.,
Mikami T.;
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
N.LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kiyomasu T., Miyazawa T., Furuya T., Shibata R., Sakai H.,
Sakuragi J.I., Fukasawa M., Maki N., Hasegawa A., Mikami T.,
                                                                                                                                                                                                                                                   Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or senu w...

EMBL; M59418; AAA43074.1; ..

EMBL; M5557; R45557.

Interpro; IPR002050; Env_polyprotein.

Pfam; PF00429; ENV_POlyprotein; 1.

Pfam; PF00429; ENV_POlyprotein; 01, Coat protein; Polyprotein; 01, Coat protein; Polyprotein; 01, Coat myAop GIYCOPROTEIN GP100.

GLYCOPROTEIN GP36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular characterization and heterogeneity of feline immunodeficiency virus isolates."; Arch. Virol. 123:29-45(1992).
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feline immunodeficiency virus (isolate TM2) (FIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=31676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 AA
                                                                                                                                                                                                                                                 DB 7
                                                                                                                                                                                                                                                     Score 41; DB.
Pred. No. 34;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91303718; PubMed=1649349;
                                                                                                                                                                                                                                                            45.18;
                                                                                                                                                                                                 136082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GP100; GLYCOPROTEIN GP36]
                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                           || :|:|| : |
| :|:|| : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                              2 SRRYSIGRYSVRFSW 16
    737
775
793
1227
270
515
637
936
                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786
135
220
228
258
274
```

;

Gaps

Indels

5;

Mismatches

5

```
Conservative
   9;
                                                                                                                                      BCHH_RHOCA
P26152;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             plants.";
                                                                                                                        BCHH_RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                           ВСНН
    Matches
                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                õ
                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
Wood V., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.;
Submitted (MAR-1998) to the EMBL/GenBark/DBD databases
-1- MISCELLANGOUS: THERE ARE THREE GENES FOR L16 IN POWBE.
-1- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.
                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 855;
Pred. No. 34;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                     BC2DFABB6245D70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C529CC6BB55E77D6 CRC64;
                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                           (GLCNAC.
(GLCNAC.
(GLCNAC.
                                                                                                                       (GLCNAC.
                                                                                                                                                 (GLCNAC.
                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                 (GLCNAC
                               GLCNAC
                                               (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 AA
N-LINKED N-L
                                                                                                                                                                                                                                                                                       LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom: PD001791; RIbosomal_Li3; 1. PROSITE; PS00783; RIBOSOMAL_Li3; 1. Stibosomal protein; Multigene family SEQUENCE 197 AA; 22333 MW; CS294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL022103; CAA17885.1; -.
InterPro; IPR001074; Ribosomal_L13.
Pfam; PF00572; Ribosomal_L13; 1.
                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.48;
52.98;
                                                                                                                                                                                                                                                                                                                                               44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIBOSOMAL PROTEIN L16-C.
                                                                                                                                                                                                                                                                                                   98238
                                                                                                                                                                                                                                                                                                                                                                                                                            :|:|:| |: | | 449 KSKRHSEARFRIRCKW 464
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                           3342
3372
4118
4422
4422
5518
5518
5518
7716
7720
7738
813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPL16C OR SPBC2G2.05
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                  855 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
2298
3330
3330
3342
3342
4422
4423
4423
7426
7426
813
813
                                                                                                                                                                                                                                                                                                                                                                             ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R16C_SCHPO
043004;
                                                                        CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                     CARBOHYD
                               CARBOHYD
                                                                                                                                                                                                                                                                                                   SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                                                                                                                                                                                                                                             Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This EWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- PATHWAY: BACTERIOCHLOROPHYLL BIOSYNTHESIS.
-1- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNIT H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang 2., Bauer C.E.;
"Rhodobacter capsulatus genes involved in early steps of the bacteriochlorophyl biosynthetic pathway.";
J. Bacteriol. 172:5001-5010(1990).
--- FUNCTION: INVOLVED IN HLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
20-MAG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT H (MG-PROTOPORPHYRIN IX CHELATASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burke D.H., Alberti M., Hearst J.E.; "bchRughal bacteriochlorophyll synthesis genes of Rhodobacter capsulatus and identification of the third subunit of light-independent protochlorophyllide reductase in bacteria and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bactéria; Proteobactería; alpha subdivísion; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 1194;
Pred. No. 72;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003672; Cobn/Mg_chelatase.
Pfam; PF02514; cobn-Mg_chel; 1.
Photosynthesis; Chlorophyll biosynthesis.
SEQUENCE 1194 AA; 129361 MW; 6341816A58774EE5 CRC64;
                                                                                                                                                                                                           PRT; 1194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SB1003;
MEDLINE-93224465; PubMed-8385667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 175:2414-2422(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1170-1194 FROM N.A. MEDLINE-90368552; PubMed=2203738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z11165; CAA77524.1; -. EMBL; M34443; AAA26097.1; -. PIR; S17808. S17808. PIR; A36716; A36716. PIR; D49851; D49851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.9%;
                                  Query Match
Best Local Similarity 42.>
Best Local 6; Conservative
2 SRRY-SIGRYSVRFSWK 17
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTOROPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :|||:
|| SYLVGRYADNRDWR 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodobacter.
NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.5; DB 1; Length 197; Pred. No. 8.9;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. DAMEd=2161319; Bohni R., Brown C.M., Cerny R., Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Carny R., Chee M.S., Bankier A.T., Beck S., Bohni R., Martignetti J.A., Horshison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomilnson P., Weston K.M., Barrell B.G.; Preddie E., Satchwell S.C., Tomilnson P., Weston K.M., Barrell B.G.; Preddie E., Satchwell S.G.; Tomilnson P., Weston K.M., Barrell B.G.; Preddie E., Martignetti A.D., Tomilnson P., Weston K.M., Barrell B.G.; Cytomegalovirus Strain AD169."; Cytomegalovirus Strain AD169."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 protein.
662 AA; 74435 MW; B8B58F7ADBF25341 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                       Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
                                                                                                                                                                                                                                                                                       "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                                           no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
HYPOTHETICAL PROTEIN UL65.
                                   01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL GENE 63 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 AA
662 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
 PRT;
                                                                                                                                                                                                                                                         MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M75136; AAA88167.1; -. PIR; I36792; I36792.
                                                                                                                                                   Viruses; dsDNA viruses, no unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 RRAALPGKFSARFTW 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RRYSI-GRYSVRFSW 16
   STANDARD;
                                                                                                                                                                                                                                                                                                                Virology 186:9-14(1992)
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=10401;
                                                                                                                                                                                                                                               STRAIN=AUBURN
                                                                                                                                                                                                                                                                                 Davison A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UL65_HCMVA
P17148;
 VG63_HSVI1
Q00159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UL65_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TT recognition surface.";

AL nature 387:312-315(1997).

AL Nature 387:312-315(1997).

C. I FUNCTION: ICAMP PROTEINS ARE LIGANDS FOR THE LEUKOCYTE ADHESION

C. I-FUNCTION: ICAMP PROTEINS ARE LIGANDS FOR THE LEUKOCYTE ADHESION

C. I-FUNCTION: ICAMPORTES ADHESIVE INTERACTIONS IMPORTANT FOR ANTIGEN-

C. ADHESTON. IT MEDIATES ADHESIVE INTERACTIONS IMPORTANT FOR ANTIGEN-

C. SPECIFIC IMMUNE RESPONSE, NK-CELL MEDIATED CLEARANCE, LYMPHOCYTE

C. IMMUNE RESPONSE AND SURVEILLANCE.

C. IMMUNE RESPONSE AND SURVEILLANCE.

C. I-SIMILARITY: BELONGS TO THE ICAM FAMILY.

C. I-SIMILARITY: BELONGS TO THE ICAM FAMILY.

C. I-SIMILARITY: MAD OTHER CONTAINS OF THE ICAM FAMILY.

C. I-DATABASE: NAME-PROW; NOTE-CD Guide CD102

C. I-DATABASE: NAME-PROW; NOTE-CD Guide CD102

C. I-MWWH-"http://www.ncbi.nlm.nh.gov/prow/cd/cd102.htm".
                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-216.
MEDLINE-97297767; Pubmed-9153399;
Casasnovas J.M., Springer T.A., Liu J.-H., Harrison S.C., Wang J.-H.;
"Crystal structure of ICAM-2 reveals a distinctive integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X15606; CAA33630.1; -.
PIR; S03967; S03967.
PDB; 12XQ; 04-SEP-97.
MIM; 146630; --
Immunoglobulin domain; Cell adhesion; Glycoprotein; Transmembrane;
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCELLULAR ADHESION MOLECULE-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-Endotherial cells; TISSUE-Endotherial cells; MEDLINE-80238547; PubMed-2497351; Staunton D.E., Dustin M.L., Springer T.A.; Staunton D.E., Dustin M.L., Springer T.A.; homologous to ICAM-2, a cell adhesion ligand for LFA-1 homologous to ICAM-1."; Mature 339:61-64(1989).
                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                           ICA2_HUMAN STANDARD; PRT; 2/5 AA.
P13598;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 40, Last annotation update)
INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR (ICAM-2) (CD102).
                                                                                                         Length 102;
                                                                                                                                                 Indels
                                                        95955B885D797665 CRC64;
                                                                                                           Score 38; DB 1;
Pred. No. 8;
}; Mismatches
                                                                                                                                                                                                                                                                                                                     275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Signal; 3D-structure.
SIGNAL 1 21 E
CHAIN 22 275
                                             l protein.
102 AA; 11524 MW;
                                                                                                                   41.8%;
58.3%;
   EMBL; X17403; CAA35380.1; -. PIR; S09828; S09828.
                                                                                                                   Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                            1 RSRRYSIGRYSV 12
                                                                                                                                                                                                                 | || |:|||::
83 RRRRCSLGRYAL 94
                                               Hypothetical
SEQUENCE 10
                                                                                                                                                                                                                                                                                                           ICA2_HUMAN
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                     οy
S R R R S
```

S

```
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                          [3]
[DENTIFICATION.
                                                                                                                                                                                                                   STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Grivell L.A., de Haan M., Maat M.J.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YCR102C/YLR460C/YNL134C FAMILY.
                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                          Score 38; DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%; Score 38; DB 1; Length 368; 57.1%; Pred. No. 31;
                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                        N-LINKED (GLCNAC...).
EXTRACELLULAR (POTENTIAL).
         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inc; 1.
40121 MW; OBEE4FB4DB04AF8B CRC64;
                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
40.1 KDA PROFEIN IN GIT1-PAU3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                368 AA.
                                                                                                                                                                   Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002085; Adh_zinc.
Pfam; PF00107; adh_zinc; 1.
SEQUENCE 368 AA; 40121 MW;
                                                                                                                                30653 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59720; CAA42244.1; -. PIR; S19414; S19414.
                                                                                                                                                           41.8%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                             Conservative
                                                                                                                                                                                                           1: :| | || :|:
253 RQQRMGTYGVRAAWR 267
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1:| |||| : | |
287 RTRLYSIGGHEVPF 300
                                                                                                                                                                                               3 RRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD; S0000699; YCR102C.
223
248
275
275
98
197
190
47
47
82
1105
1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSRRYSIGRYSVRF 14
22
224
224
41
127
48
52
134
47
82
105
115
1176
275 AA;
                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4932;
                                                                                                                                                                                                                                                             YC22_YEAST
P25608;
                                                      DISULFID
DOMAIN
TRANSMEM
                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                             DISULFID
                                                                         CARBOHYD
                                                                                  CARBOHYD
                                                                                          CARBOHYD
                                                                                                     CARBOHYD
                                                                                                                               SEQUENCE
                            DOMAIN
                                                                                                                                                                                                                                                                                                                     YCR102C
                   DOMAIN
                                                                                                                                                                                                                                                     YCZ2_YEAST
ID YCZ2_Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                õ
                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
5111111111111
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or sens u..

(EMBL; 029579; AAA69271.1;

R EMBL; AE000359; AAC75803.1; -..

R EMBL; (07525; -; NOT_ANNOTATED_CDS.

DR ECGene; EG12634; ygGB.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR001405; Helicase_C.

DR InterPro; IPR001650; Helicase_C.

DR RARY; SM00490; HELICC; 1.

DR SMARY; SM00490; HELICC; 1.

DR PROSITE; PS00662; T2SP_E; FALSE_NEG.

Hypothetical protein; Transport; ATP-binding; Complete proteome.

WP BIND 118 118 G -> PL (IN REF. 2).

NP_BIND 134 331 ATP (ON TERTIAL).

NP_BIND 135 ATP (ON TERTIAL).

NP_BIND 138 ATP (ON TERTIAL).

NP_BIND 1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-RIZ / MG1652,
STRAIN-RIZ / MG1657;
Pubbed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Greger J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau E., Shao Y.;
                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-95075655; PubMed-7984428;
Borodovsky M., Rudd K.E., Koonin E.V.;
Intrinsic and extrinsic approaches for detecting genes in a bacterial genome.";
Nucleic Acids Res. 22:4756-4767(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krone F.A., Westphal G., Schwenn J.D., "Characterisation of the gene cysH and of its product phosphoadenylylsulphate reductase from Escherichia coli."; Mol. Gen. Genet. 225:314-319(1991).
YGCB_ECOLI STANDARD; PRT; 888 AA.
P38035; Q4602;
01-0CT-1994 (Rel. 30, Created)
01-NV-1997 (Rel. 35, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
YGCB OR B2761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.8%; Score 38; DB 1; Length 888; 38.5%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91172132; PubMed-2005873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-335 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 YSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : ||:::|| :|
HDIGKFDIRFQYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                             Escherichia coli.
```

11

RESULT

RESULT 10 YGCB_ECOLI

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
STRAIN-SZBBC / AB972;
Hunt S., Bowman S., Barrell B.G., Rajandream M.A.;
Buntt S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYS
-i- FUNCTION: THIS MAGNESIUM DEPENDENT OF PHOSPHOLIPIDS (POTENTIAL).
OF ATP COUPLED WITH THE TRANSPORT OF PHOSPHOLIPIDS
                                                20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT H (MG-PROTOPORPHYRIN IX CHELATASE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                View.v. 1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last annotation update)
POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 5 (EC 3.6.3.13).
YMR162C OR YM6520.11C.
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales.
                                                                                                                                                                        Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- PATHWAY: BACTERIOCHLOROPHYLL BIOSYNTHESIS.
-i- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNIT H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 1193;
Pred. No. 1.1e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003672; CobN/Mg_chelatase.
Pfam; PF02514; cobN-Mg_chel; 1.
Photosynthesis; Chlorophyll biosynthesis.
SEQUENCE 1193 AA; 129205 MW; 13DDEBD375223151 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
               1193 AA
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF195122; AAF24273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.8%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | : ||| :|
193 RYLVSRYSANRAW 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                           NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATC8_YEAST
Q12674;
                                                                                                                                                                                                                              Rhodobacter
                        BCHH_RHOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
ATC8_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                             Q9RFD5;
      BCHH_RHOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-97373830; PubMed=9230313;

Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Lee J.J., Tilghman S.M., Gumbliner B.M., Costantini F.;

The mouse Fused locus encodes Axiv, an inhibitor of the Wnt signaling

pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                          PEDUCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN-REGULATES PETACATEMIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATEMIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATEMIN AND APC BY GSK-3B.
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATEMIN. THE INTERACTION BETWEEN AXIN AND BETA-CATEMIN COCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN.

PERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATEMIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΒY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGS.
GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APC, DVL AND PP2A.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
-!- PIM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 900;
Pred. No. 79;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EE5F990B11FC7B3B CRC64;
                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
900 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD0013639; DIX; 1.
SMART; SM00021; DAX; 1.
SMART; SM00315; RGS; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SIMILARITY: CONTAINS 1 RGS DOMAIN.
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF009674; AAC51624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.8%;
56.2%;
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001158; DIX.
InterPro; IPR000342; RGS.
Pfam; PF00178; DIX; 1.
Pfam; PF00615; RGS; 1.
ProDom; PD001580; RGS; 1.
ProDom; PD003639; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 SRRYSEGREFRYGSWR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      900
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      818
900 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                               NCBI_TaxID=9606
                                                                                                                                AXINI OR AXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603816;
    AXN1_HUMAN
015169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
```

DOMAIN

DOMAIN DOMAIN

ţ

ò q

ö

Gaps

ö

HYDROLYSIS

ï

```
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMYA_PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   furiosus.
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       AMYA_PYRFU
ID AMYA_P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49057
                                                                                                 CHAIN
     DR
DR
FT
SO
                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a new hepatitis B virus (HBV) genotype from Brazil that expresses HBV surface antigen subtype adw4.";
J. Gen. Virol. 74:1627-1632(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  PSO0154; ATPASE_E1_E2; 1.
:Ical protein; Hydrolase; Transmembrane; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Naumann H., Schaefer S., Yoshida C.F.T., Gaspar A.M.C., Repp R., Gerlich W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus (subtype adw4 / strain Brazil / isolate w4B).
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 1; Length 1656;
Pred. No. 1.5e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
MAJOR SURFACE ANTIGEN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                     SGD; S0004772; YMR162C.
InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93346970; PubMed-8345355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                               EMBL; 249705; CAA89798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X69798; CAA49455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00702; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472
516
1178
1339
1386
1416
1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnesium; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1355 YSYGRLSQGFNW 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=45410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMSA_HPBVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  005496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
VMSA_HPBVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDT TO DD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. BIOL. Chem. 268:24394-24401(1993).

-!- FUNCTION: DISPLAYS A BROAD RANGE OF SUBSTRATE SPECIFICITY, WITH THE CAPACITY TO HYDROLYZE CARBOHYDRATES AS SIMPLE AS MALTOTRIOSE.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4 -ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- PATHWAY: POLYSACCHARIDE DEGRADATION.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: HOMODIMER.
-!- MISCELLANEOUS: THE ISOELECTRIC POINT IS 4.3. THE ENZYME DISPLAYS OPTIMAL ACTIVITY, WITH SUBSTANITAL THERMAL STABILLITY, AT 100 DEGREES CELSIUS.

DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anfinsen C.B.; "Alpha-amylase from the hyperthermophilic archaebacterium Pyrococcus furiosus. Cloning and sequencing of the gene and expression in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laderman K.A., Davis B.R., Krutzsch H.C., Lewis M.S., Griko Y.V., Privalov P.L., Anfinsen C.B.;
"The purification and characterization of an extremely thermostable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha amylase from the hyperthermophilic archaebacterium Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-94043280; Pubmed-8226990;
Laderman K.A., Asada K., Uemori T., Mukai H., Taguchi Y., Kato I.,
                                                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                         Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 AA; 76178 MW; BF7A495F084E0FB1 CRC64;
                                                                                                                                    MAJOR SURFACE ANTIGEN.
4A5A2212E4B3E117 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Glycosidase; Carbohydrate metabolism.
INIT_MET 0 0 SEQUENCE 648 AA; 76178 MW; BF7A495F084E0FB1
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                      Score 37.5; DE Pred. No. 41; 4; Mismatches
InterPro; IPR000349; Hepadnavir_surfAg.
Pfam; PF00695; vMSA; 1.
Antigen. 1 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 268:24402-24407(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94043279; Pubmed-8226989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                              400 AA; 43551 MW;
                                                                                                                                                                                                                                                         41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 1,22346; AAA72035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Last
ALPHA-AMYLASE (EC 3.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                               330 WALGKYLWEWASARFSW 346
                                                                                                                                                                                                                                                                                                                                                                                    5 YSIGRY----SVRFSW 16
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                    174
                                                                                                                                                                                                                            Query Match
Best Local Similarity
'-hnc 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
```

1;

```
Ouery Match 41.2%; Score 37.5; DB 1; Length 648;

Best Local Similarity 26.3%; Pred. No. 68;

Matches 5; Conservative 8; Mismatches 1; Indels 5; Gaps

Qy 4 RYSIGRYSVRFS----WK 17

Db 587 KYAVGKFALKFEDEMEVWK 605

Search completed: February 12, 2002, 12:39:54

Job time: 807 sec
```

058921 pyrococcus 09nef4 drosophila 06792 hepatitis b 0599x1 arabidopsis 067927 hepatitis b 09ftm7 oryca sativ

O9w4yO drosophila P91233 caenorhabdi O96498 marah macro

sed

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

09xuv8 caenorhaddi 09p1b2 homo sapien 09p1b2 homo sapien 09m1h3 arabidopsis 091jg4 arabidopsis 091jg4 arabidopsis 091jg4 arabidopsis 0961jg4 arabidopsis 096540 feline immu 066947 feline immu 062ug0 arabidopsis

Q45282 corynebacte P87681 feline immu Q9zkk2 helicobacte P89340 feline immu

Q85536 feline immu

```
SEQUENCE FROM N.A.
STRAIN=NORRISTONN, PA;
STRAIN=NORRISTONN, PA;
MEDLINE-97296227; PubMed-9151811;
Bachmann M.H., Mathiason-Dubard C., Learn G.H., Rodrigo A.G.,
Sodora D.L., Mazzetti P., Hoover E.A., Mullins J.I.;
"Genetic diversity of feline immunodeficiency virus: dual infection,
recombination, and distinct evolutionary rates among envelope sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20078 MW; 7E68D346AF26CCCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 12;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                               P89340

09XUV8

09YRU8

09RBB1

09LJG4

09LJG4

09LJG4

09LJG9

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940

066940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               089177 PRELIMINARY; PRT; 089177: 01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                09W4Y0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Create 01-NOV-1996 (TrEMBLrel. 01, Last s 01-NOV-1998 (TrEMBLrel. 08, Last g 01-NOV-1998 (PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clades.";
J. Virol. 71:4241-4253(1997).
EMBL; US7018; AAC57313.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.58;
                                                                                                                                  :|:|:| ||: :| |
92 KSKRHSEGRFRIRCRW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               066944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 089177
ID 01
AC 01
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSna5 arabidopsis
Q6942 feline immu
Q9416 escherichia
Q66961 feline immu
Q91y83 arabidopsis
Q66962 feline immu
Q8539 feline immu
Q8539 feline immu
Q85402 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogna43 arabidopsis
Oglbp3 western equ
Oglbk1 western equ
Ogluvd8 alternaria
Oggut8 leishmania
O89185 feline immu
O89186 feline immu
O86106 feline immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q66944 feline immu O89177 feline immu
                                                                                                                                (without alignments)
10,689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                               February 12, 2002, 12:38:42; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                              473505
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SNA5
Q66942
Q96416
Q66961
Q9LY83
Q66962
Q66962
Q66962
Q95539
Q94W2
Q9H9V5
Q9H9V5
Q9H9V5
Q9H9V5
Q9H9V7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GUT8
089185
089186
Q86106
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                             US-09-485-571-30
91
1 RSRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
112
113
113
115
115
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_mhc:*
```

ö

Gaps ö

40.5 40 40

Score

Result

```
Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E., Kaper J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete Nucleotide Sequence and Analysis of the Locus of Enterocyte Effacement from Rabbit Diarrheagenic Escherichia coli RDEC-1."; Enfect. Immun. 69:2107-2115(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K., Lai L.C., Walmara B.P., Donnenberg M.S., Kaper J.B.;
Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.;
rhe complete sequence of the locus of enterocyte effacement (LEE) from enteropathogenic Escherichia coli E2348/69.";
Mol. Microbiol. 28:1-4(1998).
                                                                                                                                                   STRAIN-PORTOLA VALLEY, CA;
MEDLINE-97296227; PubMed-9151811;
Bachmann M.H., Mathiason-Dubard G., Learn G.H., Rodrigo A.G.,
Bachmann M.H., Mazzetti P., Hoover E.A., Mullins J.I.;
Sodora D.L., Mazzetti P., Hoover E.A., Mullins J.I.;
"Genetic diversity of felline immunodeficiency virus: dual infection,
"Genetic diversity of felline immunodeficiency virus: dual infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 675;
                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 12; Length 170;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675 AA; 75150 MW; CDBCE6B243B04160 CRC64;
                                                                                                                                                                                                                                                                                                                                    1FC2B684A054D688 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
             Last sequence update)
Last annotation update)
                                                                     Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core 43; DB 2;
red. No. 62;
Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
01, Created)
01, Last sequ
08, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RDEC-1;
MEDLINE=21153569; PubMed=11254564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RDEC-1;
MEDLINE=98254123; PubMed=9593291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
01-NOV-1996 (TrEMBLrel. 01, Crea 01-NOV-1996 (TrEMBLrel. 01, Last 01-NOV-1998 (TrEMBLrel. 08, Last GP100 SURFACE PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                        20003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                                               clades.";
J. Virol. 71:4241-4253(1997).
EMBL; U57016; AAC57311.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       47.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 KSRTHSSGRFRIRCRW 107
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RRYSIGRYSVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             170 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                              1
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AJ16
Q9AJ16;
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q9AJ16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                            Wateri T., Tsujimoto H., Hasegawa A.; Wateri T., Tsujimoto H., Hasegawa A.; "Genetic heterogeneity of ENV gene of Feline immunodeficiency virus "Genetic heterogeneity of ENV gene of Papan."; obtained from several districts in Japan."; Submitted (JAM-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AB010397; BAA31442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Choisne N., Robert C., Brottier P., Wincker P., Cattolico L., Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Length 124;
                                                                                                                                                                          Nishimura Y., Goto Y., Hai P., Momoi Y., Endo Y., Mizuno T.,
                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 12; Length 208;
Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUR Arabidopsis sequencing project;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ALI33298; CAB62022.1;
Hypothetical protein.
SEQUENCE 124 AA; 13994 MW; 7B398B9C8AD44E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                        CD2AAECE2CEA777B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or mai-zoud (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
HYPOTHETICAL 14.0 KDA PROFEIN.
               01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) ENVELOPE GLYCOPROTEIN (FRAGMENT).
                                                                                           Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBL_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1
6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                              208 208 ...
208 AA; 24090 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%;
                                                                                      Feline immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                           49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| |: : |||:||
95 SKRASLKGEVVRFTWK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 KSRKYSEARFRIRCKW 105
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
1.20 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Envelope protein.
                                                                                                                                                                      STRAIN-AIC02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             066942
066942;
```

Q9SNA5

RESULT Q9SNA5

δy g

ö

SEQUENCE NON_TER

ö

4

RESULT Q66942

A D

οy.

q

Gaps ö

Indels

066961;

066961 9

RESULT Q66961

g

```
"Nucleotide sequence of feline immunodeficiency virus: classification of Japanese isolates into two subtypes which are distinct from non-dapanese subtypes.";
J. Virol. 69:3639-3646(1995).

EMBL; D37817; BAA07063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mullins J.I.;
"Identification of three felline immunodeficiency virus (FIV) env gene
"Identification of the FIV and human immunodeficiency virus
subtypes and comparison of the FIV and human immunodeficiency virus
type 1 evolutionary patterns.";
J. Virol. 68:2230-2238(1994).
ENEL: U02421; AAA18045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodora D.L., Shpaer E.G., Kitchell B.E., Dow S.W., Hoover E.A.,
                                                                                                                                                                                                                                                                                                                                                                                   Kakinuma S., Motokawa K., Hohdatsu T., Yamamoto J., Koyama H.,
Hashimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 12; Length 855;
Pred. No. 1.2e+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein; Envelope protein.
SEQUENCE 855 AA; 98196 MW; 1158C3FA8DA06BED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26039 MW; C33E18FFB5458C58 CRC64;
                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ENVELOPE POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                    Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feline immunodeficiency virus.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
5
                                                                                                                                                    855 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002050; Env_polyprotein.
Pfam; PF00429; ENV_polyprotein; 1.
                                                                                                                                                                                    01, Created)
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95264455; PubMed-7745712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=USOKLGRL02B;
MEDLINE=94187063; Pubmed=8139008;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 08,
                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|::|| |::| | 449 KSKKYSEARFRIRCKW 464
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                  (TrEMBLrel.
                             S RRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TremB
01-NOV-1996 (TremB
01-NOV-1998 (TremB
GP100 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                        STRAIN-AOMORI
                                                                                                                                                                                  01-NOV-1996
01-NOV-1996
01-JUN-2001
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TEF.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                               Q66962
Q66962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  085539
                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Matches
                                                                                                                 RESULT
Q85539
                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of feline immunodeficiency virus: classification of Japanese isolates into two subtypes which are distinct from non-Japanese subtypes."
J. Virol. 69:3639-3646(1995).
EMBL: D37816; BAA07062.1; -.
InterPro; IPR002059; ENV_polyprotein.
Pfam; PF00429; ENV_polyprotein; I.
Polyprotein; Envelope protein.
SEQUENCE 855 AA; 97876 MW; IFDD34E0DACFE204 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F18022_250. Arabidopsis thaliana (Mouse-ear cress). Eukaryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Bevan M., wurphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W. Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                           .
MEDLINE-95264455; PubMed-7745712;
Kakinuma S., Motokawa K., Hohdatsu T., Yamamoto J., Koyama H.,
Hashimoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL163817; CAB87785.1;
InterPro; IPR002501; TruB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61475 MW; A9379FFDB44ED803 CRC64;
                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRNA SYNTHASE-LIKE PROFIN.
                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 12;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 10;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 540 AA.
                                                                                                855 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                  Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%;
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||:| |: :| |
449 KSRRHSEARFRIRCKW 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01509; TruB_N;
SEQUENCE 540 AA; 614
                                                                                                                                                                                ENVELOPE POLYPROTEIN.
11: :||||||
563 RRHILGRYSVR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
```

LY83;

Q9LY83

RESULT Q9LY83

q

ò

ö

Gaps

ö

Indels

```
REGISTER FROM N.A.

SEQUENCE FROM N.A.

AN ING. CCOLUMBIA;

RA LIU S.X., Sakano H., Yu G., Toriumi M., Lenz C., Lee J.M., Li J.,

RA Liu S.X., Sakano H., Yu G., Toriumi M., Lenz C., Hwong B., Chol E.,

Liu A., Gonzalez A., Liu K., Vaysberg M., Chin C., Hwong B., Chol E.,

RA Liu A., Conway A.B., Hansen M., Johnson-Hopson C., Khan S., Kim C.,

RA Conn L., Conway A.B., Hansen M., Johnson-Hopson C., Khan S., Kim C.,

RA Lam B., Nguyen M., Palm C., Shinn P., Tambunga G., Davis R.W.,

Lam L., Federspiel N.A., Theologis A.;

RATALIGORS J. AAFE3900.1 T.

BEER J. AAC09999; AAFE3900.1 T.

BEBL; AC09999; AAFE3900.1 T.

BEBL; AC09999; FYICH.C.

DR INTERPRO; IPR003888; FYICH.C.

DR INTERPRO; IPR003888; FYICH.C.

DR INTERPRO; IPR003189; FYICH.C.

DR INTERPRO; IPR003145; PRIC.

DR INTERPRO; IPR003145; PRIC.

DR INTERPRO; IPR001214; SET.

DR INTERPRO; IPR001214; SET.

DR SMART; SW00541; FYRN; 1.

DR SMART; SW00541; FYRN; 1.
                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4F2B3D5776A30DF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TIEMBLEEL. 15, Created)
01-OCT-2000 (TIEMBLEEL. 15, Last sequence update)
01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
                                                                                                                     01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2001 (TrEMBLrel. 17, Last annotation update)
T20M3.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 39.1%; Pred. No. 2.5e+02;
Matches 9; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1235 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00293; PWWP; 1.
SMART; SM00317; SET; 1.
PROSITE; PS00190; CYTCCHROME_C; UNKNOWN_1.
PROSITE; PS00280; SET; 1.
SEQUENCE 1193 AA; 135416 MW; 4F2B3D577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-259 FROM N.A.
STRAIN-MCMILLAN;
MEDLINE-96097271; PubMed=8535272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| |:|
564 RKYSSGKYQDHPTGYRPVRVEWK 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 RRYSIGRYS-----VRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PostSET; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
STRUCTURAL POLYPROTEIN.
                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-11039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00249;
SMART; SM00508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9IBP3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IBP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
Q9IBP3
                                                                                                Q9MA43
                                              RESULT 12
                                                                            09MA43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SO DE TENERS OF SERVICE OF SERVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Ota T., Sugano S., Shiratori A., Sudo H.,

Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Vamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.;

Ninomiya K., Iwayanagi T.;

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ CRC64;

SEQUENCE 734 AA; 83064 MW; A35CC38F95C39F7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12525 FIS, CLONE NT2RW4000030, WEAKLY SIMILAR TO LAS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 4; Length 734;
Pred. No. 1.5e+02;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 5; Mismatches 5; Indels
Score 41; DB 12; Length 225;
Pred. No. 41;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1999). SEQUENCE 717 AA: 81242 MW; 651B7F0FFB3FD07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           734 AA
                                                                                                                                                                                                                                                                                                                   717 AA
                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.1%;
                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, C1
01-NOV-1999 (TrEMBLrel. 12, Li
01-MAY-2000 (TrEMBLrel. 13, Li
DJ475B7.2 (NOVEL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             437 ARRESAGOWEARRGWR 452
              45.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11:1 1:: 1 1:
420 ARRESAGQWEARRGWR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SRRYSIGRYSVRFSWK 17
:|::|| |::| |
107 KSKQYSEARFRIRCKW 122
                                                                                                                        1 RSRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
```

Q9H9V5

RESULT 11

g ò

RESULT 10
09Y4W2
C 09Y4W2
AC 09Y4W2
DT 01-N0V

Ω ŏ

7

g δλ

1;

Gaps

; 8

S

ö

Gaps

ö

```
"Complete genomic RNA sequence of western equine encephalitis virus and expression of the structural genes.";
J. Gen. Virol. 8:1151-159(2000).
EMBL, AF214040; AAF28140.1; -
InterPro; IPR001836; Alpha_core.
InterPro; IPR001836; Alpha_EL_glycop.
InterPro; IPR0002533; Alpha_E2_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF00589; Alpha_E2_glycop.
InterPro; IPR000930; Togavirin.
Pfam; PF01589; Alpha_E2_glycop; I.
Pfam; PF01589; Alpha_E2_glycop; I.
Pfam; PF01589; Alpha_E2_glycop; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Dothideomycetes,
Pleosporales, Pleosporaceae, mitosporic Pleosporaceae, Alternaria.
NCBL_TaxID=5599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

A TRANSPOSON=LTR-RETROTRANSPOSON REAL;
A TRUGE T. Kaneko I.;
STRAIN-15A; TRANSPOSON=LTR-RETROTRANSPOSON REAL;
A TSUGE T. Kaneko I.;
"REAL: an LTR-retrotransposon of the plant pathogenic fungus alternaria alternata.";
Alternaria alternata.";
Submitted (MAR: 1999) to the EMBL/GenBank/DDBJ databases.
I SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE TRANSCRIPTASE).
REMBL; AB025309; BAA89272.1; -
R InterFro; IPR000953; Chromo.
R InterFro; IPR000504; RRW.
R InterFro; IPR000477; RVTse.
R InterFro; IPR000737; Squash.
R Pfam; PF00665; rve; I.
R Pfam; PF006075; rve; I.
                                                                                                                                                                                                                                                                                 Score 41; DB 12; Length 1236;
Pred. No. 2.6e+02;
4; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 3; Length 120
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                        1236 AA; 136266 MW; 56B752C0D19CD3F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144367 MW; 6E5DAF287D461C6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00293; SQUASHINHBTR.
SMART; SM00298; CHROMO; 1.
PROSITE; PS50013; CHROMO_2; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.18;
                                                                                                                                                                                                                                                                                      45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-directed DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                        PRINTS; PR00798; TOGAVIRÍN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|| || | : ||
1116 QQYSTGRSSKKLDWK 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                       635 SRNFSVGREGLEYVW 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                   2 SRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 RRYSIGRYSVRFSWK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternaria alternata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 1265 AA;
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POL (FRAGMENT).
                                                                                                                                                                                                                         Polyprotein.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UVD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9UVD8
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              90VD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
    δ
                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
 Uryvaev L.V., Lebedev A.Iu, Sokolova T.M., Iuferov V.P.; "Primary structure of the nucleocapsid gene C and the protein coded by it from the Western equine encephalomyelitis virus."; botl. Akad. Nauk 344:397-401(1995).
                                                                                                                                                                                                                                                   Uryvaev L.V., Lebedev A.Iu, Sokolova T.M., Iuferov V.P.; "Cappid glycoprotein of E2 Encephalitis Virus, Western Equine: primary structure of gene and its product."; bokl. Akad. Nauk 357:134-139(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Netolitzky D.J., Schmaltz F.L., Parker M.D., Rayner G.A., Fisher G.R.,
Trent D.W., Bader D.E., Nagata L.P.;
                                                                                                                         Uryvaev L.V., Lebedev A.Iu.; "Comparative analysis of primary structure of nucleocapsid protein from Western equine encephalomyelitis virus and other alphaviruses."; Vopr. Virusol. 41:252-259(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Western equine encephalitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                            Primary structure of WEEV 26S RNA.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AF229608; AAPG0166.1;
InterPro; IPR001836; Alpha_core.
R InterPro; IPR001836; Alpha_E1_glycop.
R InterPro; IPR002548; Alpha_E2_glycop.
R InterPro; IPR002936; Alpha_E3_glycop.
R InterPro; IPR002939; Alpha_E3_glycop.
R Pfam; PF00944; Alpha_Core; 1.
R Pfam; PF00944; Alpha_E1_glycop; 1.
R Pfam; PF00594; Alpha_E2_glycop; 1.
R Pfam; PF01569; Alpha_E2_glycop; 1.
R Pfam; PF01569; Alpha_E3_glycop; 1.
R Pfam; PF01569; Alpha_E3_glycop; 1.
R Pfam; PF01569; Alpha_E3_glycop; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 12; Length 12
Pred. No. 2.6e+02;
4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27AD7CED71EEBD4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
STRUCTURAL POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E3-POLYPEPTIDE.
E2-PROTEIN.
6K-POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E1-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-71V-1658;
MEDLINE-20109043; Pubmed-1064053;
                                                                                                            MEDLINE-97130212; PubMed-8999681;
                                                                                                                                                                                                                      STRAIN-MCMILLAN;
MEDLINE-98100973; PubMed-9471275;
                                                                                                                                                                                                        SEQUENCE OF 320-742 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1235 AA; 136352
                                                                              SEQUENCE OF 1-259 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 SRNFSVGREGLEXVW 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SRRYSIGRYSVRFSW 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
319
742
807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11039;
                                                                                               STRAIN-MCMILLAN;
                                                                                                                                                                                                                                                                                                                                                STRAIN-MCMILLAN;
                                                                                                                                                                                                                                                                                                                                                                Uryvaev L.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9J1K1
Q9J1K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

ö

Gaps

us-09-485-571-30.rspt

Search completed: February 12, 2002, 12:38:43 Job time: 756 sec

Wed Feb 13 07:51:52 2002

Page

```
February 12, 2002, 12:30:30 ; Search time 242.57 Seconds (without alignments) 5.497 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_1101:*

| SIDSB/gcgdata/geneseq/geneseqp/AA1980_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1982_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1984_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1984_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1985_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1987_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1987_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1981_DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AA1991_DAT:*
| SIDSB/gcgdata/geneseqf/geneseqp/AA1991_DAT:*
| SIDSB/gcgdata/geneseqp/AA1991_DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS8/gcgdata/geneseg/genesegp/AA1993.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1994.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqp/AA1997.
/SIDS8/gcgdata/geneseq/geneseqp/AA1998.
/SIDS8/gcgdata/geneseq/geneseqp/AA1999.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 XGGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-485-571-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	New DNA sequence i	KIAA0160 polypepti	Human secreted pro	Eucalyptus grandis	Human potassium ch	Human Signal pepti	A human proliferat	Human protein segu	Protein encoded by	SUP-B27 t(1;19) tr	E2A/prl fusion pro
	;	ID	AAW56163	AAB00066	AAG02285	AAB32776	AAY79674	AAY87291	AAY84906	AAB94371	AAY02540	AAR13949	AAR15158
	:	: 8	19	77	21	21	21	21	21	22	20	12	13
	Query	Length	738	803	102	129	394	394	526	526	623	736	742
ф	Query	March	51.5	51.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5	48.5
		score	17	17	16	16	16	16	16	16	16	16	16
	Result	Q	7	7	e	4	ഗ	9	7	80	6	10	11

SUP-B27 t(1:19) tr E2A/Pr1 fusion pro Human secreted pro Protein encoded by Spider recombinant Rice beta-glucanas Rice Gag CDS prot C glutamicum prote Protein encoded by Spider recombinant Spider recombinant Human colon cancer A. fumigatus aller Human protein HP10 Arabidopsis thalia Rat mACHR-6 protein Rat mACHR-6 protein Rat G protein coup Human protein HRAF Human protein HRAF Human protein HP10 Arabidopsis thalia Arabidopsis thalia	de . d as r
AAR13948 AAR13951 AAG02803 AAY022803 AAY09298 AAY09296 AAY09296 AAY02541 AAB2609 AAB2609 AAG26489 AAG26489 AAG26489 AAG26489 AAG26489 AAG26489 AAG26489 AAG26489 AAG32977 AAM40773 AAM40773 AAM413373 AAM13373 AAM13373 AAM13373 AAM1373 AAM71374 AAG41762 AAG41762 AAG41762 AAG41762	ALIGNMENTS ; 738 AA. cosmetic. cosmetic. 1. 9. K. K. Sents protein encoded by ata. The protein be use
\$\text{6.5} \text{5.5}	d; Protein; rst entry) isolated f protein; c 7JP-0138461 6JP-0184459 SEIYAKU KK 723 vector, h ide in high -11; 15pp; ence repres
00000000000000000000000000000000000000	AW56163 stan AW56163; 8-JUL-1998 ew DNA seque inctada fuca inctada fuca P10080285-A. 1-WAR-1998. 8-MAY-1997; 5-JUL-1996; MIKI-, MIKIP PI; 1998-254 -PSDB; AAV22 ew CDNA and roduce polyFlaim 9; Page he present solated from
	RESULT AAW 56 LIT AAW 56 LIT

in cosmetics

Sequence

SXXC

AAB00066;

AAB00066 ID AAB0

g ò

```
The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs expressed from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3. Contranslated region (UTR) of the mRNA because they are often obtained untranslated region (UTR) of the mRNA because they are often obtained isolating cohn sequences derived from the 5. ends of mRNAs and even in isolating cohn sequences derived from mRNAs with intext 5. Those cases where longer cDNA sequences have been obtained, the full 5. The isolating can therefore be used to obtain full length cDNAs and genomic DNAs. 5. ESTs are derived from mRNAs with intext 5. DNAs. 5. ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream chromosome mapping procedures. They are used to obtain upstream croulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
                                                                                                                                                             ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis transcription factor protein sequence #234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 21; Length 10
Pred. No. 4.5e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; SEQ ID 6366; 71pp + CD-ROM; English.
                                                                                                                                Juman secreted protein, SEQ ID NO: 6366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB32776 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                             AA.
                         AAG02285 standard; Protein; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                        21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                             99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXX 18
                                                                                                     06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 ggsssgtttttttttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC02291
                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999;
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                    EP1033401-A2.
                                                                                                                                                                                                                                                                                                         06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB32776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                AAG02285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AAB32776
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid sequences obtained from the VRNZ locus of a plant encode polypeptides which are capable of affecting one or more vernalization responses such as, flowering time, leaf size and/or shape or the shade avoidance response of a plant into which the nucleic acid is introduced. Introducing such sequences into plants to alter these characteristics maximises the reproductive success of the plant. This protein is encoded an isolated human sequence which has homology to the Arabidopsis thaliana VRNZ gene over a short region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated vernalization gene VRN2 is used to produce transgenic plants with altered vernalization response, flowering time, leaf size and/or shape or shade avoidance response for maximized reproductive success
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Vernalization gene; VRN2; plant characteristic; flowering time; leaf size; leaf shape, shade avoidance response; reproduction; breeding; pollination; cultivation; human.
                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21; Length 803;
                                                                                           DB 19; Length 738;
1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 21; Length 80
Pred. No. 1.1e+04;
0; Mismatches 14; Indels
                                                                                                                                    14; Indels
                                                                                                                                        0; Mismatches
                                                                                                   Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 79; 105pp; English.
                                                                                                                                                                                                                                                                                                   AAB00066 standard; Protein; 803 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2000; 2000WO-GB00248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 ggsysasssssaaaag 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99GB-0001927
                                                                                                   51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                             280 ggsaaaaaaaaaagg 296
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                       2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-499333/44.
N-PSDB; AAA47759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  KIAA0160 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gendall A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                    738 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200044918-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000
```

Dean C,

ö

Gaps

; 0

Sequence

4

ŏ Db

Length 102;

```
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY87291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY87291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, belix.loophelix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain cys2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-halix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TASK1; TWIK-related acid-sensitive K+ channel 1; human; potassium channel; drug screening; hypertension; hypotensive; epilepsy; arrhythmia; vascular diseases; neurodegenerative disease; ischaemia; anoxia; endocrine disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 21; Length 129;
Pred. No. 5.3e+03;
F. Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Wood M, McGrath A, Shenk MA, Glenn M;
                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY79674 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 300; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human potassium channel TASK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%;
                                                                                                                                                                                                                                             09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                                                                                                        99US-0266513
                                                                                                                                                                                                                                                                                                            99US-0149485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 17.00;
Angle 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 ggssssaaraassseag 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-579369/54
                                                                                                            Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 AA;
                                                                                                                                                     WO200053724-A2.
                                                                                                                                                                                                                                                                                      11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2000
                                                                                                                                                                                                14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
      $\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\times_{\time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
Human; signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of human TASK1 (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675). TASK1 is expressed in many different tissues, and at particularly high levels in pancreas and placenta. C Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anoxia, endocrine diseases associated with anomalies of hormone secretion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human signal peptide containing protein HSPP-68 SEQ ID NO:68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 21;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                   "O-phosphorylated"
                                                                                                         "O-phosphorylated"
                                                                                                                                                          "O-phosphorylated"
                                                                                                                                                                                                                   "O-phosphorylated"
'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY87291 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lazdunski M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 8; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0107692.
99US-0436265.
                                                                                                                                                                                                                                                                                                                                                                                     99WO-IB01886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 ggsahttdtasstaaag 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                   /note-
                                                                                                         /note=
392
                                                                                                                                                               /note=
                                                                                                                                                                                                                        /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duprat F, Lesage F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Locai Similarity
The 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 3000-376487/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and muscle diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB: AAA27746
                                                                                                                                                                                                                                                                         40200027871-A2
                         Modified-site
                                                                             Modified-site
                                                                                                                                   Modified-site
                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1998;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-2000
                                                                                                                                                                                                                                                                                                                               18-MAY-2000
```

A human proliferation and apoptosis related protein.

21-AUG-2000 (first entry)

AAY84906;

AAY84906 standard; Protein; 526 AA.

```
AAY84906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ AAZ98109 to AAZ98242 encode AAX87224 to AAX87357 which represent the chuman signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have controlled and entiasthmatic activities, and can neuroprotective, cardiovascular and antiasthmatic activities, and can neuroprotective, cardiovascular and antiasthmatic activities of associated with decreased activity or function of HSPP. Such diseases include cell proliferation (HSPP act used to treat or prevent diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, (including cancer), inflammation, cardiovascular, neurological, creproductive or developmental disorders, (e.g. arteriosclerosis, corganic assemic heart disease, microbial or other infections, congestive or schman, can be used for the recombinant production of HSPP diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP diseases, schizophrenia, ovulatory defects, muscular dystrophy), HSPP diseases, schizophrenia, ovulatory defects, muscular dystrophy), HSPP diseases, schizophrenia, ovulatory defects, muscular dystrophy), HSPP cucleic acids can be used for the recombinant production of HSPP, cor genetic variations, and for chromosomal mapping HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and cancer diseases (Ab) and to screen for agonists or antagonists (potential therapeutic agents). Ab are used to diagnose, or antagonists forcential therapeutic agents). Ab are used to diagnose, or antagonists, in competitive drug screens, and for purification of HSPP controlled antagonists, and an amplement or succession of the prerepeutic antagonists, in competitive drug screens, and for purification of HSPP controlled to the control or purification of HSPP controlled or antagonists, and an advanced to diagnose, or some drugonists and antagonists, and controlled the control or purification of HSPP controlled to the control or purification of HSPP controlled 
antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
m IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 21; Length 394; Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 207-208; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0090762.
98US-0094983.
98US-0102686.
98US-0112129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US14484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-160673/14.
N-PSDB; AAZ98176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA;
                                                                                                                                                                                                                                                           muscular dystrophy
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200000610-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akerblom IE,
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandman 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal P,
```

```
Human; proliferation and apoptosis related protein; PROAP; psoriasis; cell proliferative disorder; immunological disorder; hepatitis; reproductive disorder; arteriosclerosis; cirrhosis; melanoma; lymphoma; cancer; acquired immune deficiency syndrome; AIDS; allergy; anaemla; asthma; diabetes mellitus; osteoarthritis; endometriosis; uterine fibroid; menstrual cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "potential phosphorylation site"
383
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "potential phosphorylation site"
407
                                                                                                                                                                                                                                                                                                                              /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                          /note= "potential phosphorylation site"
285
                                                                                                                                                                                                                                                                                                                                                                     /note= "potential phosphorylation site"
290
                                                                                                                                                                                                                                                                                                                                                                                          "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                              'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                           'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                "potential phosphorylation site"
                                                                                                                                                                                                        "potential phosphorylation site"
                                                                                                                                                                                                                           "potential phosphorylation site"
                                                                                                                                                                                                                                                                    /note= "potential glycosylation site"
                                                                                                                                                                                                                                                                                       "potential glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "potential phosphorylation
                                                                                                                                                                                l..25
⁄note= "signal peptide"
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0172216.
99US-0118559.
99US-0172229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US24511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
470
                                                                                                                                                                                                                                                                                                                                                                                                /note= '
342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
436
                                                                                                                                                                                                                                 /note=
137
                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200023589-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-1998;
04-FEB-1999;
11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-0CT-1999;
                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                Peptide
```

ö

Gaps

.; 0

Indels

14;

0; Mismatches

Conservative

276 ggsahttdtasstaaag 292

g δà

RESULT

2 GGXXXXXXXXXXXX 18

S

```
WO9909:174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY02540;
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY02540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
  δ
                                                                                                                                                                        The present sequence represents a human proliferation and apoptosis related protein (PROAP). The polypeptides and polynuclectides can be used for the diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. Disorders associated with decreased expression or activity of include arteriosclerosis, cirrhosis, hepatitis, psoriasis, melanoma, lymphoma and cancers of the breast, brain and prostate, acquired immune deficiency syndrome (AIDS), allergies, anaemla, asthma, diabetes mellitus, osteoarthritis, andergies, uterine fibroids and disruptions of the mensitual cycle. Antibodies against PROAP can be use in diagnosis of disorders characterized by PROAP e.g. in ELISA (enzyme linked immunosorbent systs) and the polynuclectides may be used to detect and quantify gene expression in biopsied tissues. These techniques can also be used to monitor regulation of PROAP levels during therapeutic intervention.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                          New human proliferation and apoptosis related protein polypeptides used for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                           Lal P;
                                                                                                                                                                                                                                                                                                                                                                             Length 526;
                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 21; Length 52
Pred. No. 1.4e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sogai T, Nishikawa T, Hayashi K, Saito K, Y
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                           Guegler KJ, Corley NC, Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:14909.
                                                                                                                                                     Claim 1; Page 106-107; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94371 standard; Protein; 526 AA.
                                           Hillman JL, G
n MR, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0248036
 99US-0154336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ggsssgttttttttgg 39
                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                       Azimzai Y, Baughn MR,
                                                                          WPI; 2000-339688/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                           Yue H,
                                                                                       N-PSDB; AAA15006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1074617-A2.
22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T, IS
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB94371;
                                                                                                                                                                                                                                                                                                                                               Sequence
                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94371
                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
The present invention describes primer sets for synthesising 5602

full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence. Where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide of the primer sets can be used in antisense therapy and
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03658 and
AAH03633 to AAH03629 to AAH03629
condection and condec
                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobitrazol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 22; Length 526; Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by wheat Rht clone 5al genomic sequence.
                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 14909; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY02540 standard; Protein; 623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB02383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 ggsssgttttttttgg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harberd NP, Peng J,
WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum.
                                                                                                                                                                                                                                                 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 AA;
```

```
736 AA;
N-PSDB; AAQ13673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09113172-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-1991
                                                                                                                                                                                                                                                                       homeodomains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR15158;
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR15158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                 Qγ
  The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with used to produce Rht mutant plants which are dwarfed compared with which the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the wheat Rht clone Sal genomic sequence.
                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin; enhancer-binding factor; E12; E47; E2A; homeoprotein;
chromosomal translocation; leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                                       Gaps
                                   New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ρ;
                                                                                                                                                                                                                                                                                               Score 16; DB 20; Length 623;
Pred. No. 1.5e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mccaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUP-B27 t(1;19) translocation fusion protein - clone KJ9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478..736
/note= "chromosome 1-derived sequence"
621..684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murre C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..477
/note= "E2A identical sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltimore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13949 standard; Protein; 736 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (STRD ) LELAND STANFORD JR UNIV. (WHIT-) WHITEHEAD INST BIOMED RE.
                                                                                  Disclosure; Fig 8b; 88pp; English.
                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-0484063.
                                                                                                                                                                                                                                                                                                   48.5%;
milarity 17.6%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91WO-US01168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mellentin JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    181 ggsstsssssslgg 197
                                                                                                                                                                                                                                                                                                                                                2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-281484/38.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
           WPI; 1999-181040/15.
N-PSDB; AAX36279.
                                                                                                                                                                                                                                                                        623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9113172-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleary ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13949;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                            qq
              ò
```

```
The E2A gene (see AAQ13669), encoding immunoglobulin enhancer-binding CC factors E12 and E47 (see AAQ13670 and AAQ13671), is localised to the breakpoint of a consistently recurring chromosomal translocation composed in many acute leukemias and is structurally altered by most present in many acute leukemias and is structurally altered by most (17.19) chromosomal translocations. The translocation results in cypthesis of a fusion mRNA (see AAQ13672 for fusion cDNA) that crosses synthesis of a fusion mRNA (see AAQ13672 for fusion cDNA) that crosses composite nucleotide sequences of the SUP-B27 fusion cDNAs were composed and represented in a composite sequence (see AAQ13672). CC determined and represented in a composite sequence (see AAQ13672). Cc clone KJ9 differs from the other four fusion cDNAs in that it has a cloodes a predicted 80 KD protein. The KJ9 variant concodes a predicted fusion proteins contd. the amino two-thirds of although the predicted fusion proteins contd. the amino two-thirds of dimerisation motif, which was replaced by a polypeptide encoded by conclaps with a region in homeoproteins that correspond to their correspond to their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin; enhancer-binding factor; chromosomal translocation;
leukemia; fusion protein.
Detection of t(1,19) break-point-associated genes E2A and prl in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E2A/prl fusion protein TYPE II from clone 697-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%; Score 16; DB 12;
17.6%; Pred. No. 1.7e+04;
iive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= E2A/pr1_breakpoint
485.742
/label= pr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR15158 standard; Protein; 742 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRD ) LELAND STANFORD JR UNIV. (WHIT-) WHITEHEAD INST BIOMED RE.
                                                                                                                                            Disclosure; Fig 8; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0484063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..484
/label= E2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91WO-US01168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 ggsaaaaaaaaaggag 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484..485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also AAQ13669-75.
```

```
present in many acute leukemias and is structurally altered by most tilly chromosomal translocation present in many acute leukemias and is structurally altered by most tilly) chromosomal translocations. The translocation results in synthesis of a fusion mRNA (see AAQ13672 for fusion cDNA) that crosses the breakpoint between chromosome 1 and 19.

The complete nucleotide sequences of the SUD-B27 fusion cDNAs were determined and represented in a composite sequence (AAQ13672).

The fusion cDNAs encode a 85 kD protein. Clone KJ9 differs from the other four fusion cDNAs in that it has a small deletion of chromosome 1-derived DNA (see AAQ13673).

Although the predicted fusion proteins contd. the amino two-thirds of EZA, they no longer retained the helix-loop-helix DNA-binding and climatisation motif, which was replaced by a polypeptide encoded by overlaps with a region in homeoproteins that correspond to their
factors E12 and E47 (see AAQ13670 and AAQ13671), is localised to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin; enhancer-binding factor; chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of t(1,19) break-point-associated genes E2A and prl in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mccaw P;
                                                                                                                                                                                                                                                                                                                                                                                               Length 819;
                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleary ML, Mellentin JD, Baltimore D, Murre C,
                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 12;
Pred. No. 1.8e+04;
); Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E2A/prl fusion protein TYPE I from clone 697-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484..485
/label= E2A/prl_breakpoint
485..825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13951 standard; Protein; 825 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STRD ) LELAND STANFORD JR UNIV. (WHIT-) WHITEHEAD INST BIOMED RE
                                                                                                                                                                                                                                                                                                                                                                                               48.5%;
ilarity 17.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-US01168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0484063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485..825
/label= pr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 ggsaaaaaaaaaggag 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                        See also AAQ13669-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-281484/38.
N-PSDB; AAQ13674.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                            819 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9113..72-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13951;
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR13951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin; enhancer-binding factor; E12; E47; E2A; homeoprotein; chromosomal translocation; leukemia; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The E2A gene (see AAQ13669), encoding immunoglobulin enhancer-binding
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of t(1,19) break-point-associated genes E2A and prl -
in chromosomal translocation, and prods. useful in diagnosis and
therapy of human neoplasm, esp. acute lymphoblastic leukaemia
                                                                                                     Detection of t(1,19) break-point-associated genes E2A and pr1 in chromosomal translocation, and prods. useful in diagnosis and therapy of human neoplasm, esp. acute lymphoblastic leukaemia
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mccaw P;
                  Mccaw P;
                                                                                                                                                                                                                                                                                                                         Length 742;
                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478.819
/note= "chromosome 1-derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murre C,
                  Murre C,
                                                                                                                                                                                                                Fusion protein Type I is represented in AAR13951
See also AAQ13669-75.
                                                                                                                                                                                                                                                                                                                         Score 16; DB 12;
Prèd. No. 1.7e+04;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "E2A identical sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUP-B27 t(1;19) translocation fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleary ML, Mellentin JD, Baltimore D,
                  Baltimore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- homeodomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13948 standard; Protein; 819 AA.
                                                                                                                                                                              Disclosure; Fig 4B; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STRD ) LELAND STANFORD JR UNIV. (WHIT-) WHITEHEAD INST BIOMED RE.
                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91WO-US01168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0484063
                                                                                                                                                                                                                                                                                                                                                                                                                                519 ggsaaaaaaaaaggag 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                  Mellentin JD,
                                                                                                                                                                                                                                                                                                                                                                                               2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-281484/38.
N-PSDB; AAQ13672.
                                                  WPI; 1991-281484/38.
                                                                                                                                                                                                                                                                      742 AA;
                                                                       N-PSDB; AAQ13674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9113172-A.
                  Cleary ML,
                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR13948
```

ö

Gaps

ö

ò

g

Gaps

; 0

Indels

14;

Mismatches

; 0

Conservative

э; Э

21

δ g

```
Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Triticum Aestivum polynucleotides - encode a polypeptide whi
provides inhibition of the growth of plants, which inhibition is
antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                 Protein encoded by rice EST D39460 sequence.
                                                                                                                                            AAY02538 standard; Protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                     16-JUL-1999 (first entry)
                             2 GGXXXXXXXXXXXX 18
                                                                5 ggggsskassssassag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-181040/15.
N-PSDB; AAX36277.
                                                                                                                                                                                                                                                                                                                                                                                              W09909174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                               5-FEB-1999.
                                                                                                                                                                                     AAY02538;
                                                                                                                   RESULT 15
Matches
                                                                                                                                     AAY 02538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                      Óλ
                                    ŏ
                                                                qq
                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a polypeptide encoded by one of a large number of 5. ESTs derived from mRNAs encoding secreted proteins. The 5. ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in solating cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                            Gaps
                                                                                                                                                                                            ;
0
                                                                                                                                                           DB 12; Length 825;
                                                                                                                                                                                            14; Indels
                                                   Fusion protein Type II is represented in AAR15158.
See also AAQ13669-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A, Giordano J;
                                                                                                                                                                             1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID 6884; 71pp + CD-ROM; English.
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein, SEQ ID NO: 6884.
                                                                                                                                                             Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                     AAG02803 standard; Protein; 104 AA.
                       Disclosure, Fig 4B; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2000; 2000EP-0200610.
                                                                                                                                                               48.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                     519 ggsaaaaaaaaaggag 535
                                                                                                                                                  Ouery Match
Best Local Similarity 1/.00
- hear 3; Conservative
                                                                                                                                                                                                                                2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-500381/45.
N-PSDB; AAC02809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA;
                                                                                                               825 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                             06-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                            AAG02803;
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                            AAG02803
```

which

DE;

Richards

Peng J,

97GB-0017192.

```
The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antegonised by a globerellin. The products can be used to provide Rht expression in glibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin insensitive. Taller plants wild-type, the dwarfing being gibberellin insensitive. Taller plants to the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, compounds which inhibit gibberellin biosynthesis inhibitor to keep weeds dwarfibut let crop plants grow tall. The present sequence is encoded by rice expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 20; Length 25
pred. No. 1.4e+04;
0; Mismatches 14; Indels
Claim 12; Fig 6b; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 gggstssssssslgg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

Length 104;

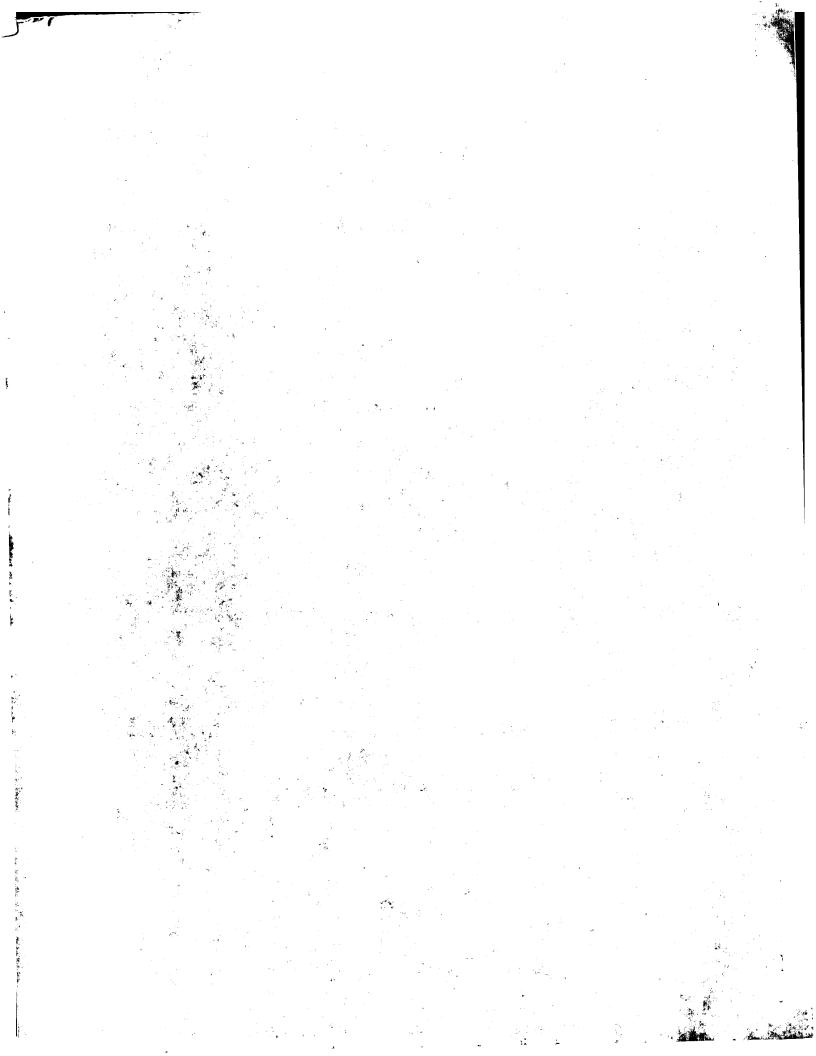
Score 15; DB 21; Pred. No. 7.8e+03;

45.5%; 17.6%;

Query Match Best Local Similarity

Search completed: February 12, 2002, 12:30:31 Job time: 364 sec

us-09-485-571-20.rag



Appli Appli Appli Appli Appli

Appl Appli Appli Appli Appli Appli Appli

```
Sequence 10,
Sequence 26,
Sequence 1, A
        Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: MORISHITA, Hideaki
APPLICANT: MOBUHARA, Masahiro
APPLICANT: FOR INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, F
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND F
TITLE OF INVENTION: TREATING USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
US-08-122-510-11
US-08-122-510-12
US-08-1174-365A-56
US-08-1174-365A-3
US-08-221-582A-3
US-08-221-027-1
US-08-251-027-7
US-08-251-027-7
US-08-321-027-7
US-08-321-027-7
US-08-321-027-7
US-08-321-13-26
US-08-303-162A-1
US-08-303-162A-1
US-08-302-178-8
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-322-171-1
US-08-323-171-2
US-08-323-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; D
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/07791213D Patent No. 5409895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-07-791-213D-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-791-213D-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFT WARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENG'TH:
             \phi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1, Appli
9, Appli
38, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
                                                                                                                                                                                                                                                                                                                                                (without alignments)
3.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 39, Appl
Seguence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the number of results predicted by chance to have a r than or equal to the score of the result being printed, ed by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                               February 12, 2002, 12:32:24; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3 Sequence 5 Sequence 6 Sequence 6 Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequence 2 Sequence 3 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
                                                                                         Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-122-510-14
US-08-191-1866D-69
US-08-291-150A-39
US-08-272-255-2
US-08-181-256-4
US-08-181-256-4
US-09-080-455-1
US-09-080-455-1
US-09-080-455-1
US-08-789-337F-102
PCT-US95-08665-2
US-07-663-413-7
US-07-663-413-10
US-07-663-413-10
US-07-663-413-10
US-07-663-413-10
US-07-181-135A-9
US-07-181-135A-9
US-07-181-135-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-122-510-7
US-08-122-510-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 XXXXXXXXXXXXXX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-485-571-31
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
```

AND ENZYME METHODS OF

```
) OTHER INFORMATION: /note= "Where X is Benzylester; CTHER INFORMATION: ); OTHER INFORMATION:
                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIFICATION 1514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
PRIOR APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR-1991
PRIOR APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 25-MAR-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
             3: Allegretti & Witcoff, Ltd. 10 S. Wacker Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312-715-1000
312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1; Conserv
                       ADDRESSEE: Alle
STREET: 10 S. W
CITY: Chicago
                                                                                                          USA
                                                                                   STATE: IL COUNTRY: USZ ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 G 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: STAUKI, Nacyoshi
APPLICANT: STAUKI, Nacyoshi
TITLE OF INVENTION: A No. 5464819el Physiologically Active Peptide Having
TITLE OF INVENTION: Immunoregulatory Activities
TITLE OF INVENTION: Immunoregulatory Activities
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: BITCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
STREET: Virginia
COUNTRY: United States of America
ZIP: 22040-0747
         ö
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USEQUATE STORT OF SEQUENCE 9, APPLICATION US/08122510

SEQUENCE 9, APPLICATION:
SEQUENCE 1. INFORMATION:
GENERAL INFORMATION:
APPLICAMY: ADSMUL-OLSEN, Stig
APPLICAMY: WIDMER, Fred
APPLICANY: WIDMER, Fred
APPLICANY: SMALL SEQUENCES: TITLE OF INVENTION: Small peptidic compounds useful for the TITLE OF INVENTION: treatment of Glaucoma NUMBER OF SEQUENCES: 14
             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2;
             Indels
             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.3%; Score 6; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/729,353
FILING DATE: 19910712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19910712
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-182714
FILING DATE: 12-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: SVENSON, LEGNARION:
REGISTRATION NUMBER: 30,330
RESPERENCE/COCKET NUMBER: 216-273P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              ; Sequence 5, Application US/07729353; Patent No. 5464819
                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-07-729-353-5
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2 amino a rype: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 G 10
                       1;
                                                                                                                                                                         RESULT 2
US-07-729-353-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 G 1
                                                              10 G 10
                                                                                                          ~
                                                                                                          7
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                          g
```

```
ö
                                   Gaps
                                   ;
0
                                                                                                                                                                Sequence 14, Application US/0812510
Patent No. 5464821
GENERAL INFORMATION:
APPLICANT: AASWUL-OLSEN, Stig
APPLICANT: WIDNER, Fred
APPLICANT: GAURI, Kailash
TITLE OF INVENTION: Ireatment of Glaucoma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                   0; Indels
        Length 2;
        Score 6; DB 1;
                        Pred. No. 0;
Mismatches
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Allegretti & Witcoff, Ltd. STREET: 10 S. Wacker Dr. CHicago
27.3%; Scut
100.0%; Pre
0;
```

```
Sequence 39, Application US/08293150A; Patent No. 5792629; GENERAL INFORMATION:
                       TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 69:
SEQUIENCE CHARACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELETAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-191-866D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-293-150A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-293-150A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: A
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                       10 G 10
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 69, Application US/08191866D

Patent No. 5783195

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D

APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Reloaning Lifectious Bovine
TITLE OF INVENTION: Reloaning Virus S-IBR-052 And Uses Thereof
NUMBER OF SEQUENCES: 99

CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 185 Avenue of the Americas
CITY: New York
STRIE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 2; . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1..2
OTHER INFORMATION: /note= "Boc-Gly Val-Obzl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                    APPLICATION NUMBER: US/08/122,510
FILING DATE: 24-SEP-1993
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0532/91
FILING DATE: 25-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/DK92/00095
FILING DATE: 25-MAR-1992
APPLICATION NUMBER: PCT/DK92/00095
FILING DATE: 10FORMATION:
NAME: IWANICATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REGISTRATION NUMBER: 34,628
REGISTRATION NUMBER: 39,848
TELECOMMUNICATION NUMBER: 93,848
TELECOMMUNICATION NUMBER: 93,848
TELECOMMUNICATION NUMBER: 31,715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 6; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-715-1234
TELEX: 910/21-5317
INFORMATION FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-191-866D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-122-510-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 G 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBURRA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
TITLE OF INVENTION: TREATING USING THE SAME
OCHRESPONDENCES: 110
CORRESPONDENCES: BURNS, DOANE, SWECKER & MATHIS
                                                             ö
                                                          0; Indels
   Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FI-POPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG(1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PROR APPLICATION NUMBER: US 2-306745
FILING DATE: 13-NOV-1990
PROF ROME APPLICATION NUMBER: US 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36.07
27.3%; Score 6; DB 1;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITX: Alexandria
```

```
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Blue Light Same
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9. 499B-69
Sequence 69, Application US/08185949B
SECONDARY: Mark D. Cochran Applicant: Mark D. Cochran Applicant: Richard D. Macdonald Applicant: Richard D. Macdonald Applicant: Richard D. Macdonald Applicant: Richard D. Macdonald Applicant: Richard D. Warden Correspondence: John P. White STREET: 1185 Avenue of the Americas CITY: New York STATE: New York STATE: New York ZIP: US36
                                                                                                                                                                                                              CIP: 19103
COMPUTER READABLE FORM:
MEDTUM TYPE: Eloppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATOMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,255
FILING DATE: 09-JUL.1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
COMPUTER: DEM 30 466 DX2
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 6; DB 2; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein US-08-272-255-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                  USA
                                                                                                                                                                              ΡA
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 G 2
                                                                                                                                                      CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                            ;
0
                                                                                                                                                                                                                                                        Sequence 6, Application US/08470837
; Sequence 6, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
    APPLICANT: Nimil, Marcel E.
    APPLICANT: Tuan, Tai-Lan
    APPLICANT: Tuan, Tai-Lan
    APPLICANT: Wu, Lingtad
    TITLE OF INVENTION: Transforming Growth Factor B Fusion
    TITLE OF INVENTION: and
    TITLE OF INVENTION: Their Use in Wound Healing
    NUMBER OF SEQUENCES: 34
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Marchant & Gould
    STREET: 11150 Santa Monica Boulevard, Suite 400
    CTTW. I TO A ADDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 2;
                                                                              0; Indels
                                   Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,837 FILING DATE:
                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
iive 0; Mismatches
                                      27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30630-1US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/08272255
; Patent No. 5824859
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY TOPOTATION:
ATTORNEY AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 3063(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cashmore, Anthony R. APPLICANT: Ahmad, Margaret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100..
Lag 1; Conservative
                      Ouery Match
Best Local Similarity 100..
Conservative 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-470-837-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-272-255-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 G 1
                                                                                                                                                                                                                                                      US-08-470-837-6
                                                                                                                           10 G 10
                                                                                                                                                                     2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                     qq
                                                                                                                               ŏ
```

```
RESULT 1.1
US-09-060-455-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 C 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08483236
Batent No. 5939385
GENERAL INFORMATION:
APPLICANT: Labroo, Virender
APPLICANT: Busby, Sharon
TITLE OF INVENTION: Transglutaminase Cross-Linkable
TITLE OF INVENTION: Polypeptides and Methods Relating Thereto NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                       .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                   Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,236
                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                               27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; DB 2
nilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-0?
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6673
REGISTRATION NUMBER: ,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 206-442-667
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               Query Match 27.3'
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             МA
                                                                                                                                                                            US-08-185-949B-69
                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-483-236-4
                                                                                                                                                                                                                                                                                                                                                                                                             US-08-483-236-4
                                                                                                                                                                                                                                                                                                     10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
G
                                                                                                                                                                                                                                                                                                                                      2 G 2
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                        ô
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sandberg, Lawrence; Roos, Phillip;
APPLICANT: Sandberg, Lawrence; Roos, Phillip;
APPLICANT: Mitts, Thomas
TITLE OF INVENTION: ELASTIN DERIVED COMPOSITION
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED SMITH SHAW & MCCLAY, LLP
STREET: PO BOX 488
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COHPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/060,455
FILING DATE: 14-APR-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/044,743
FILING DATE: 18-APR-1997
ATTORNEY AGENT INFORMATION:
NAME: MOAR: JODY M
REGISTRATION NUMBER: 38,563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0495-0005.30 TELECOMMUNICATION INFORMATION: TELEPHONE: (650)3240880
Sequence 1, Application US/09060455; Patent No. 5965118; GENERAL INFORMATION:
APPLICANT: Duncan, Ruth
APPLICANT: Evagorou, Evagoras; APPLICANT: Buckley, Robert G.
APPLICANT: Gianasi, Elisabetta
TITLE OF INVENTION: Polymer-Platinum; TITLE OF INVENTION: Compounds; NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                        ...urkSSEE: Deblinger & Associates
STREET: 350 Cambridge Ave. Ste. 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 4, Application US/09039308A; Patent No. 6069129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%
100.0%; Pix.
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-060-455-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-039-308A-4
                                                                                                                                                                                                                                                                                                                         COUNTRY:
```

```
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-07-663-413-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/0878933F

Sequence 102, Application US/0878933F

Batent No. 6153380

GENERAL INFORMATION:
APPLICANT: NO. 6153380an, Garry P

APPLICANT: NO. 6153380an, Garry P

TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR

TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES

TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES

TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES

CURRENT APPLICATION NUMBER: US/08/789,333F

CURRENT FILING DATE: 1997-01-23

PRIOR FILING DATE: 1996-01-23

PRIOR FILING DATE: 1996-01-23

NUMBER OF SEQ 1D NOS: 102

SOFTWARR: Patentin Ver. 2.0

SSEC ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: linker; OTHER INFORMATION: sequence.
US-08-789-333F-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%; Score 6; DB 4; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
                                        COUNTRIED TO THE TOTAL TO THE TOTAL THE TOTAL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; DB 3
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                           APPLICATION ...
APPLICATION ...
FILING DATE: 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MILET, RAYMONG A.
REGISTRATION NUMBER: 97-489
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 288-4392
TELEPAX: (412) 288-4392
TELEPAX: (412) 288-3300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.3%
Best Local Similarity 100.C
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-039-308A-4
Pennsylvania
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-789-333F-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
    STATE: P
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9508565
Sequence 2, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Casimore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
CORRESPONDENCES: 2
NUMBER OF SEQUENCES: 2
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2;
                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.3%; Score 6; DB:
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: US 08/272,255
APPLICATION UNBER: US 08/272,255
FILING DATE: 08-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTATION UNMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
REFERENCE/DOCKET NUMBER: UPN-1795
TELEFONDICATION INFORMATION:
TELEFONDICATION INFORMATION:
TELEFAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 2 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10112
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein pcT-US95-08565-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                            USA
```

```
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/663,413
FILING DATE: 19910301
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 38720
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEPHONE: (212) 977-9550
TELEFAX: 4223-3 COOP UI
SEQUENCE CHARACTERISTICS:
LENGTH 3 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein,
US-07-663-413-7
```

Search completed: February 12, 2002, 12:32:25 Job time: 453 sec

ö

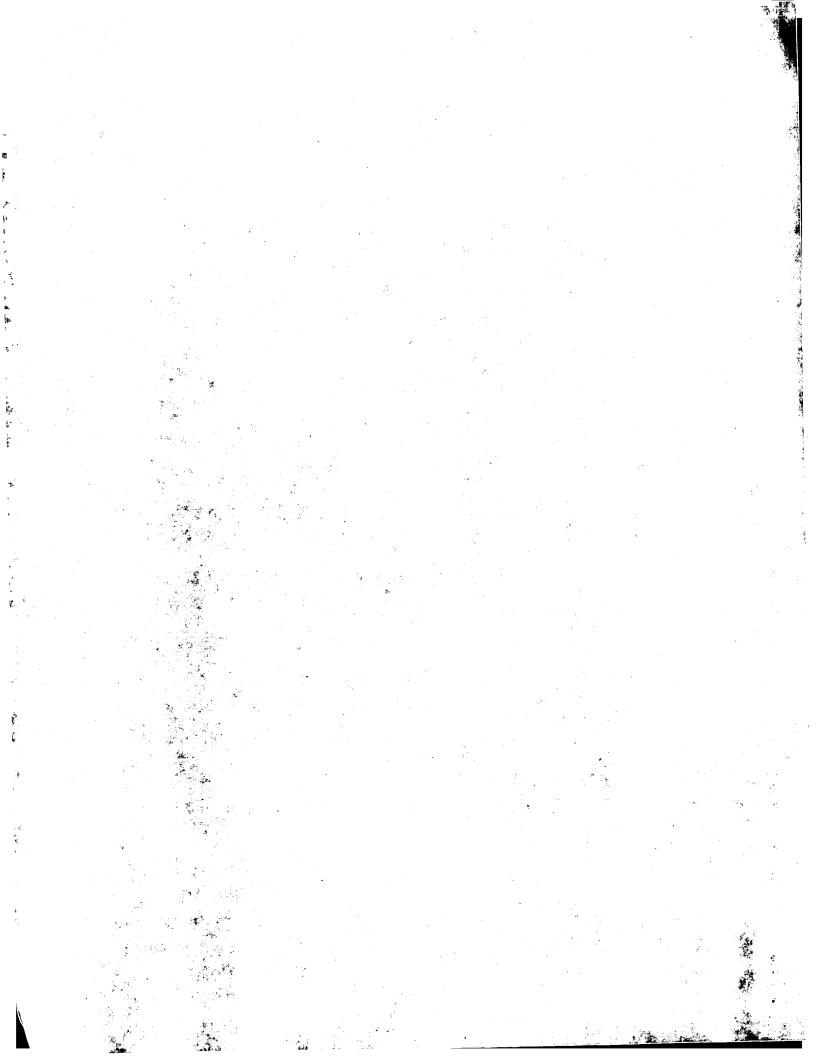
Gaps

ő

0; Indels

Query Match 27.3%; Score 6; DB 1; Length 3; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches 0; Indels

ò g



١

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:34:42; Search time 126.85 Seconds (without alignments) 10.209 Million cell updates/sec Run on:

1 XXXXXXXXXXXXXX 17 US-09-485-571-31 22 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SUMMAKIES	
Result No.	Score	Query	Length	DB	ID	Description
	9	27.3	3	7	СКНО	growth-modulating
7	9	27.3	m	~	A60898	bursin - chicken
Э	9	27.3	m	7	A23751	spinal cord peptid
4	9	27.3	m	7	B23751	cord
ហ	9	27.3	m	7	PT0636	recep
9	9	27.3	m	7	PT0571	
7	9	27.3	4	ч	ECXAA	antho-RFamide neur
8	9	27.3	4	~	A32039	tyrosine-melanocyt
6	9	27.3	4	7	PL0140	carbon-monoxide de
10	9	27.3	4	7	S09478	qlobulin IV alpha
11	9	27.3	4	7	T30569	hypothetical prote
12	9	27.3	4	7	I38888	COI intron 16 prot
13	9	27.3	4	7	A25844	autho-RF amide neu
14	9	27.3	4	7	A34626	RPCH-related neuro
15	9	27.3	4	~	A32480	achatin-I - giant
16	9	27.3	4	~	839390	myosin-light-chain
17	9	27.3	4	7	PT0240	Ig heavy chain CRD
18	9	27.3	4	7	PT0271	Ig heavy chain CRD
19	9	27.3	4	7	S43959	Ig mu chain V regi
20	9	27.3	4	~	A53284	
21	9	27.3	4	7	B53284	T-cell receptor be
22	9	27.3	4	~	PT0633	T-cell receptor be
23	9	27.3	4	~	PT0711	T-cell receptor be
		27.3	4	7	PT0698	T-cell receptor be
22	φ	27.3	4	7	PT0677	T-cell receptor be
	9	27.3	4	~	PT0706	T-cell receptor be
27	9	27.3	4	~	PT0675	T-cell receptor be
58	9	27.3	4	~	PT0721	T-cell receptor be
53	9	27.3	4	N	PT0566	T-cell receptor be

ubiquitin - rat	cholecystokinin-5	spinal cord peptid	mitosis inhibiting	copper resistance	primase - Citrobac	alkanal monooxygen	R-phycoerythrin ga	cadmium-binding pe	photosystem I 10.4	alpha-amylase - ri	actin I - malaria	hemoglobin, extrac	Leu-enkephalin - b	Met-enkephalin - b	alcohol dehydrogen
847552	A32516	223751	A26830	A41225	140702	A44955	F22565	A33882	PQ0689	S51077	B45525	S65726	B61445 ·	51445	511075
8	2 A:	;; ;;	2 A.	2 A		2 A		-			2 B			2 A(Si
4	Ŋ	S	2	S	Ŋ	Ŋ	'n	2	2	Ŋ	Ŋ	5	S	'n	_Ω
27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3
9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

```
Growth-modulating peptide - human Growth-modulating peptide - human Growth-modulating peptide - human Growth-modulating Saloct-1801 #sequence_revision 26-May-1995 #text_change 20-Jun-2000 Gracession: A01421 R. Schlesinger, D.H.; Pickart, L.; Thaler, M.M. Experientia 33, 324-325, 1977 A.Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine. A.Reference number: A01421 MUID:77162369 A.Reference number: Protein Anolecule type: protein A.Reference Type: protein C.S. Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 OB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
```

ö

RESULT 2 A60898 bursin - chicken 10 G 10 1 G 1 δ qq

Dutsin curuses.
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus data (cispecies)
Cispecies: Accession: A6089
Ribadhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A; Fitle: Tripeptide structure of bursin, a selective B-cell-differentiating hormone A; Reference number: A60898
A; Rocession: A60898
A; Rocession: A60898
A; Rocession: A60898
C; Superfamily: unassigned animal peptides
C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; hormone
F; 3/Modified site: amidated carboxyl end (Gly) #status experimental

Gaps ö 0; Indels Length 3; DB 2; 5. 0; Query Match 27.3%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches

10 G 10 ŏ

. G m

qq

ö

```
R.HOTVATh, A.; Kastin, A.J.
J. Biol. Chem. 264, 2175-2179, 1989
A.Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting f. Aj.Reference number: A32039; MUID:89123285
A;Reference number: A32039
                                                                                                                                                                                                                                                                                                                                                                                  R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.F.Itle: Junctional sequences of fetal T cell receptor beta chains have few N region
A.Reference number: PT0509; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthor Remaide neuropeptide - sea anemone (Anthopleura elegantissima)
anthopleura elegantissima
C.Species: Anthopleura elegantissima
C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 08-Dec-1995
C.Accession: A2666
R.Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of CGlu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea A; Reference number: A26666; MUID:87092339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
C;Accession: A32039
                                                                                                                                                                                                                    T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molocule type: protein
A;Residues: 1-4 <GRI>
C;Comment: The function of this peptide is not known but it could act as a C;Comment: The function of this peptides had identical properties.
C;Comment: Synthetic and natural peptides had identical properties.
C;Superfamily: Remaide neuropeptide
C;Superfamily: Remaide neuropeptide in neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
F;4/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: PT0571
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-3 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; DB 2;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; DB 1
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 G 3
                                                              3 G 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                 qq
       ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell receptor beta chains have few N regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
B123751
Spinal cord peptide SCP-5 - pig
Spinal cord peptide SCP-5 - pig
Spinal cord peptide SCP-5 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 28 -Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 18-Aug-2000
C;Date: 28-Sep-1987 #sequence_revision 26: Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425
A;Accession: B23751
A;Status: preliminary
A;Mescieule type: protein
A;Residues: 1-3 - 4815>
C;Superfamily: unassigned animal peptides
                                                                                       A23751 cord peptide SCP-4 - pig spinal cord peptide SCP-4 - pig cybinal cord peptide SCP-4 - pig cybinal cord peptide SCP-4 - pig cybinal cybi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: newborn thymus, strain BALB/c C, Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.3%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 6; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A.Pitle: Junctional sequences of fetal T (A:Reference number: PT0509; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: profein
A; Residues: 1-3 <HSI>
C; Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-3 <FEE>
                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A23751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

a transmit

ö

Gaps

ô

ö

Gaps

0;

ô

Gaps

ö

Indels

; 0

07:52:35

Wed Feb 13

```
RMorrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.

Curr. Genet. 34, 379-385, 1998
A; Filte: Isolation and characterisation of the acetyl-CoA carboxylase gene from Asp.
A; Reference number: 220869; MUID:99087906
A; Reference number: 220869; MUID:99087906
A; Reterence number: preliminary; translated from GB/EMBL/DDBJ
A; Rotcus: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-4 < AMOR>
A; Residues: 1-4 < AMOR>
A; Residues: 1-4 < AMOR>
A; Cross-references: EMBL: X15996; NID:e12185512; PID:e1218041; PIDN:CAA75927.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collintron 16 protein - Podospora anserina mitochondrion
C;Species: mitochondrion Podospora anserina
C;Species: mitochondrion Podospora anserina
C;Date: 0.5-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C;Accession: 13888
B;Cummings, D.J.; Michel, F; McNally, K.L.
Curr. Genet. 16, 381-406, 1989
A;Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit
A;Reference number: A48327; MUID:90124722
A;Accession: 138888
A;Status: preliminary
A;Molecule type: DNA
A;Status: greliminary
A;Molecule type: DNA
A;Cross-references: GB:X55026; GB:M30937; GB:M61734
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rigrimmelikhuijzen, C.J.P.; Groeger, A.
PERS Lett. 21, 105-108, 1987
A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid
A;Reference number: A25844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
A25844
author RF anide neuropeptide - sea pansy (Renilla koellikeri)
C; Species: Renilla koellikeri (Koelliker's sea pansy)
C; Date: 21-Way-1988 #sequence_revision 30-Sep-1993 #text_change 11-Jul-1997
C; Accession: A25844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;4/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOlecule type: protein
A;Residues: 1-4 <GRI>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                                                                                Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.3%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                           27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%; Score 6; DB 3 100.0%; Pred. No. 0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                             Query Match 27.3
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A25844
C; Accession: T30569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 G 10
                                                                                                                                                                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 G 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 G 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I38888
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Accession: PLO140
R.Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Mcrobiol. 152, 335-341, 1989
A.Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop A. Reference number: PLO138; MUID:90055678
A. Accession: PLO140
A. Molecule type: protein
A. Residues: I-4 «KRA»
C. Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me C. Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       910bulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
N;Alternate names: 11S globulin alpha subunit gamma chain
C;Species: Cucurbita sp. (cucurbit)
C;Species: Cucurbita sp. (cucurbit)
C;Species: Cucurbita sp. (cucurbit)
C;Accession: S09478
R;Ohmiya, M.; Hara, I.; Matsubara, H.
Plant cll Physiol. 21, 157-167, 1980
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A;Reference number: S0906
A;Reference number: S0906
A;Reference number: S0906
A;Residues: 1-4 <OHM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena
C;Species: Pseudomonas carboxydohydrogena
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                  Gaps
                    A:Residues: 1-4 <HOR>
A:Experimental source: brain
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:4/Modified site: amidated carboxyl end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
                                                                                                                                                                                               Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                          Query Match 27.3%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1; Conservat
  A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 G 10
                                                                                                                                                                                                                                                                                                                              4
G –
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 6 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
G
                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
achatin. achains achain. Aschains and a chain a filican snail N; Contains: achain. I C; Species: Achain. II
N; Contains: Achain a fulica (giant African snail)
C; Species: Achain a fulica (giant African snail)
C; Species: Achain. I contains (c) accession: A32480
R; Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sun R; Kamatani, Y.; Minakata, H.; Kenny, Dilloron, 1015-1020, 1989
Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A; Title: Achain. I, an endogenous neuroexcitatory tetrapeptide from Achaina fulica feru A; McCession: A32480; MUID: 89273551
A; McCession: A32480
A; Mote: stereochemistry of the active form confirmed by chemical synthesis
R; Rshida, T; Inn, Y; Inoue, M; Yasuda-Kamatani, Y; Minakata, H; Iwashita, T.; Nomotc FEBS Lett. 307, 253-256, 1992
A; Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
                                                                                                                                                                                                                                                A34626

When the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (n-gy fine riu map m.)
A; Reference number: A44691; MUID:92354723
A; Contents: annotation; X-ray crystallography, 0.85 angstroms A; Note: achatin-II has L-phenylalanine
C; Keywords: D-amino acid
F; Z/Modified site: D-phenylalanine (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 6; DB 2;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 12, 2002, 12:34:42 Job time: 560 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 G 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 G 3
10 G 10
                                                                                 2 G 2
                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                 qq
         ò
```

us-09-485-571-31.rsp

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:39:54; Search time 67.2 Seconds (without alignments) 9.275 Million cell updates/sec Run on:

US-09-485-571-31 22 1 XXXXXXXXGXXXXXX 17 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	á	on	homo sapien	achatina fu	osendomonas	homo sapien	carcinus ma	pardachirus	canis famil	mus musculu	chlamydia t	mytilus edu	mytilus edu	moniezia ex	locusta mig	carcinus ma	carcinus ma	carcinus ma	carcinus ma	cydia pomon	helisoma tr	hirudo medi	dactylium d	carnobacter	leptinotars	mus musculu	rattus norv	pinus pinas		gryllus bim	tabanus atr	carcinus ma	carcinus ma	carcinus ma	carcinus ma
	1,100	Description	-			_	-	_	_	_	-			_		-	-	_	-	_		-	_	-		_		_		-		_	<u>-</u>	_	P81820 ca
SUMMARIES	ď.		GRWM_HUMAN	ACH1_ACHFU	DCML_PSECH	EOSI_HUMAN	AL14_CARMA	PAP2_PARMA	TPIS_CANFA	UF01_MOUSE	UXA4_CHLTR	CIP1_MYTED	CIP2_MYTED	FARP_MONEX	LOK1_LOCMI	ALL2_CARMA	ALL3_CARMA	ALL4_CARMA	ALL5_CARMA	ALL7_CYDPO	FAR1_HELTI	FAR5_HIRME	IGAO_DACDE	LANC_CARUI	MNP1_LEPDE	UF04_MOUSE	UH11_RAT	ONO6_PINPS	ACI_THUAL	AKHG_GRYBI	AKH_TABAT				AL17_CARMA
	ac	:	1 G	1 A	1 D	1 E	1 P	1	1 1	1 0	1 0	7	1	1	1	1 P	1	1 P	1 7	1 A			1		Ξ	п П	1	-	1 P	1. P	7 7	1 Y	1 1	٦ ٦	∢ .
	4		e	4	4	4	S	S	S	വ	Ŋ	9	9	9	9	7	7	7	7	7	7	7	7	7	7	7	7	7	æ	σ ο	œ	æ	ω.	æ	Φ
ø	Query	Maccin	27.3	27.3	27.3		27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	27.3	•	27.3	27.3	27.3	27.3	27.3	•	27.3	•	27.3	٠	27.3	27.3	27.3
	9	2006	9	9	9	9	9	ø	9	9	9	ø	9	ø	9	9	9	9	9	9	9	ø	9	φ	9	9	9	9	9	9	9	9	φ,	9	9
	Result	2	П	7	e	4	2	9	7	æ	σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

[2]

RN

ma con con con con ma ma ma				0;		
P81821 carcinus ma P82152 cydia pomon P82154 cydia pomon P82155 cydia pomon P82155 cydia pomon P82155 cydia pomon P82156 cydia pomon P82157 cydia pomon P82157 cydia pomon P82187 cydia pomon P81815 carcinus ma P81812 carcinus ma P81812 carcinus ma P81812 carcinus ma		A. ;) te) rtebrata; Euteleostom1; Hominidae; Homo.	M.; glycyl-histidyl-lysine."; DE HAS BEEN FOUND TO STIMULATE HHIBIT OTHER TYPES IN VITRO.	Length 3; 0; Indels 0; Gaps		A. (te) Pulmonata; Stylommatophora; Pulmonata: Stylommatophora; nashita T., Watanabe K., Movales-Li P., moto K.; restapptide from Achatina residue.";
ALIB_CARMA ALIJ_CYDPO ALIJ_CYDPO ALIJ_CYDPO ALIJ_CADVO ALIJ_CYDPO ALIJ_CADPO ALIJ_CARWA ALIJ_CARWA ALIJ_CARWA ALIJ_CARWA CADI_ENTFA	ALIGNMENTS	PRT; 3 A ced) sequence update annotation upda ans; Craniata; Ve ss; Catarrhini;	356; Thaler M. Peptide is TRIPEPTII S AND TO IN	Score 6; DB 1; Pred. No. 0; 0; Mismatches		PRT; 4 A A sequence update annotation update annotation update ansall). a; Gastropoda; Chatina. AND SYNTHESIS. 97281; enny P.T.M., Iweny P.T.M., Iweny P.T.M., Iwakeuchi H., No euroexcitatory a do-amino acid an. 160:1015-10
27.3 8 1 1 27.3 8 1 2		N STANDARD; 86 (Rel. 01, Created) 86 (Rel. 01, Last seq 86 (Rel. 01, Last ann DULATING PEPTIDE. ens (Human). Metazoa; Chordata; Eutheria; Primates;	ng n	27.3%; Similarity 100.0%; 1; Conservative		T 2 ACHLEUCH ACHEU ACHLEUCH P35904; 01-JUN-1994 (Rel. 29, Created) 15-JUN-1994 (Rel. 29, Last sequen 15-JUL-1998 (Rel. 36, Last annota ACHATIN-I. ACHATIN-I. ACHATIN-I. ACHATIN-ERAZOA; MOILUSCA; Gas ACHATINIACCA; ACHATINIAGE; ACHATINIACCA; CHARACTERIZATION, AND SSTRAIN-FERUSSAC; TISSUE-Ganglion; MEDLINE-89273551; Pubmed-2597281; Manatani Y., Minakata H., Kenny P. Kunase K., Sun X.P., Yongsiri A., Novales E.T., Kanapi C.G., Takeuc 10-ACHATINIAC ACHATINIAC ACHATINIACCA ACHATINIAC AC
33.33.4 44.0 45.0 44.1 45.0 46.0 46.0 46.0 46.0 46.0 46.0 46.0 46		UMAN UMAL RWM_HUMA 01157; 1-JUL-19 1-JUL-19 ROWTS-MO OMO SADA UKARYOTA AMMALYOTA	[1] SEQUENCE. MEDLINE=7716386; SECHESINGER D.H., "Growth-modulation Experientia 33:32 -!- MISCELLANDOUS GROWTH OF SOW PIR; A01421; GKUM SEQUENCE 3 AA;	Query Match Best Local Simi Matches 1;	10 G 10 G 1	RESULT ACH1_ACHFU BC P35904; DT 01-JUN-1994 (Rel. DT 01-JUN-1994 (Rel. DT 15-JUL-1998 (Rel. DE ACHATIN-I. CC ACHATIN-I. CC ACHATIN-I. CC EUKARYOTA; METAZOO CA ACHATINA-I. CC ACHATINA-I. CC EUKARYOTA; METAZOO CA ACHATINA-I. CC EUKARYOTA; METAZOO CA ACHATINA-I. CC EUKARYOTA; METAZOO CA ACHATINA-I. CC EUKARYOTA; MEDLINB-89273551; RX MEDLINB-89273551; RX MEDLINB-89273551; RA FAMATATINA-I. RA FUNASE K., SAN X.I. RA FUNASE K., SAN X.I. RA HONVAIES E.T., KANG RY "ACCHATION IN TOTAL IN TOTA
		RESULT GRAWLH GRAWLH AC P P P P P P P P P P P P P P P P P P	S D C C R R R R R R S S	JO B	yo da	REPARENCE OF THE STREET OF THE

```
NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                               anaphylaxis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL14_CARMA
P81817;
                                  EOSI_HUMAN P02731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
0 –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL14_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~
                  EOSI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                      Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                   MEDLINE-93014529; PubMed=1399265; Ishida T., In Y., Dol M., Inoue M., Yasuda-Kamatani Y., Minakata H., Ishida T., In Y., Dol M., Inoue M., Yasuda-Kamatani Y., Minakata H., Ishida T., In Y., Dol M., Inoue M., Yasuda-Kamatani Y., Minakata H., Iwashita T., Nomoto K.; "Crystal structure and molecular conformation of achatin-I (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid residue."; Incl. J. Pept. Protein Res. 39:258-264(1992).
Incl. J. Pept. J. Pept. Protein Res. 39:258-264(1992).
Incl. J. Pept. J. Pept. Pept. Pept. Pept. Pept. Pept. Pept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1 - SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
     STRAIN=FERUSSAC; TISSUE=Heart atrium; MEDLINE=91264856; PubMed=1675568; Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Furification of achatin I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-PEG-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Microbiol, 152:335-341(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 4 AA; 441 MW; 7761E876F000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                        2 D-PHENYLALANINE.
4 AA; 408 MW; 6AADD9C810000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 6; DB 1
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90055678; PubMed=2818128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Molybdenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - COFACTOR: MOLYBDENUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                           Hormone; D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
"-hes 1; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PL0140; PL0140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arch. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCML_PSECH
P19916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 6 2
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 G 1
                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
DCML_PSECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-I. MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS

(ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING EDSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                         "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).

-I. FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

NOUR DES.

AMIDATION (POTENTIAL).

SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 1 V -> A (IN OTHER PEPTIDE).
/FTId=VAR_005201.
4 AA; 390 MW; 6B05B862A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eubrachyura; Portunoidea; Portunidae; Carcinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
5. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
EOSINOPHILOTACTIC PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 6; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
PRT;
                                                                                                                                                                                                                                                                                                                 MEDLINE=76078412; PubMed=1060093;
Goetzl E.J., Austen K.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A03190; ETHUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARCINUSTATIN 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6759;
```

ö

m

ö

Gaps

ö

G 4

τ ð g

2 4 RESULT 6 PAP2_PARMA

SEQUENCE

```
Mus musculus (Mouse).
Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamma.ia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_FaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=L2/434/BU;
SIni L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fibroblast;
MEDLINE-85009907; PubMed-7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
                                                                               Isomerase; Glycolysis; Gluconeogenesis; Fatty acid blosynthesis; Pentose shunt.
-!- SUBDATT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC.-2DPAGE; P54714; DGG.
InterPro: IPR000652; Trioseph_isomrse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               using.preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS
PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
                                                                                                                                                         64444862C9A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                            5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AA.
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                            DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6; I
Pred. No.
                                                                                                                                                                                                                Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                       PARTIAL.
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                              27.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.3%;
100.0%;
                                                                                                                                                         550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                    PROSITE; PS00171; TIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
...hog 1; Conservē
                                                                                                                                                                                                                             L Similarity
1; Conserva
                                                                                                                           2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pallini V.;
                                                                                                                                                                                                                                                                                                                                                                                                            UF01_MOUSE
P38639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UXA4_CHLTR
P38005:
                                                                                                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                  G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G 10
                                                                                                                                                                                                                                                                                                                    ო
ლ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ა
ლ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
UXA4_CHLTR
                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Skin secretion;
MEDLINE-87057369; PubMed-3782138;
Lazarovici P., Primor N., Loew L.M.;
Purification and pore-forming activity of two hydrophobic
polypeptides from the secretion of the Red sea moses sole (Pardachirus marmoratus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Heart;
MEDLINE-98163340; PubMed-9504812;
Dunn M.J.; Corbett J.M., Wheeler C.H.;
"HSC-2DPAGE and the two-dimensional gel electrophoresis database of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. BIOL. Chem. 261:16704-16713(1986).

-!- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.

-!- SUBBUXIT: MONOMER. IN AQUEDOUS SOLUTION EXISTS AS A TETRAMER.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
                                                                                                                                                                                                                                            Pardachirus marmoratus (Red sea moses sole).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Edrinopteryyji; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Pardachirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-ocT-1996 (Rel. 34, Created)
01-ocT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          614 MW; 7769C9C9C8100000 CRC64;
                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
PARDAXIN II (PXII) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                          5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETONE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPIS_CANFA
ID TPIS_CANFA
AC P54714;
                                                                                                                                          PARMA
              G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 G 10
```

G.

-

g

à

SEQUENCE

ö

Gaps

ö

UNKNOMN

```
RESULT 12
FARP_MONEX
ID FARP_MONEX
AC P41966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOK1_LOCMI
P41491;
MUSCLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
                                                             SEQUENCE
                                                                                                                                                   10 G 10
                                                                                                                                                                       1 G 1
                                                                                                                                                                                                                                                                                                                                                                  Moniezia.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - ტ
                                                 MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
LOK1_LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                          qq
                                                                                                                                                    δλ
 CC CC CC SQ EFT SQ SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                ö;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILNE-88240357; PubMed-3377776; Hirata T., Ikeda T., Muneoka Y.; Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.; Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.; Structures and actions of Mytilus inhibitory peptides."; "Structures Res. Commun. 152:1376-1382(1988).

i. FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Pedal ganglion;
MEDLINE-88240357; PubMed=3377776;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
Structures and actions of Mytlius inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-:- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE II (MIP II).
Mytilus edulis (Blue mussel).
Edwaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea; Mytilidae; Mytilidae; Mytilidae; Mytilidae; Mytilus.
NCBI_TAXID=6550;
  Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
NON_TER
                                                                                                                                                                                                                                                                                                      Mytilus edulis (Blue mussel).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
                                                                                        Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION.
72C9C68775B81000 CRC64;
                                           Score 6; DB 1;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE I (MIP I).
                                                                                        27.3%; Score 6; DB 1;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Scor
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO MIP II. PIR; A27696; A27696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA; 637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                      1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Pedal ganglion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIP2_MYTED P13737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSCLES
                                                                                                                                                                                                                                  CIP1_MYTED P13736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                             10 G 10
                                                                                                                                                                    3 G 3
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 G
                                                                                                                                                                                                            RESULT 10
CIPL_MYTED
DI CIPL_MAC
DT 01-JAN
DT 01-JAN
DT 01-JAN
DT 15-DEC
DE CONTRA
OC EURALY
OC EURALY
OC MYTILO
OC MYTILO
OC MYTILO
OC MYTILO
OC MYTILO
OC HITATA
RR SEQUEN
RR SECUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIP2_MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                    g
                                                                                                                                                δλ
          SUCE
```

```
ö
                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-33312289; PubMed-8323531; Manle A.G., Shaw C., Halton D.W., Thim L.; Robytide isolated from "GNFFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
Rhabditophora; Eulecithophora; Revertospermata; Mediofusata;
Neodermata; Cestoda; Eucestoda; Cyclophyllidea; Anoplocephalidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the sheep tapeworm, Moniezia expansa.";
Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Corpora cardiaca;
MEDIINE-92262851; PubMed-1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
de Loof A.;
                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta; Perygota; Neoptera; Orthopteroldea; Orthoptera; Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                          9
                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 6 AMIDATION.
6 AA; 787 MW; 69D409C9C4481000 CRC64;
                                                                  AMIDATION.
72C9C6876DD81000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE GNFFRF-AMIDE.
                                                                                                                                                      27.3%; Score 6; DB 1;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                                                              6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.3%; Score 6; DB 100.0%; Pred. No. 0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Locusta migratoria (Migratory locust)
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moniezia expansa (Sheep tapeworm)
                                                                                          6 AA; 621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation.
MOD_RES 6 6
SEQUENCE 6 AA; 787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
-!- SIMILARITY: TO MIP I. PIR; B27696; B27696. Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=28841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUSTAKININ I.
```

```
Search completed: February 12, 2002, 12:39:54 Job time: 807 sec
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                        Thorne A.;
                                                                                                                                                                                                                                                                                                                                                                                      10 G 10
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                      ö
"Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis."; Regul. 37:49-57(1992).
-!- FUNCTION: MYOTROPIC PEPTIDE. MAY BE IMPORTANT IN THE STIMULATION OF ION TRANSPORT AND INHIBITION OF DIURETIC ACTIVITY IN MALPIGHIAN
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thorpe A.;
"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blochem. 250:727-734(1997).
-:- FUNCTION: MAY ACTA AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-:- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.

MOD_RES.

7

AMIDATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 3.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
NCBL_TaxID-6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 6; DB 1; Length 7; 100.0%; Pred. No. 0; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 7 AMIDATION (POTENTIAL).
7 AA; 770 MW; 672879CDCB5DDB70 CRC64;
                                                                                                                                                                        AMIDATION.
686365A5B9CDB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 2.
                                                                                                                                                                                                                                                       Query Match 27.3%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                          MOD_RES 6 6
SEQUENCE 6 AA; 654 MW;
                                                                                                                           PIR; A61068; A61068.
Neuropeptide; Amidation.
MOD_RES 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                          TUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALL3_CARMA
P81806;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALL2_CARMA
P81805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 G 10
                                                                                                                                                                                                                                                                                                                                            10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 0 9
                                                                                                                                                                                                                                                                                                                                                                                   9 9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALL2_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALL3_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
```

ò g

```
TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE-98121193; PubMed-9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
```

ö 0; Indels Length 7; DB 1; 27.3%; Score 6; DB 1 100.0%; Pred. No. 0; Live 0; Mismatches 1; Conservative

g

ð

ö

Gaps

us-09-485-571-31.rspt

protein

ĕ

Run on:

Sequence:

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9xsyl canis famil
Q9tt78 canis famil
Q9try3 sus sp. ins
Q9ps69 gallus gall
                  saccharomyc
aspergillus
homo sapien
                                                                                                                                                                                                                                                                                                                                                           periplaneta
periplaneta
periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                   megaptera n
canis famil
                                                                                                                                                                                                                                                                                                  perinereis
periplaneta
periplaneta
  saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                   0.09hds4
0.15889
0.15889
0.15889
0.016468
0.094x6
0.090mm7
0.0900mm7
0.094638
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.094633
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09463
0.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aust. J. Chem. 52:0-0(1999).
-!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY
ANTIBLOTIC ACTIVITY.
-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
Amphibian skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RUBELLIDIN 3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 13; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     047029 PRELIMINARY; ' PRT; 047029; 01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9TT78
Q9TRY3
Q9PS69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                           0.09 Y 4 X 6 0.09 Y 6 2 8 0.09 Y 6 9 5 0.00 
                                   Q9HDS4
Q15889
Q15901
                                                                                                                                                                                                                                                                                                                                                                                                                                        09xsy1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.vv
'-heq 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-SKIN SECRETION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_CaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P82073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P82073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q47029
ID Q4
AC Q4
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
P82073
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04923 glycine max
PB2445 nicotiana t
Q9c5b3 arabidopsis
063668 rattus norv
063184 rattus norv
007524 rous sarcom
00928 synechococc
056140 streptococc
056429 thermus aqu
084463 agrobacteri
084463 agrobacteri
084463 agrobacteri
09571 prochloroco
09572 shigella dy
0974M3 enterococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P82073 litoria rub
                                                                                                                                                        (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q47029 enterobacte
Q47505 escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   February 12, 2002, 12:38:43; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PB2073
Q47029
Q47029
Q49223
Q63568
Q63568
Q63480
Q63480
Q63480
Q65184
Q05140
Q056140
Q56140
                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9X3K1
Q9R5R2
Q9R4M3
Q9AGP4
                                                                                                                                                                                                                                                        1 XXXXXXXXXXXXX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                   US-09-485-571-31
22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
```

Minimum DB A

Database

Result õ

Searched:

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
NCBI_TaxID=3847;
                                                                                                                                                                                     Laux T., Goldberg R.B.;
"Aax plant DNA binding protein shares highly conserved sequence motifs
with HMG-box proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
10 KDA CELL WALL PROFIEIN (FRAGMENT).
Nicotiana tabacum (Common tobacco).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotlana.
NCBL_TaxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. PETIT HAVANA; SIRCHell G.P., Robertson D., Slabas A.R., Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R., Wojtaszek P., Bolwell G.P.; Proteonic study of secondary cell wall proteins from transformed theorem on time ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 7;
                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. ESSEX; TISSUE-ROOTS;
Mahalingam R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA; 850 MW; 6AAAAB378637810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 6; DB 10;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                      Nucleic Acids Res. 19:4769-4769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9C5B3;
01-JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: CELL WALL -!- TISSUE SPECIFICITY: XYLEM.
                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. ESSEX; TISSUE-ROOTS;
MEDLINE-91367679; PubMed-1891369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 1; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Planta 0:0-0(2000)
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tobacco culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 G 4
                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 G 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P82445
P82445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09C5B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9C5B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-94079349; PubMed-8257126;

Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;

Rather P.N., Mann P.A., gene encoding a novel 3-N-

"Analysis of the aac(3)-VIa gene encoding a novel 3-N-

acetyltransferase."

Antimicrob. Agents Chemother. 37:2074-2079(1993).

EMBL; M88012; AAA16193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=9609297; PubMed=8522520; Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.; Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.; translation of plasmid genes required to produce the translation inhibitor microcin C7."; J. Bacteriol. 177:7131-7140(1995). EMBL; X57583; CAA40808.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pMccC7.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
WCBL_TaxID=562;
                                                                                                              Enterobacter cloacae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 08, Last annotation update)
HMG-1-LIKE PROTEIN (FRAGMENT).
Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PLASMID PMCCC7 MCCA, B, C, D, B, F GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644DD44861B406F0 CRC64;
                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA; 744 MW; 633862D2C321A030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 6; DB 2;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA; 763 MW;
                                    01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
AAD AI PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Thes 1; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                      NCBI_TaxID=550;
                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 G 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
0
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                049223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    047505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
049223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRACTOR OF STANCE OF ST
```

ö

Gaps

.; 0

ò Dp

ö

Gaps

ö

ID DE DIT OS

g ŏ

us-09-485-571-31.rspt

```
MEDLINE-96198747; PubMed-8612486; Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M., Detera-Wadleigh S.D.; "Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                              Endocrinology 137:1562-1571(1996).
EBML; U59125; AAB02827.1; --
NON IER
SEQUENCE 7 AA; 758 MW; 672AA87
   TR4-NS ORPHAN RECEPTOR (FRAGMENT).
                                                                      [1]
SEQUENCE FROM N.A.
                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                   10 3 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                    - ₩
                                                                                                                                                       domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · O
                                                                                                                                                                                                                                                                                                                                                                    055184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                              RESULT
055184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
   δ
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mandon B., Bellanger A.C., Elalouf J.M.;
Inverse PCR-mediated cloning of the promoter for the rat vasopressin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                           TISSUE-ROOTS;
MEDLINE-21171025; PubMed-11277426;
Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
Varadidopsis Indiana genes expressed in the early compatible interacion with root-knot nematodes.";
Mol. Plant Microbe Interact. 14:288-299(2001).
EMBL; AJ286350; CAB71014.2;
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                           0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.3%; Score 6; DB 11; Length 7; 100.0%; Pred. No. 0; O; Indels 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Length 7;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 0.7 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V2 receptor gene.";
Pflugers Arch. 430:12-18(1995).
EMBL; X83264; CAA58237.1; -
SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;
                                                                                                                                                                                                                                                7 AA; 719 MW; 6732C7287EB325D0 CRC64;
                                                                                                                                                                                                                                                                                  DB 10;
o. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                                                  27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY; MEDLINE-95396550; PubMed-7667072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, VASOPRESSIN V2 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01,
01,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                  Query Match 27.3
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                               10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 G 10
                                                                                                                                                                                                                                                                                                                                                    - D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q63480
Q63480;
                                                                                                                                                                                                                                                                                                                                                                                                                899690
                                                                                                                                                                                                                                                                                                                                                                                                                            063668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q63668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             063480
ID 06
AC 06
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
 à
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
ö
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96198747; PubMed-8612486; Yoshikawa T., Makino S., Gao X.M., Xing G.O., Chuang D.M., Deterra-Wadlejgh S.D.; Bottora-Wadlejgh S.D.; Splice variants of rat TR4 orphan receptor: differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96299786; PubMed-8661150; Syshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.; Syshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.; New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene.";
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
7 AA; 758 MW; 672AA87864005350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
. 0;
                                                                  27.3%; Score 6; DB 11;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORPHAN RECEPTOR TR4-NS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology 137:1562-1571(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U59454; AAB91433.1; -.
NON_TER 1
SEQUENCE 7 AA; 663 MW; 6D
                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLRel. 06, 01-JUN-1998 (TrEMBLRel. 06, 01-NOV-1998 (TrEMBLRel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35:361-366(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Conservative
                                                                                                                     1; Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                         Best_Local Similarity
Matches. 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCB1_TaxID=10116;
```

ô

Gaps

;

```
STRAIN=HB-8;
MEDLINE=88025722; PubMed=3052437;
BOWen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
Bowen D., Littlechild J.A., phosphoglycerate kinase gene from the
"Nucleotide sequence of the phosphoglycerate kinase gene from the
extreme thermophile Thermus thermophilus. Comparison of the deduced
extreme thermophile Thermus thermophilus.
                                                                                                                                                           Constable A., Mollet B., "Isolation and characterisation of promoter regions from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coxiella burnetii.
Bacteria: Proteobacteria; gamma subdivision; Legionellaceae group;
Coxiella group; Coxiella.
Streptococcus thermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermus aquaticus (subsp. thermophilus).
Bacteria: Thermus/Deinococcus group; Thermus group; Thermus.
NCBL_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GAPDH (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 8 AA; 885 MW; 33C873333732C72B CRC64;
                                                                                                                                                                                                                                                                                  8 AA; 846 MW; ED086772D5B045B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Score 6; DB 2;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA.
                                                                                                                                                                                                                                                                                                                                            Query Match 27.3%; Score 6; DB 2; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequenco
01-NOV-1998 (TrEMBLrel. 08, Last annotat.
HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                          thermophilus.";
FEMS Microbiol. Lett. 122:85-90(1994).
EMBL, X78210; CAA55045.1; -.
SEQUENCE 8 AA, 846 MW; ED086772D5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                 STRAIN=ST11;
MEDLINE=95047254; PubMed=7958782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blochem. J. 254:509-517(1988).
EMBL; X12464; CAA31005.1; -
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                             [1]
SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=1308;
                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 G 7
                                                                                                                                                                                                                                                                                                                                                                                                                                 10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 6 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   085406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      085406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 056429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            056429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        056429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OC OC DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                 OS
OC
OC
OX
OX
RR
RR
RT
RT
RT
RT
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                   STRAIN-PRACUE C;
MEDLINE-93010967; PubMed-1327749;
Donze O., Spahr P.F.;
"Role of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO. J. 11:3747-3757(1992).
EMBL. X67587; CAA71862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801). Bacteria; Cyanobacteria; Chrococcales; Cyanothece.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF001780; AAC33369.1: NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                              Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
(ST11) STP6 CONTROL REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
Rous sarcoma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA; 672 MW; 776045A7687DD6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 6; DB 1
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВВ ,
0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. v,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%; Score 6; L
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLiel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-AUG-1998 (TrEMBLrel. 07, NIFH (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=11886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RF-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 G 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
Q56140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     009258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
009258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIFH.
                             11D 0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
0007624
00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF DE DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
```

ô

Gaps

; 0

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
AGROBACTERIUM TUMEFACIENS TI PLASMID VIRD3 AND VIRD4 GENES (FRAGMENT).
Agrobacterium radiobacter.
Plasmid prikanc.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
[1]
SEQUENCE FROM N.A.
SEDIENE-88015611; PubMed-3658701;
Portner S.G., Yanofsky M.F., Nester E.W.;
"Molecular characterization of the virD operon from Agrobacterium tumefaciens.";
                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%; Score 6; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 0; Matches 1; Conservative 0; Mismatches 0; Indel.
                                                                                                                                       Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 15:7503-7517(1987).

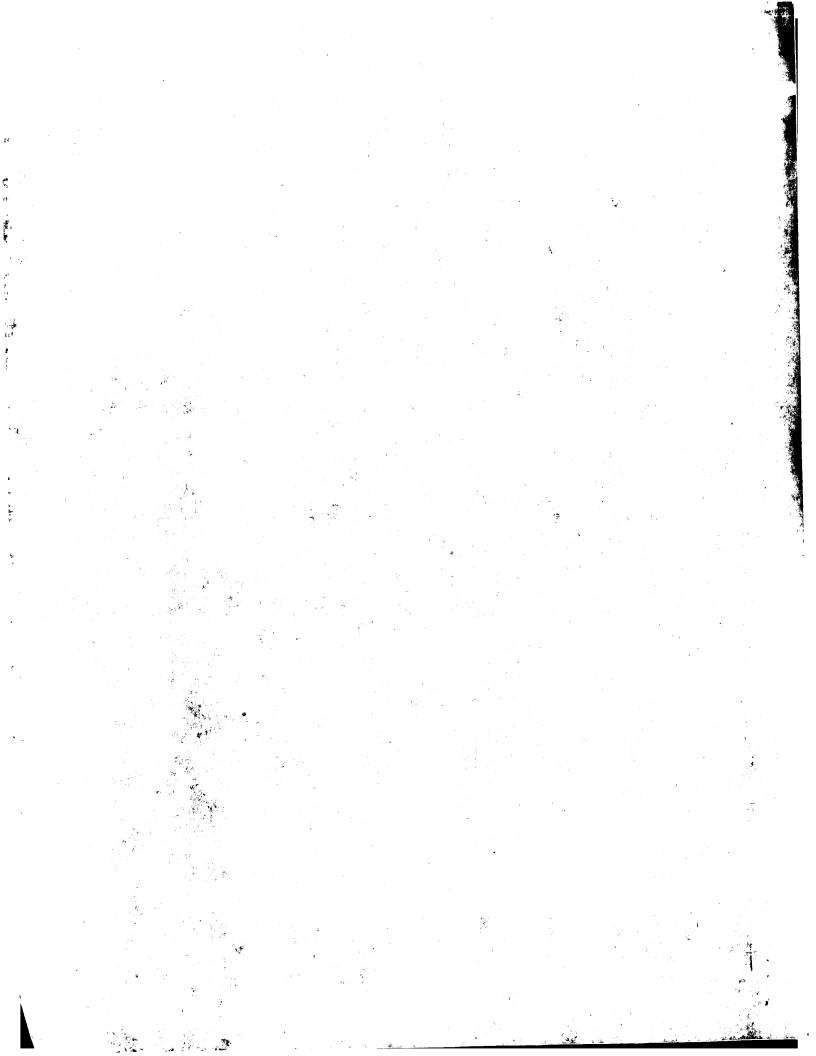
EMBL; X06045; CAA29439.1; -.

Homid:

NON TER

SEQUENCE 8 AA; 887 MW; F8F2C325B33861A6 CRC64;
                                                                                                                                     27.3%; Score 6; DB 2;
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                                                                                                                       8 AA.
                                                                                                                                                                                                                                                        PRT;
                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 1; Conservative
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 G 10
                                                                                                                                                                               10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 G 3
                                                                                                                                                                                            დ
- ს
8
                                                                                                                                                                                                                                                       Q44463
Q44463;
                                                                                                                                                                                                                                  RESULT 15
Q44463
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Search completed: February 12, 2002, 12:38:43 Job time: 756 sec



```
February 12, 2002, 12:30:34; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                      522463
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                             1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                               US-09-485-571-32
90
                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                     Run on:
```

Databa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Tachyplesin deriva	Antimicrobial tach	Tachyplesin analog	Tachyplesin deriva	Antimicrobial tach	Tachyplesin deriva	Peptide which may	Antimicrobial tach	Antimicrobial tach	Generic tachyplesi	Antimicrobial tach
SUMMARIES	AAW99416	AAR75806	AAY69610	AAW99417	AAR75808	AAW99413	AAY93617	AAR75819	AAR75807	AAY69609	AAR75816
ОВ	20	16	21	20	16	20	21	16	16	21	16
% Query Match Length DB	17	17	17	17	17	17	17	17	17	17	21
8 Query Match	100.0	74.4	74.4	68.9	67.8	67.8	67.8	66.7	65.6	9.59	9.59
Score	06	67	67	62	61	61	61	9	59	59	59
Result No.		7	e	4	Ŋ	9	7	æ	6	10	11

Antimicrobial tach Antimicrobial tach Tachyplesin deriva New lipopolysaccha Antiviral peptide. Tachyplesin II. Tachy Bacterial shock tr Tacyplesin.III. T Tacyplesin.III. T Tacyplesin. III. T Tacyplesin an an Cationic peptide t Cationic peptide t Cationic peptide t Cationic peptide t Tachyplesin analog Antimicrobial tach Tachyplesin analog Antimicrobial tach Tachyplesin iII. L Bacterial shock tr Tachyplesin III. Ta Antimicrobial tach Tachyplesin III. Ta Antimicrobial tach Cationic peptide t	Tachyplesin analog Tachyplesin analog Tachyplesin analog Antimicrobial tach Antimicrobial tach S	beta-sheet; secondary structure; ntitumour agent; antiviral; passive transport; cytoplasm; rek M; ng disulfide bridges - used o cells
AAR75810 AAR75812 AAW99414 AAR91671 AAR08202 AAR08202 AAR08202 AAR75805 AAR75805 AAR75805 AAR75805 AAR75805 AAR75803 AAR75813 AAR75813 AAR75813 AAR75813 AAR75818	AAY69617 AAY69615 AAY69611 AAR75811 AALIGNMENT ALIGNMENT 7 AA.	antibiotic; ribozyme; a 11 membrane 7 G, Kaczo y G, Kaczo gents int
11. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	7 21 7 21 7 21 7 16 7 16 7 16 7 16 7 16	
666 666 666 666 666 666 666 666 666 66	60.0 558.9 55.6 55.6 55.6 (first	OF E
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	54 53 50 50 50 50 416 416; N-19	Linear; tachh disulphide bhanti-inflamme nucleus; bloc Synthetic. WO9907728-A2 18-FEB-1999. 06-AUG-1998; 12-AUG-1997; (SYNT-) SYNT Calas E, Chawer; 1999-199 WPI; 1999-199 as carriers (
11111111111111111111111111111111111111	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	XX XX Linea KW disul KW anti- XX OS Synth XX XX XX XX YX YX YX YX YX YX YX YX YX

Length 17;

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao AG;
                                                                                                                                                           AAY69610
ID AAY6
                                                                                                                                            RESULT
                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                             .;
0
                           This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                Length 17;
                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                               100.0%; Score 90; DB 20; 100.0%; Pred. No. 4.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR75806 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                .;
0
      Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0168809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                   17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09516776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75806;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75806
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
```

셤 δ

```
Sequences AAV69610-V69611 and AAV69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala. Leu and Asp. respectively. Tachyplesin (AAV69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (V696912-AAV69614, AAV69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native techyplesin are replaced by the hydrophobic amino acids isoleucine, rachyplesin are replaced by the hydrophobic amino acids isoleucine, rachyplesin are replaced by the hydrophobic amino acids isoleucine, rachyplesin are replaced by the hydrophobic amino acids isoleucine, rachyplesin are replaced by the analogues are useful for intramolecular disulphide bonds, the analogues are functional as intramolecular disulphide bonds, the analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, and viruses. Note: The present sequence is not shown in the specification, but is derived from the generic tachyplesin analogue
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tachyplesin analogue; generic; antimicrobial; disulphide bond;
                                                                                     ;
0
Score 67; DB 16; Length 17.
Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page -; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAY69610 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence given in column 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0962034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tachyplesin analogue, TPA.
                                                                                               Conservative
                                                                                                                                                                                                                     13
                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-126327/11.
                                                                                                                                                                                                 Best Local Similarity
Matches 12; Conserv
                                                                                                                                                          1 KWAFRVAYRGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT:1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6015941-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY69610;
```

DB 21;

74.4%; Score 67;

Query Match

```
Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Essarium moniforme, Sclerotinia sclerotiorum, Sclerotinia trifolorum and Aspergilus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                          Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.8%; Score 61; DB 16; Length 17; 76.9%; Pred. No. 0.00048; Live 1; Mismatches 2; Indels
                                                                                                                                                     Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachyplesin derivative peptide SM1726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99413 standard; peptide; 17 AA.
                                       AAR75808 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                  94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999 (first entry)
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 AA;
                                                                                                                                                                                                                                                                                                                                                              19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9907728-A2
                                                                                                                07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1993;
                                                                                                                                                                                                                                                                                       W09516776-A1
                                                                                                                                                                                                                                                                                                                          22-JUN-1995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                            infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW99413;
                                                                            AAR75808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW99413
                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are linear and lack the gents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus,
                                       ö
                                                                                                                                                                                                                                                                                                                                                            Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 20; Length 17;
Pred. No. 0.00032;
4; Mismatches 0; Indels
                                       Indels
Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaczorek M;
                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                        Tachyplesin derivative peptide SM2192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grassy G,
                                                                                                                                                                                                          AAW99417 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.9%;
75.0%;
                 92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Nle
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.9
Best Local Similarity 75.0
Matches 12; Conservative
                                     12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWAFRVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chavanieu A,
                                                                          1 KWAFRVAYRGIRY 13
                                                                                                WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA.
                   Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
```

Key Modified-site

Synthetic.

08-JUN-1999

AAW99417;

AAW99417

q

ò

WO9907728-A2

18-FEB-1999.

12-AUG-1997; 06-AUG-1998;

Calas B,

Sequence

S

RESULT

g

õ

ö

Gaps

ö

```
07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putman RJ,
                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                          infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                        AAR75819;
                                                                                                                                                                              Query Match
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animals
                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                            AAR75819
                                                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                      g
This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active apents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic
                                                                                                                                                                                                                                            and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                           - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                        Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                  Score 61; DB 20; Length 17;
Pred. No. 0.00048;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colin De Verdiere A;
                                                                                       Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93617 standard; peptide; 17 AA.
                                                                                       Grassy G,
                                                                                                                                                         Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98FR-0015073.
                                                                                                                                                                                                                                                                                                                     67.8%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-FR02939.
                              98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaczorek M,
                                                   97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       Query Match 67.8
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                        Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                        ||:|||:|||| |
| kwsfrvsyrgisy 13
                                                                                                                                                                                                                                                                                                                                                           1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                          WPI; 1999-190034/16
                                                                     (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    remsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-2000
                                06-AUG-1998;
                                                   12-AUG-1997;
                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer.
                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93617
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                              à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hosemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium moniforme, Sclerotinia sclerotiorum, Sclerotinia articolorum, and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                              The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.8%; Score 61; DB 21;
76.9%; Pred. No. 0.00048;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75819 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 35; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US14619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09516776-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-1995.
```

Ŋ

```
08-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                        WPI; 2000-126327/11.
                                                                                                                             Misc-difference 12
                                                                                          Misc-difference 3
                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                 31-OCT-1997;
                                                                                                                                                                                                                                                                    31-OCT-1997;
                                                                                                                                                                                                              US601.5941-A.
                                                                                                                                                                                                                               18-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and viruses
                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                        Rao AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                              AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fundi, in particular for fundi pathogenic to plants e.g. Fusarium morificarme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                    New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                    0;
                                                                                                                                                                                          Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                  Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                 Score 60; DB 16; Length 17
Pred. No. 0.00072;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 16;
Pred. No. 0.0011;
L; Mismatches 2
                                                                                                                                                                        Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY69609 standard; peptide; 17 AA.
                                                                                                                   AAR75807 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 30; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.6%;
llarity 76.9%;
Conservative
                  66.7%;
76.9%;
                                                                                                                                                                                                                                                                                              93US-0168809
                                                                                                                                                                                                                                                                                                                                  Rao A;
                                                                                                                                                        (first entry)
                                    Conservative
                                                               1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || ||| ||| ||||:|
| kwlfrvnyrgiky 13
                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                  Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-231570/30
                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 AA;
                                                                                                                                                                                                                                       W09516776-A1
                                                                                                                                                                                                                                                                            19-DEC-1994;
                                                                                                                                                                                                                                                                                              17-DEC-1993;
                                                                                                                                                       07-FEB-1996
                                                                                                                                                                                                                                                         22-JUN-1995
                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                     Infection
                                                                                                                                     AAR75807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY 69609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                  Φ
                                                                                                 RESULT
AAR75807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                      ò
                                                                      a
                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This sequence represents a generic tachyplesin (TP) analogue which has antimicrobial activity. Tachyplesin (AAK09608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which help to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y696912-AAK09614, AAK09616) in which cert ecysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophoic amino acids isoleucine, value, methionine, phenylalanine or tyrosine, the same amino acid being present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tachyplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Ile, Val, Met, Phe, Tyr
/note= "The molecule has the same amino acid at all four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                           Tachyplesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB 21; Length 17;
Pred. No. 0.0011;
0; Mismatches 3; Indels
Generic tachyplesin (TP) analogue antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Ile, Val, Met, Phe, Tyr
Misc-difference 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the above positions"
                                                                                                                                                                                                                                                                                                                                                                                  'label= Ile, Val, Met, Phe, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Ile, Val, Met, Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "C-terminal amide"
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 23; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
```

ö

Gaps

ö

W09516776-A1

infection. Synthetic. 22-JUN-1995

07-FEB-1996

AAR75816;

19-DEC-1994; 17-DEC-1993;

```
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocyptes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungi pathogenic to plants e.g. Fusarium graminearum, Fusarium monificame, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin
                                                                                                                                                                New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 16; Length 35
Pred. No. 0.0023;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                       Claim 1; Page 31; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75822 standard; peptide; 17
                                                                    (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.68;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rao AG, Rao A;
          94WO-US14619
                                                                                                        Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-231570/30.
                                                                                                         Putman RJ, Rao AG,
                                                                                                                                         WPI; 1995-231570/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWAFRVAYRGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 kwlfrvnyrgiky
                                                                                                                                                                                                                                                                                                                                                                                                                             35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putman RJ,
          19-DEC-1994;
                                          17-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR75822;
                                                                                                                                                                                                                                                                                                                                                                                                animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungi pathogenic to plants e.g. Fusarium moliforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                               Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 16;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial tachyplesin peptide derivative.
                                                                                                                  Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR75810 standard; peptide; 35 AA.
                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 34; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                      (PION-) PIONEER HI-BRED INT INC.
                     AAR75816 standard; peptide; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.68;
76.98;
                                                                                                                                                                                                                                                                                                      94WO-US14619.
                                                                                                                                                                                                                                                                                                                                      93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                         Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 76.9
Matches 10; Conservative
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || ||| ||| ||||:|
| kwlfrvnyrgiky 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                         Putman RJ, Rao AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1996
```

Sequence

animals

Query Match

ò g infection. Synthetic

AAR75810;

RESULT 12 AAR75810

ö

Gaps

ó

ö

Gaps

ö

Pred. No. 0.0016;

69.28;

8888888888888

```
Lipopolysaccharide-binding polypeptide; bacterial infections; lipopolysaccharide (LPS) endotoxins; antibacterial agents; LPS-mediated immune disorders; inflammatory disorders;
                                                                                                                                                                                                                                                                          New lipopolysaccharide-binding polypeptide(s).
                                                                                                                                                                      AAP91671 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"H-Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88WO-JP00823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87JP-0206258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEGK ) SEIKAGAKU KOGYO KK.
                                                                                                                                                                                                                                        29-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                             horseshoe crab haemocytes
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iwanaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \frac{3..16}{7..12}
                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-068854/09.
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                Horseshoe crab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W08901492-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1989
                                                                                                                                                                                                        AAP91671;
                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                          q
                                                     ò
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, tibozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and nor-liver active agents, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
               haemocytes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungi, in particular for fungi pathogenic to plants e.g. Fusarium monilforme, Sclerotinia sclerotiorum, Sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nseq
 (AAR75805) a small peptide isolated from japanese horseshoe crab
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                      Score 58; DB 16; Length 17;
Pred. No. 0.0016;
); Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tachyplesin derivative peptide SM2307.
                                                                                                                                                                                                                                                                                                                                                                                             AAW99414 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grassy G,
                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleus; blood-brain barrier.
                                                                                                                                                                                                        64.48;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                   Ouery Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                             || ||| ||| |||| |
| kwrfrvryrgiey 13
                                                                                                                                                                                                                                                                          1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                      17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                     animals
                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                             AAW99414
```

/note="Arg-OH or Arg-NH2"

/label=OTHER

Location/Qualifiers

q

à

/label=OTHER

```
ö
                                                                                                                                                                                                                    The lipopolysaccharide-binding polypeptides may be prepd. by either solid-phase peptide synthesis followed by oxidn. to form the disulphide bridges or, subjecting horseshoe crab haemcoytes to hypotonic extraction, extracting the residue with acid, and purifying the extract. The polypeptides have high affinity for lipopolysaccharide (LPS) endotoxins and are useful for removing such toxins from fluids, as antibacterial agents, eg active against Salmonella spp. and S. aureus, and for treating LPS-mediated immune and inflammatory disorders, eg superior trachebonochial infections, unimary tract infections, bedsores, burns, colitis, cirrhosis, hepatic insufficiency and post-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 10; Length 17;
Pred. No. 0.0024;
0; Mismatches 3; Indels
New lipo:polysaccharide binding polypeptide(s) - useful for treating bacterial infections and immune and
                                                                                                                                                         Claim 2; Page 27; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.38;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                              inflammatory disorders.
```

Length 17;

64.4%; Score 58; DB 20;

Query Match

Miyazaki

Σ

Ohno

Qy

1 KWAFRVAYRGIRY 13 || || || || || || | 1 kwcfrvcyrgicy 13

Search completed: February 12, 2002, 12:30:34 Job time: 367 sec

Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 8, Al Sequence 8, Al Sequence 8, Al Sequence 11, Al Sequence 14, Sequence 14, Sequence 5, Al Sequence 1, Al Sequence 3, Al Sequence 3, Al Sequence 1, Al Sequence 1, Al Sequence 2, Al Sequence 1, Al Sequence

App]

4, Appli 14, Appl

Sequence 4 Sequence 1 Sequence 2 Sequence 2

```
APPLICANT: Putnam, Rebecca J.
APPLICANT: Reo, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 1; Length 17;
Pred. No. 2.1e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITX: Des Moines
PCT-US95-10219-7

US-08-282-030-8

PCT-US95-10219-8

US-08-168-809-11

US-09-230-180-36

US-08-168-809-11

US-08-105-809-11

US-08-037-77A-1

US-08-037-77A-1

US-08-37-039C-1

US-08-35-039C-1

US-08-426-550-5

US-08-426-550-5

US-08-426-0368-3

US-07-856-0268-3

US-07-856-0268-14

US-07-856-0268-14

US-07-856-0268-14

US-07-856-0268-14

US-07-856-0268-14

US-07-856-0268-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: ROCH, MICHAEL J.
REGISTRATION NUMBER: 0.342
REFERENCE/DOCKET NUMBER: 0.173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515.245-3595
TELEPHONE: 515.245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
         118
117
117
118
118
118
118
118
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EL
IA
RY: USA
50309
FEAD?
                                                                                                 552.2
552.2
552.2
552.2
552.2
552.2
552.2
550.0
550.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
650.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE:
US-08-168-809-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-168-809-5
         STATE:
         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Appl
Sequence 6, Appli
Sequence 2, Appli
Sequence 15, Appli
Sequence 9, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             App]
                                                                                                                                                                                         (without alignments)
3.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Ap Sequence 1, Ap Sequence 16, Ap Sequence 16
                                                                                                                                                                 ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1
Sequence 2
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-168-809-5
US-08-168-809-7
US-08-168-809-18
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-08-168-809-15
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
US-08-168-809-16
US-08-168-809-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5-08-168-809-17
5-08-426-550-2
5-08-168-809-10
5-08-168-809-12
5-08-168-809-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -07-876-883-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-426-550-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-282-030-7
                                                                                                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                 February 12, 2002, 12:32:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                           US-09-485-571-32
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
60
55
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                      OM protein
                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                 Run' on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
```

ö

Gaps

ö

Length 17;

g

```
GENERAL INFORMATION:
APPLICANT: PUtnam, Rebecca J.
APPLICANT: Rao, Aragula G.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 60; DB 1; Length 17;
Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                          0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMDUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-TOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08168809
Patent No. 5580852
                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION UNBER: 29,342
REFERENCE/POOKET NUMBER: 0173F
TELECOMMUNICATION INFORMATION:
TELEFAX: 515-245-3595
TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INPORTATION:
NAME: RCth, Michael J. 3.
REGISTRATION NUMBER: 29,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEFAX: 515-245-3634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 515-245-3634 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.7
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWKFRVKYRGIKY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
US-08-168-809-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                  Sequence 7, Application US/08168809
Sequence 7, Application US/08168809
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pao, Aragula G.
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINGER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 50309
COMPUTER: ELORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1; I
Pred. No. 0.00023;
1; Mismatches 2,
                                                                                                                                                                                                                                                                                    ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-168-809-18; Sequence 18, Application US/08168809; Patent No. 5580852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
CLASSIFICATION: 100
ATTORNEY/AGENT INFORMATION:
NAME: ROICH, MICHAEL J.
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELECHONE: 515-245-3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 513-24 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KWLFRVTYRGIKY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRY 13
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                           RESULT 2
US-08-168-809-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                        STATE:
```

δ

ö

Gaps

```
Sequence 9, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: DIRIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: LINIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
Sequence 15, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 1; Ler
Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
                                                                                                                                         NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.6%; Scur.
76.9%; Pred. No. v...
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROCH, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 01731
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 515-245-3634
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                            Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: D
HYPOTHETICAL: D
HYPOTHETICAL: NO
HYPOTHETICAL: NO
US-08-168-309-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                  50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50309
                                                                                                                                                                                                                                               STATE: I,
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 3; Length 17;
Pred. No. 0.0005;
0; Mismatches 3; Indels
                                                                                                                                                                                                                        Length 17;
                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rao, A. GUTULA)
TITLE OF INVENTION: PEPTIDE DERIVATIVES OF TACHYPLESIN
TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer IP Group of Alston & Bird
STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: NC
COUNTRY: US
ZIP: 27622-1107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,034
FILING DATE:
                                                                                                                                                                                                                      Score 59; DB 1;
Pred. No. 0.0005;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: 5718-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08962034 Patent No. 6015941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.68;
76.98;
                                                                                                                                                                                                                          65.6%;
76.9%;
                    LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                    Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
  SEQUENCE CHARACTERISTICS
                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-168-809-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                            1 KWLFRVNYRGIKY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWXFRVXYRGIXY 13
                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-168-809-15
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-962-034-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-962-034-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                          g
```

;

```
.;
0
                                                                                                                         Score 58; DB 1; Length 17;
Pred. No. 0.00074;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-07-926-965-1
US-07-926-965-1
Sequence 1, Application US/07926965
Patent No. 5416194
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OHNO, MOTONORI; IWANAGA, SADAAKI;
APPLICANT: OHNO, MOTONORI; IWANAGA, SADAAKI;
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND METHOD FOR TITLE OF INVENTION: NOVEL POLYPEPTIDE AND METHOD FOR TITLE OF INVENTION: PREPARING THE SAME
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSE: ADDRESSEE: ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: NAME/KEY: LPS-binding polypeptide, or LPB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIE: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT MODDERFRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/926,965
FILING DATE: 19920807
CLASSIFICATION TO PATA:
APPLICATION NUMBER: 07/665,819
FILING DATE: 07-MAR-1991
PRIOR APPLICATION NUMBER: 07/348,487
FILING DATE: 19-APR-1989
ATORNEY/AGENT: HFORMATION:
NAME: CHARLES A. MUSERLIAN
NAME: CHARLES A. MUSERLIAN
REGISCHATTON NUMBER: 19,683
REFRENCE/DOCKET NUMBER: TSU-4B
TELECOMMUNICATION INFORMATION:
TELEDHONE: 212-661-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : HORSESHOE CRAB
TACHYPLEUS TRIDENTATUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        64.48;
76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: POLYPEPTIDE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 17 AMINO ACIDS
                                                                                                                                            Query Match 64.4
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEW YORK
: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL LINE:
ORGANELLE:
HYPOTHETICAL:
                      ; ANTI-SENSE:
US-08-168-809-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: 1
STATE:
                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21. Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, Rebecca J.
APPLICANT: Putnam, DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNCI
NUMBER OF SEQUENCES:
ADDRESSEE: Ploneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.6%; Score 59; DB 1; Length 35; 76.9%; Pred. No. 0.0011; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Des Moines
STATE: IA
COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: DESTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/168,809
   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0173R US
                                                                                                                                                                                                                                                        0173R US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTATION NUMBER: 29,342
REFERENCE/POCKET NUMBER: 0173F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPHONE: 515-245-3595
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0173F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.6
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                     FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-168-809-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-168-809-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
Sequence 4, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGI
                                                                                                                          APPLICANT: Fulli, No. 5449752utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Minohimori
TITLE OF INVENTION: Lipopolysaccharides With Affinity To
TITLE OF INVENTION: Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 1; Length 17;
Pred. No. 0.0011;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPA: DC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PC-DOS/MS-DOS
SOFTWARE: PATCHIN PATA: US/07/876,883
APPLICATION NUMBER: US/07/876,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International
STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION UNUARE: 24,576
REFERENCE/DOCKET NUMBER: 7569:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELERAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                    ; Sequence 3, Application US/07876883; Patent No. 5449752; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19920429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPCLOGY: unknown

MOLECULE TYPE: peptide
US-07-876-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-168-809-4
         US-07-876-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                 WHEREIN CYS-3 AND CYS-16 CAN FORM A DISULE BOND, AND CYS-12 CAN FORM A DISULE BOND, AND CYS-7 AND CYS-12 CAN BE ANIDATED; WHERE BOND; WHEREIN CARBOXYL GROUP OF ARG-17 CAN BE ANIDATED; WHERE OR ALL OF THE RESIDUES CAN BE PROTECTED WITH PROTECTIVE GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Yamamoto, Naoki
APPLICANT: Watsumoto, Akiyoshi
TITLE OF INVENTION: Lippolysaccharides With Affinity To
TITLE OF INVENTION: Lippolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPED: Pennie & Edmonds
STREET: Pennie & Edmonds
STREET: New York
COUNTRY: U.S.A
ZIP: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A
ZIP: 10036-271
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE FORM:
COMPUTER: IBM PC C
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.3%; Score 57; DB 1; Length 17; 76.9%; Pred. No. 0.0011; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                           Score 57; DB 1; Length 17; Pred. No. 0.0011; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 19920429
CLASSIFICATION: S10
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: 212 869-9741
TELEXX: 66141 PENNIE
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-876-883-1
Sequence 1, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                              63.3%;
76.9%;
; IDENTIFICATION METHOD:
; OTHER INFORMATION: WHER
; OTHER INFORMATION: FORM;
; OTHER INFORMATION: OR AI
US-07-926-965-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                       Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                        1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-876-883-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                               ð
```

ö

Gaps

ö

Gaps

```
APPLICANT: FUJII, No. 5710128utaka
APPLICANT: FUJII, No. 5710128utaka
APPLICANT: Wanamoto, Naoki
APPLICANT: Water Matsumoto, Akiyoshi
APPLICANT: Water Michinori
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
AUDHER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Annue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.3%; Score 57; DB 1; Length 17; ilarity 76.9%; Pred. No. 0.0011; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                               Score 57; DB 1; Length 17; Pred. No. 0.0011; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New YOLK
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MAILLER, Charles E.
REGISTRATION NUMBER: 24,576
REGISTRATION NUMBER: 24,576
REGISTRATION NUMBER: 24,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/08426550
; Patent No. 5710128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 7561
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEX: 56141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 17 amino acids
              LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPOPLOGY: unknown
                                                                                                                                                                                                       Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-426-550-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                             , MOLECULE TYPE: peptide US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || || || || || || || KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-426-550-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1. Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Tanamorio, Nacki
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 1; Length 17; Pred. No. 0.0011; 0; Mismatches 3; Indels
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
SOFTWARE PATENTIN RAIS:
APPLICATION NUMBER: US/08/168,809
FILING DATE:
CLASSIFICATION NUMBER: US/08/168,809
ATTONENY/AGENT INFORMATION:
NAME: RCITCATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
REGISTRATION NUMBER: 29,342
RELECOMMUNICATION INFORMATION:
TELECHONE: 515-245-3595
TELECOMMUNICATION SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/426,550 FILING DATE: 21-APR-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MILLEr, Charles E.
REGISTRATION NUMBER: 24,576
REPERENCE/POCKET UNBER: 7568
TELECOMMUNICATION INFORMATION:
TELECHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212 790-909
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 63.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-168-809-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-426-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

ö

```
US-89'952'034.

US-89'952'034.

Sequence I. Application US/08962034.

Patent No. 6015941.

GNERRAL INFORMATION: PEPTIDE DERIVATIVES OF TACHYPLESIN TITLE OF INVENTION: HAVING ANTIMICROBIAL ACTIVITY NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: ADDRESSE: Bell Seltzer IP Group of Alston & Bird STREET: NC

COUNTRY: US

INFORMATING STEEN IN COUNTRY: US

COMPUTER: US

COMPUTER: IBM PC COMPATIBLE

OPPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

COMPUTER: IBM PC COMPATION:

MEDICATION NUMBER: US/08/962,034

FILICATION NUMBER: 32,943

REGISTRATION NUMBER: 32,943

REGISTRATION NUMBER: 5718-19

TELECOMMUNICATION INFORMATION:

NAME: Spruill, W MUNICAY

REFERENCE/DOCKET NUMBER: 5718-19

TELECHONE: 919 420 2202

TELECHONE: 919 420 2202

TELECHONE: 17 amino acids

TYPPE: amino acids

TYPPE: amino acids

TOPOLOGY: Linear

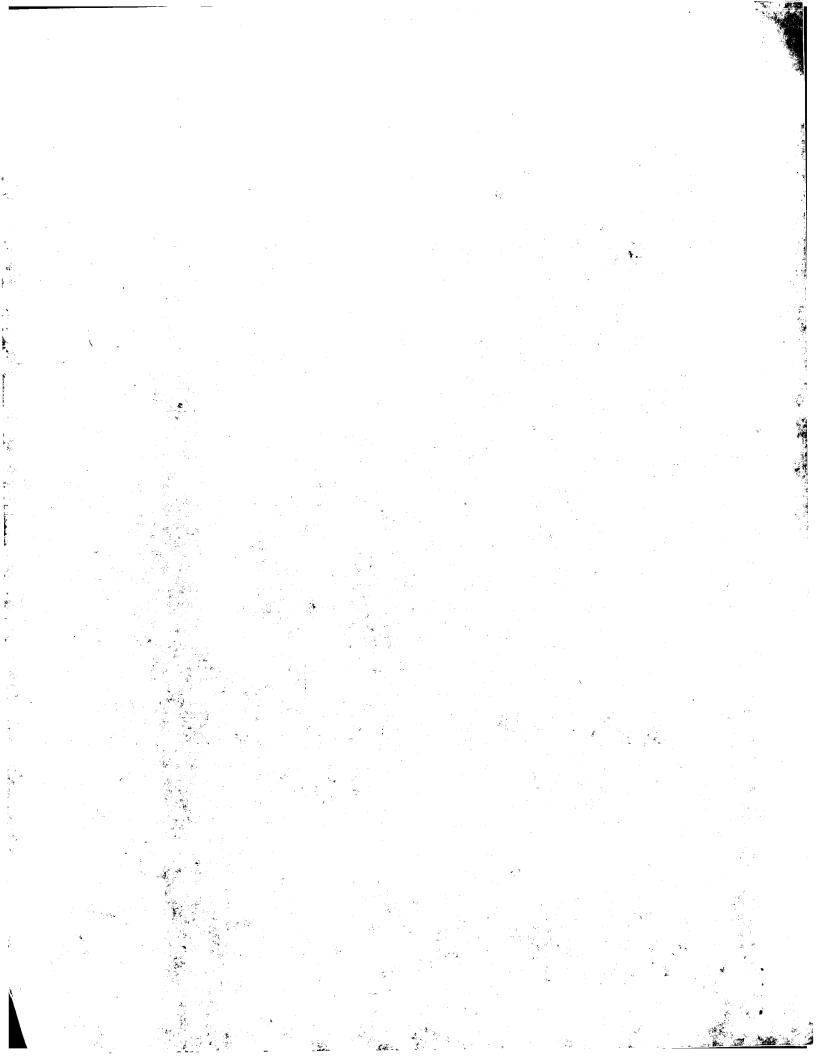
MOLECULE TYPE: peptide

US-08-962-034-1
US-08-962-034-1
```

Gaps ö 63.3%; Score 57; DB 3; Length 17; 76.9%; Pred. No. 0.0011; tive 0; Mismatches 3; Indels Query Match 63.39
Best Local Similarity 76.99
Matches 10; Conservative 1 KWAFRVAYRGIRY 13 ð qq

; 0

Search completed: February 12, 2002, 12:32:25 Job time: 453 sec



```
February 12, 2002, 12:34:42 ; Search time 126.85 Seconds
(without alignments)
10.209 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       219241 segs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                       US-09-485-571-32
90
                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pirl:* pir2:* pir3:* PIR_68:*

Database :

Description	(4 . F a:00 (a:40a+	+ +	7		tachyplesin I prec	H	polyphemusin I - A	- II uishemnsin II	hypothetical prote	_	٦	_	hypothetical prote	alpha-1,3-mannosy1	hypothetical prote	alpha-1,3-mannosyl	atpase inhibitor p	granulocyte colony	hypothetical prote	gamma-crystallin 5	probable membrane	hypothetical prote	conserved hypothet	protein F1504.37 [	pyruvate (flavodox	titin, cardiac mus	proteinase II VCA0	hypothetical prote	Env/v-mpl fusion p	hypothetical prote
SUMMARIES	75005K	A30024	370123	JX0124	A38345	B38345	JU0124	JU0125	F84162	A84161	T21986	T21993	S76323	T43341	669860	T16401	T41548	T10268	877356	A26912	E64862	D71489	н81650	G86476	S58236	I38344	E82506	S68196	79	T29365
DB		4 (	7 (	7	7	7	~	~	~	~	7	~	~	7	7	7	~	~	~	7	7	7	7	7	7	-	~	7	7	7
Length	17	+ -	7,	19	77	77	18	18	307	378	1661	1663	302	467	611	702	90	174	282	174	521	529	529	767	1165	26926	665	225	284	298
% Query Match			500		63.3		55.6	52.2	48.9	48.9	48.9	48.9	47.8	•	•	•	٠	45.6	45.6	44.4	44.4	44.4	44.4	44.4	44.4	44.4	٠	43.3	43.3	43.3
Score	5.7	ָרְ נְי	70	57	57	54	20	47	44	44	44	44	43	43	43	43	42	41	41	40	40	40	40	40	40	40	39.5		39	39
Result No.	-	4 (	7 (	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

ö

Gaps

;

Query Match 63.3%; Score 57; DB 2; Length 17; Best Local Similarity 76.9%; Pred. No. 0.0017; Matches 10; Conservative 0; Mismatches 3; Indels

30 39 43.3 300 2 A69351 31 39 43.3 350 2 727577 32 43.3 357 2 72577 34 39 43.3 516 2 E70779 34 43.3 516 2 E70779 35 43.3 516 2 E70779 36 43.3 1152 2 B00566 37 39 43.3 1152 2 B00566 37 39 43.3 1152 2 B00566 38 42.2 174 2 B72239 44.3 38 42.2 174 2 B72239 44.3 38 42.2 182 2 E64771 42 38 42.2 182 2 E64771 42 38 42.2 182 2 E64771 43 42.2 182 2 E64771 44 38 42.2 182 2 E64771 45 38 42.2 182 2 E64771 45 38 42.2 182 2 E64771 46 38 42.2 182 2 E64771 47 38 42.2 182 2 E64771 48 38 42.2 182 2 E64771 48 38 42.2 182 2 E64771 49 38 42.2 182 2 E64771 40 38 42.2 182 2 E64771 41 18 42.2 182 2 E64771 42 38 42.2 182 2 E64771 43 8 42.2 182 2 E64771 44 38 42.2 182 2 E64771 45 88894 46 188 42.2 188 2 E64771 47 188 42.2 188 2 E64771 48 188 48 48 48 5 E6477 48 188 48 48 5 E6477 48 188 48 5 E6477 48 188 5 E6477 48 18 18 18 18 18 18 18 18 18 18 18 18 18	heterodisulfide re hypothetical prote probable glpbl pro probable glycarol- hematopoietic grow prote-oncogene - m protenin Tyl/copia- probable respirato hypothetical prote conserved hypothet probable transfera hypothetical proce	) S. southeast Asian horseshoe crabs ((#status experimental	2; Length 17; 17; 3; Indels 0; Gaps 0;	as) 92 #text_change 11-Jul-1997 S. isoutheast Asian horseshoe crabs (firstatus experimental)
30 39 43.3 31 39 43.3 32 39 43.3 33 39 43.3 34 43.3 35 39 43.3 36 39 43.3 37 39 43.3 38 43.3 38 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 42.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 39 44.2 3	00000000000000000	IGNMENTS leus gigas 30-Jun-19 ; Iwanaga, mocytes of 357 redicted end (Arg)	63.3%; Score 76.9%; Pred. Live 0; Mi 3	cab (Tachypleus gig revision 30-Jun-19 ljima, H.; Iwanaga, l from hemocytes of ursor. IID:91035357 Eend end status predicted sarboxyl end (Arg)
manarere to a transfer to the	39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 43.3 39 44.3 39 45.3 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 46.3 39 39 39 46.3 39 39 39 46.3 39 39 39 46.3 39 39 39 39 46.3 39 39 39 39 39 39 49 49 39 39 39 49 49 39 39 49 49 39 39 39 49 49 39 39 39 49 49 39 39 39 49 49 39 39 49 49 39 39 49 49 39 39 49 49 39 39 49 49 39 39 49 49 39 39 49 49 39 39 39 49 49 39 39 49 49 39 39 49 49 49 49 49 49 49 49 49 4	SULT 1 8824 chyplesin I - horseshoe Species: Tachypleus gig Accession: A3824 Muta, T: Fulimoto, T:, Biochem. 108, 261-266, Tille: Tachyplesins iso ing intermediate of its Reference number: JX012 Accession: A3824 Molecule type: protein Residues: 1-17 AMUT. Experimental source: he Keywords: amidated carb 3-16,7-12/Disulfide bon 17/Modified site: amida	Query Match Best Local Similarity Matches 10; Conserva 1 KWAFRVAYRGIRY 1 1	Collians 2 (2012) Collians 2 (2012) Species: Tachypleus gig Date: 30-Jun.1992 #sequ Accession: JX0125 Muta, T.; Fujimoto, T.; Biochem. 108, Z61-266, Title: Tachyplesins iso Sing intermediate of its Reference number: JX0125 Accession: JX0125 Molecule type: protein Residues: 1-17 AMUTa Experimental source: he Keywords: amidated carb 3-16,7-12/Disulfide bon 17/Modified site: amida

```
Query Match 60.0%;
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| ||| ||| |
2 RWCFRVCYRGFCY 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
JU0125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A38345
tachyplesin I precursor - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Species: Tachypleus tridentatus
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 01-Dec-2000
C;Accession: A38345; A3068
R;Shiganaga, T.; Tok, Y.; Tokunaga, F.; Iwanaga, S.
J. Biol. Chem. 265, 21350-21354, 1990
A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localiza
A;Recence number: A38345; MUID:91065956
A;Accession: A38345
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7 CSHT>
A;Cross-references: GB:M57242; GB:J05689; NID:g161659; PID:g161660
A;Accession: A38345
A;Title: Tachyplesin, a class of antimicrobial peptide from the hemocytes of the horsesh
A;Reference number: A30068; MUID:89034158
A;Accession: A30068
A;Molecule type: proctein
A;Residues: 24-40 cNAK>
                                                                                                                                                                       tachyplesin I precursor - horseshoe crab (Carcinoscorpius rotundicauda)
C.Species: Carcinoscorpius rotundicauda
C.Species: Carcinoscorpius rotundicauda
C.Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jul-1997
C.Accession: JX0124
B.Muta, T.: Fujimoto, T.: Nakajima, H.: Iwanaga, S.
J. Biochem. 108, 261-266, 1990
A.Fitle: Tachyplesins isolated from hemocytes of southeast Asian horseshoe crabs (Carcin A: Reference number: JX0124; MUID: 91035357
A.Accession: JX0124
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-19 AUTD:
A.Experimmental source: hemocyte
C.Keywords: amidated carboxyl end
F:1-17/Product: tachyplesin I #status experimental <AMT>
F:1-17/Product: tachyplesin I #status predicted
F:3-16,7-12/Disulfide bonds: #status predicted
F:3-16,7-12/Disulfide bonds: #status predicted
F:17/Modified site: amidated carboxyl end (Arg) (amide in mature form from following 91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tachyplesin II precursor - horseshoe crab (Tachypleus tridentatus)
C;Species: Tachypleus tridentatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.3%; Score 57; DB 2; Length 77; 76.9%; Pred. No. 0.0082; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.3%; Score 57; DB 2; 76.9%; Pred. No. 0.002; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                             1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
KWAFRVAYRGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
  ò
```

```
C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 08-Dec-2000 C;Accession: B38345; Ju0123 F;Shigenaga, T.: Muta. T.: Toh, Y.: Tokunaga, F.: Iwanaga, S. J. Biol. Chem. 265, 21350-21354, 1990 A;Title: Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization: B38345 A;Accession: B38345 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Title: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A; Reference number: A91914; MUID: 90110066
A; Reference number: A91914; MUID: 90110066
A; Accession: U10124
A; Molecule type: protein
A; Residues: 1-18 (MIY>
C; Comment: The peptide is one of the antimicrobial peptides in the Atlantic horseshocycoment: The peptide is one of the antimicrobial peptides in the Atlantic horseshocycoment: The peptide arrowyl end
F; 4-17, 8-13/Disulfide bonds: #status experimental
F; 18/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyphemusin II - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 13-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
C;Accession: JU0125
R;Miyata, T; Tokunaga, F; Yoneya, T; Yoshikawa, K; Iwanaga, S; Niwa, M.; Takao, J. Blochen. 106, 663-668, 1989
A;Fitle: Antimicrobial peptides, isolated from horseshoe crab hemocytes, tachyplesin A;Reference number: A91914; MUID:90110066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: JU0123
A, Molecule type: protein
A, Residues: 24-40 < MIY>
C, Comment: The peptide is one of the antimicrobial peptides found in the Japanese hc C; Keywords: amidated carboxyl end
F; 26-39, 30-35/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;26-39,30-35/Disulfide bonds: #status preutcus F;40/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: JU0124
R;Miyata, T.; Tokunaga, F.; Yoneya, T.; Yoshikawa, K.; Iwanaga, S.; Niwa, M.; Takao,
J. Biochem. 106, 663-668, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyphemusin I - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Score 50; DB 2; Length 18; 61.5%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 54; DB 2; Length 77;
Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JU0125
A; Molecule type: protein
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein February 12, 2002, 12:34:42; Search time 126.85 Seconds Run on:

(without alignments) 10.209 Million cell updates/sec

US-09-485-571-33 93

1 KYAWRVAHRGIRWLLRX 17 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

219241

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	45	48.4	2083	7	T42721	CRP-ductin-alpha p
7	44	47.3	481	Н	S57294	carboxypeptidase D
3	44	47.3	567	7	F81682	phosphoenolpyruvat
4	43	46.2	125	~	T02519	hypothetical prote
2	43	46.2	183	7	B83183	
9	43	46.2	221	~	T29509	
7	42	45.2	311		PABY1	phosphoprotein pho
89	42			~	C83874	arsenical pump-dri
σ	41.5	44.6		-	JC5713	25-hydroxyvitamin
10	41.5	44.6		~	D82055	conserved hypothet
11	41	44.1	345	7	T46962	8-oxoquanine DNA-q
12	41	44.1	371	~	S04880	probable transposa
13	41	44.1	372	Н	QQEC47	
14	41	44.1	571	~	C71528	probable pts pep p
15	41	44.1	1009	~	S20538	chitin synthase (E
16	40.5	43.5	464	~	F69587	L-arabinose transp
17	40	43.0		7	C65134	hypothetical 16.9K
18	40	43.0	-	~	B86016	
19	40	43.0		-	QQBED6	⊆.
20	40	43.0	256	~	E75401	hypothetical prote
21	40	43.0	e	-	TVBE13	42.9K protein kina
22	40	43.0		~	T50894	hydroxyneurosporen
23	40	43.0	4	~	E81357	glutamatetRNA li
24	40	43.0	502	~	A86019	probable xylulose
22	40	43.0	536	~	T41652	hypothetical prote
56	40	43.0	1594	~	T30549	hensin - rabbit
27	39		4	~	S55073	env polyprotein -
28	39	41.9		~	S55072	env polyprotein -
59	39	41.9	108	7	T30659	hypothetical prote

thiopurine methylt	aldo/keto reductas	ubiquinolcytochr	ubiquinolcytochr	ubiquinolcytochr	ubiquinolcytochr	signal-transducing	beta-glucosidase (	conserved hypothet	probable excision	AMP deaminase (EC	hypothetical prote	AMP deaminase (EC	cell division cont	env protein gp120(	env polyprotein pr
A83291	D69826	CBZM	CBVF	CBRZ	T14263	C69431	S34570	D83043	858300	859996	A72393	A44313	S49940	A47665	VCLJS2
7	7	-	-	Н	~	7	7	~	7	~	~	~	7	~	7
218	331	388	392	397	397	438	446	478	496	605	611	760	836	869	880
41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9
39	39	39	33	39	39	39	33	39	39	33	33	39	39	33	39
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

T42721 CRP-ductin-alpha precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 11-7an-2000 #sequence_revision 11-Jan-2000 #text_change 23-Mar-2001

C,Accession: T42721
R;Cheng, H.; Bjerknes, M.; Chen, H.
Anat. Rec. 244, 327-343, 1996
A;Title: CRF-ductin: a gene expressed in intestinal crypts and in pancreatic and he A;Reference number: 222241; MUID:96362470
A;Reference number: 222241; MUID:96362470

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-2083 < CHBA
A;Residues: 1-2083 < CHBA
A;Cross-references: EMBL:U37438; NID:g1276646; PID:g1276647; PIDN:AAC52505.1
A;Experimental source: strain BALB/c; jejunal epithelial cells
C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
C;Keywords: transmembrane protein
C;Keywords: signal sequence #status predicted <SIG>
E;29-2083/Product: CRP-ductin-alpha #status predicted <MAT>

Gaps ;; Length 2083; 2; Indels Score 45; DB 2; Pred. No. 86; 1; Mismatches 48.48; Query Match
Best Local Similarity 61.5
Matches 8; Conservative

1;

2 YAWRVAHRGIRWL 14 οy

# | | | :||| || | 112 YLWRCSHRG--WL 122 g

Carboxypeptidase D (EC 3.4.16.6) - Penicillium janthinellum
N;Alternate names: penicillopeptidase S3
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
C;Species: Penicillium janthinellum
S;Sedate: 124 kov-1999 #sequence_revision 24 Nov-1999 #text_change 24-Nov-1999
C;Accession: S57294; S57293
R;Syendaen, 1: Pay, B3;
R;Syendaen, 1: Portein
R;Residues: 1-481 <SVE>
R;Syendaen, 1: Portein Sequence Database, September 1995

A; Reference number: S57293

A; Accession: S57293

A;Molecule type: protein A;Residues: 1-481 <SVW> A;Experimental source: strain IBI 3991

```
46.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYAWRVAH--RGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 KFAWRIPHFVYGATWTL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 YAWRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 YGFTVSHQGKRWYL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:W05H7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: PA3698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236236
A.Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236236
A.Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236236
A.Experimental source: cultivar Columbia
B.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID:20083487
A.Status: preliminary
C; Superfamily: serine carboxypeptidase
C; Keywords: glycoprotein; hydrolase; serine carboxypeptidase
C; L481, Product: carboxypeptidase D *status experimental <MAT>
F; 1-481, 218, 256, 326, 384, 392, Binding site: carbohydrate (Asn) (covalent) *status experimenta
F; 71-322, 191-289, 232-279, Disulfide bonds: #status experimental
F; 71-88, 378, 456, Active site: Ser, Asp, His *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: GB:AE002330; GB:AE002160; NID:g7190649; PIDN:AAF39444.1; PID:g719065
A)Experimental source: strain Nigg (MoPn)
C:Genetics: RC0613
A;Gene: TC0613
C;Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I hq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g37530 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F13M22.3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Mar-2001
C;Accession: T02519; H84793
C;Accession: T02519
A;Beference number: 214677
A;Accession: T02519
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C; Accession: F81682
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoenolpyruvate-protein phosphotransferase TC0613 [imported] - Chlamydia muridarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255 A;Accession: F81682 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٥:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                   Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1;
Pred. No. 30;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.3%; Score 44; DB 2; 77.8%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   47.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| |||:| : |||:
460 QYQPRVAYRHLEWLLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-567 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AHRSVRWLL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

A SECTION AND ADDRESS OF

```
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p A; Reference number: A82950; MUD: 20437337
A; Recession: B83183
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-183 <STO>
A; Cross-references: GB: AE004789; GB: AE004091; NID: g9949857; PIDN: AAG07086.1; GSPDB: G; C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein W05H7.5 - Caenorhabditis elegans
C;Species: T29509
R;Wohldmann, P.; Le, T.T.
Submitted to the EMBL. Data Library, April 1997
A;Reference number: Z20630
A;Reference number: Z20630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-221 <WOH>
A;Residues: 1-221 <WOH>
A;Residues: 1-221 <WOH>
A;Residues: 1-221 <WOH>
C;Genetics: Cass = EMBL:U97552; PIDN:AAB52865.1; GSPDB:GN00028; CESP:W05H7.5
C;Genetics: Cass = C
A;Molecule type: DNA
A;Residues: 1-125 <STO>
A;Cross references: GB:AE002093; NID:g3236236; PIDN:AAC23624.1; GSPDB:GN00139
C;Genetics: S3; At2g37530
A;Map position: 2
A;Introns: 19/2; 67/2
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g37530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA3698 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83183
R;Stover, C.K.; Pham X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb.
.; Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: X
A;Introns: 30/1; 61/1; 172/3; 183/1
C;Superfamily: Caenorhabditis elegans hypothetical protein W05H7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 2
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2
Pred. No. 17;
3; Mismatches
```

ö

M.J.

ï

Wed Feb 13

C; Superfamily: arsenical pump-driving ATPase

ö

```
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Stecesion: UC5713
C;Accession: UC5713
C;Accession: UC5713
Biochem. Biophys. Res. Commun. 239, 527-533, 1997
A;Title: Molscular cloning of cDNA and genomic DNA for human 25-hydroxyvitamin D3 1 A;Reference number: UC5713; MUID:98008873
A;Reference number: UC5713; MUID:98008873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1.508 <MON>
A;Cross-rezerences: DDBJ:AB005038; NID:g2626736; PIDN:BAA23416.1; PID:g2626737
C;Comment: This enzyme catalyzes the conversion of 25-hydroxyvitamin D3 to 1-alpha, C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **Reidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Selle I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNX Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID: 20406833
A;Accession: D82055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004327; GB:AE003852; NID:99657185; PIDN:AAF95741.1; GSPDB
A;Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein VC2600 [imported] - Vibrio cholerae (strain N16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-hydroxyvitamin D3 1-alpha-hydroxylase (EC 1.14...) precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120486; OMIM:264700
A;Map position: 12q12-12q13
C;Superfamily: human cytochrcome P450 CYP11B1; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
E;314-477/Domain: cytochrome P450 homology <P45>
F;450-470/Domain: heme-binding #status predicted <HMB>
F;455/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 622;
                                                                                                Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.5; DE Pred. No. 93; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.5; DE Pred. No. 76; 1; Mismatches
                                                                                                DB
41;
                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: GDB: PDDR; VDR; VDD1; CYP27B; CYP1ALPHA
                                                                                                Score 42;
Pred. No.
                                                                                                45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                Query Match 45.2
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                      :||| | || : ||
27 FAWRCAERGEKTLL 40
                                                                                                                                                                                                                                2 YAWRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KYAWRVAHRGIRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -622 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: D82055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: VC2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D82055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Reference number: S67560
A; Accession: S67580
A; Cross-references: Hab.
A; Cross-references: Extain S288C
C; Genetics:
A; Genetics:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCession: C83874

Frakani, H.; Maksone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20263314

A; Reference number: A83650; MUID:20263314

A; Reference number: BNA

A; Restdues: preliminary

A; Residues: 1-313 < STO>

A; Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05514.1; GSPDB:GNOC

C; Genetics:
C; Genetics:
A; Gene: BH1795
                                                                                                                                                                                                                                                                                                                                                      phosphoprotein phosphatase (EC 3.1.3.16) SIT4 - yeast (Saccharomyces cerevisiae)
N;Alternate names: PPH1 protein; protein D2693; protein YDL047w; suppressor protein SIT4
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000
C;Accssion: A31874; 567580
R;Arndt, K.T.; Styles, C.A.; Fink, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A suppressor of a HIS4 transcriptional defect encodes a protein with homology A;Reference number: A31874; MUID:89136000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arsenical pump-driving ATPase BH1795 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Bacillus halodurans
.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Accession: A31874
A; Molecule type: DNA
A; Residues: 1-311 < ARN>
A; Cross-references: EMBL:M24395; NID:g341163; PIDN:AAA56864.1; PID:g598433
B; Paulin, L.; Saren, A.M.; Laamanen, P.
Submitted to the Protein Sequence Database, July 1996
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                 5
   Score 43; DB 2; Length 221;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.2%; Score 42; DB 1; Length 311; 58.3%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 40;
2; Mismatches
                                                                 3; Mismatches
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 58.3،
ابت 7; Conservative
                                                              Conservative
                                                                                                                               1 KY--AWRVAHRGIRW 13
                                                                                                                                                                                              58 KYGGTWKLRHLGMRW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AWOVSPRGAGWL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AWRVAHRGIRWL 14
                               Local Similarity
hes 7; Conserv
Query Match
Best Local S
Matches 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                               ò
```

Ĥ

Σ

g õ

```
A; Molecule type: mRNA
A; Residues: 3-355, SHRWIS', 362-363, EVPDPKRRRTNSLWRITKMVIWSLQVAIRGTVSLTAYKTQLKNARHRL'
A; Cross-references: GB:X03123; NID:943689; PIDN:CAA26900.1; PID:943690
A; Experimental source: insertion sequence 1S186
C; Comment: This protein is encoded by an insertion sequence isolated from a cDNA lib
probable transposase T31 - Escherichia coli insertion sequence IS186
N.Alternate names: protein b2394
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 13-Feb-1998 #text_change 16-Jun-2000
C;Date: 31-Mar-1988 #sequence_revision 13-Feb-1998 #text_change 16-Jun-2000
C;Accession: G65013; D64791; H64721; S40538; A25031; A24221
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Accession: G65013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 372;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Mobile element: insertion sequence IS186
C; Superfamily: IS186 probable transposase T31
C; Keywords: transmembrane protein
F; 337-353/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Mobile element: insertion sequence IS186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.1%;
ilarity 61.5%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A24221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics: <Y12>
A;Gene: yi81_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics: <YIl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transposase I (insertion sequence IS421) - Escherichia coli
NyAlternate names: probable membrane protein I
C;Specias: Escherichia coli
C;Specias: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C;Accession: S04880
B;Sato, S:/ Nakada, Y:/ Shiratsuchi, A.
FEBS Lett. 249, 21-26, 1989
A;Title: IS421, a new insertion sequence in Escherichia coli.
FEBS Lett. 249, 21-26, 1989
A;Rocession: S04880
A;Rocession: S04880
A;Rocession: S04880
A;Rocession: S04880
A;Rocession: Source: S121 (SAT)
A;Cross-references uncleotide sequence is not complete
A;Rocestic translation of the nucleotide sequence is not complete
A;Note: translation of the nucleotide sequence from Fig. 3 is inconsistent with the nucleotide:
A;Note: translation of the nucleotide sequence is not complete
A;Note: translation of the nucleotide sequence is not complete
C;Genetics:
A;Wobifamily: IS188 probable transposase T31
C;Superfamily: IS186 probable transposase T31
C;Superfamily: IS186 probable transposase T31
C;Keywords: transmembrane #status predicted <TWM>
                                                                                                                                                                                                            8-oxoguanine DNA-glycosylase [validated] - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: J7-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 16-Feb-2001
C;Accession: 746962
R;RoSENGUIST, T.A.; ZHARKOV, D.O.; GROLLMAN, A.P.
Proc. Natl. Acad. Sci. U.S.A. 94, 7429-7434, 1997
A;Title: Cloning and characterization of a mammalian 8-oxoguanine DNA glycosylase.
A;Reference number: 208708; MUID:97352815
A;Accession: 746962
A;Reference number: 208708; MUID:97352815
A;Accession: 746962
A;Reference number: 208708; MUID:97352815
A;Rolecule type: mRNA
A;Residues: 1-345 <ROS>
A;Cross_references: EMBL:U96711; NID:g2078295; PIDN:AAB81133.1; PID:g2078296
C;Genetics:
A;Note: mogg1
C;Function:
A;Description: removes mutagenic base 8-oxoguanine, formed by oxidative DNA damage, by ]
C;Superfamily: mouse 8-oxoguanine DNA-glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description: removes mutagenic base 8-oxoguanine, formed by oxidative DNA damage, by Superfamily: mouse 8-oxoguanine DNA-glycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11arity 41.7%; Score 41; DB 2; ilarity 41.7%; Pred. No. 63; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.1%; Score 41;
61.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                          | | |: | ||:||:
161 KLAQRIQHSRGVRWV 175
                                                              1 KYAWRVAH-RGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db. 191 YIVRVHWRGLRWL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 HVWQIAHRDYGW 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQEC47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

ö

Gaps

ö

Indels

```
Search completed: February 12, 2002, 12:34:43 Job time: 561 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
S20538
chilin synthase (EC 2.4.1.16) CHS2 - yeast (Candida albicans)
C; Species: Candida albicans
C; Species: C; Scott S20538; A38192
R; Chen-Wu, J.L.; Zwicker, J.; Bowen, A.R.; Robbins, P.W.
Mol. Microbiol. 6, 497-502.1992
A; Title: Expression of Chilin synthase genes during yeast and hyphal growth phases of Candidates preliminary
A; Reference number: S20538; MuID:9219994
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 11009
C; CHS
A; Cross-references: GB: MB2937; NID:9170844; PIDN: AAB59308.1; PID:9170845
A; Cross-references: GB: MB2937; NID:9170844; PIDN: AAB59308.1; PID:9170845
A; Cross-references: GB: MB2937; NID:9170844; PIDN: AAB59308.1; PID:9170845
A; Reference number: A38192; MUID:92115692
A; Title: Classification of fungal chitin synthases.
A; Reference number: A38192; MUID:92115692
A; Residues: 333-463; FH', 466-510, 'AS' < BOW>
A; Residues: 333-463; FH', 466-510, 'AS' < BOW>
A; Robertamily: chilin synthase chsa
C; Superfamily: chilin synthase chsa
C; Keywords: 91ycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                           probable pts pep phosphotransferase - Chlamydia trachomatis (serotype D, strain UW3/Cx) c.Species: Chlamydia trachomatis c.Species: 13-69p-1998 #sequence_revision 13-Sep-1998 #text_change 21-Jan-2000 c.Accession: C71528 R.Stephens, R.S.: Kalman, S.: Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998 A.; Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A:Reference number: A71570; MUID:99000809 A;Reference number: A71670; MUID:99000809 A;Reference number: A71670 A;Reference number: A71670 A;Reference number: A71670 A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.1%; Score 41; DB 2; Length 1009; Best Local Similarity 72.7%; Pred. No. 1.7e+02; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 44.1%; Score 41; DB 2; Length 571; Best Local Similarity 66.7%; Pred. No. 1e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                         2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 SHRSVRWLL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                         q
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
```

.

(5

(5) - 4

•

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:39:54 ; Search time 67.2 Seconds
(without alignments)
9.275 Million cell updates/sec Run on:

US-09-485-571-33 93 1 KYAWRVAHRGIRWLLRX 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	Description	W O90k57 chlamvdia	009758		015528	008160	070249	LI P08409 escherichia	I P11901	084340		P09707	860000	014061		P04165	P29757	P0571		P1483	P07747	033843	008638	_	P06102 sacch		· P11267 simian	P0588			ы		P34431	111111111111111111111111111111111111111
SUMMARIES	ΩI	PT1 CHLMU	YA71_SCHPO	PP11_YEAST	CP2B_HUMAN	OGG1_MOUSE	OGG1_RAT	INST_ECOLI	T421_ECOLI	PT1_CHLTR	CHS2_CANAL	US31_HCMVA	KR16_HSVI1	YC35_SCHPO	GS69_BACSU	CYB_MAIZE	CYB_SOLTU	CYB_VICFA	CYB_OENBE	CYB_ORYSA	CYB_WHEAT	BGLA_THENE	BGLA_THEMA	YA31_SCHPO	NOT3_YEAST	AMD2_HUMAN	ENV_SIVML	ENV_SIVMK	ENV_SIVM1	POL_HTL1C	MML3_MYCLE	IF2P_PYRAB	YL51_CAEEL	0,000
	DB	-	-	Н	٦	П	Н	-	_	7	-	7	-	Н	-	Н	Н	-	-	1	-		Н	-	Ч	<del>,  </del>	-	٦	-	-	٦	٦	Н	-
	Query Match Length	:	588	311	208	345	345	370	371	571				236	331	388	392	392	394	397	398	444	446	496	836	879	880	881	882	896	955	992	1745	7.50
ф	Query Match	47.3	45.7	45.2	44.6	44.1	44.1	44.1	44.1	44.1	44.1		43.0	43.0	٠	•	٠	٠	•	٠	•	41.9	41.9	٠	•	٠	i,	;	41.9	41.9	•	41.9	41.9	7 . 7
•	Score		42.5	42	41.5	41	41	41	41	. 41	41	40	40	40	36	39	39	39	39	39	39	39	39	39	39	39	39			39	39	39	39	G.
	Result No.	,	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30		32	33

P35475 homo sapien	. P30589 neurospora	O70173 rattus norv	P11696 ectothiorho	Q50648 mycobacter1	Q52822 rhizoblum l	Q52926 rhizobium m	O22504 daucus caro	P34497 caenorhabd1	Q07430 chlamydia p	Q23623 caenorhabdi	Q9zk79 helicobacte
IDUA_HUMAN	CHS2_NEUCR	PK3G_RAT	LHB2_ECTHL	YP73_MYCTU	EXOR_RHILV	EXOR_RHIME	GLN1_DAUCA	GLNA_CAEEL	OMIN_CHLPN	TGT_CAEEL	ATPA_HELPJ
7	_	-	-	Н	н	Н	-	-	-		~
653	944	1505	65	246	267	268	352	367	389	400	503
41.4	41.4	41.4	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.9	40.9
	S	ς.	38	38	38	38	38	38	38	38	38
38.5	38.	38									

## ALIGNMENTS

311 AA.

ŏ Db

```
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C)
Paulin L., Se
     PP11_YEAST
P20604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.,
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.; Sunditted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO YEAST YGL084C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
          Length 567;
                                                                                                                                                                                                                                                                                                    YATI_SCHPO STANDARD; PRT; 588 AA.
009758, 09C025;
01-007-1995 (Rel. 32, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOPHETICAL 69.1 KDA PROTEIN C24H6.01C IN CHROMOSOME I.
SPAC24H6.01C OR SPAPB21F2.01.
SCHIZOSACCHAROMYCES POMBE (Fission yeast).
Eukaryota; Fungl; ASCOMYCOCTA; SchizOsaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetases;
                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SER-RICH.
757AB685494B8B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                DB 1;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.5;
                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΨW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 254142; CAA90845.2; -. EMBL; AL590562; CAC36890.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 211-588 FROM N.A.
                     47.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-228 FROM N.A. STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Query Match
Best Local Similarity 7/..
.- Trace 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 WRVAHRGI-RWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
588 AA;
                                                                                                                                                      360 AHRSVRWLE 368
                                                                                                                           7 AHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wood V.;
                                                                                                                                                                                                                                                         RESULT 2
1YA71_SCHPO
1YA71_SCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

428 WRAWHRSFNRWLIR 441

g

RESULT 3 PP11_YEAST

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOL. Cell. Biol. 11:2133-2148(1991).

-i- FUNCTION: INVOIVED IN THE DEPHOSPHORYLATION OF THE LARGE SUBUNIT

-i- FUNCTION: INVOIVED IN THE DEPHOSPHORYLATION OF THE LARGE SUBUNIT

OF RNA POLYMERASE II. IS REQUIRED IN LATE G1 FOR NORMAL G1 CYCLIN

OF RAR POLYMERASE D1. IS REQUIRED IN LATE G1 FOR NORMAL G1 CYCLIN

ARE PERIODICALLY EXPRESSED DURING LATE G1. ASSOCIATES WITH THE

SAF PROTEINS IN A CELL CYCLE-DEPRINDINT MANNER.

-i- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)0 = A PROTEIN +

ORTHOPHOSPHATE (THIS BUXYME IS SERINE/THREONINE SPECIFIC).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.

-i- SUBCELLULAR LOCATION: CYTOPLASMIC.

-i- SUBCELLULAR LOCATION IN THE LATE CELL CYCLE G1 PHASE FOR

-progression into the S Phase, POSSIBLY ASSOCIATED IN TWO SEPARATE

COMPLEXES WITH THE PHOSPHORYLATED FORMS OF P155 AND P190, TWO HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24395; AAA56864.1; --
EMBL; 271781; CAA96442.1; --
EMBL; 274095; CAA98609.1; --
PIR; A3184; PABY1.
HSR; PO8129; IFJM.
SGD; SO002205; SIT4.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-89136000; PubMed=2537149;
Arndk K.T., Sryles C.A., Fink G.R.;
"A suppressor of a HIS4 transcriptional defect encodes a protein with homology to the catalytic subunit of protein phosphatases.";
Cell 56:527-537(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGRATE; PS00125; SER_THR, PHOSPHATASE; 1.

PROSITE; PS00125; SER_THR, PHOSPHATASE; 1.

Hydrolase; Iron, Manganese; Cell cycle; Mitosis; Multigene family.

METAL 55 55 IRON (BY SIMILARITY).

METAL 82 82 IRON AND MANGANESE (BY SIMILARITY).

METAL 114 114 MANGANESE (BY SIMILARITY).

METAL 115 115 GENERAL ACID (BY SIMILARITY).

METAL 164 164 MANGANESE (BY SIMILARITY).

METAL 238 ANGANESE (BY SIMILARITY).

METAL 238 ANGANESE (BY SIMILARITY).

SEQUENCE 311 AA; 35537 MW; AF52BC65E4F715EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91172202; PubMed-1848673;
Sutton A., Immanuel D., Arndt K.T.;
"The SIT4 protein phosphatase functions in late G1 for progression
into S phase.";
                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V
                            01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SERTHE/CHREDOUINE PROTEIN PHOSPHAIASE PPI-1 (EC 3.1.3.16).
PPHI OR SIT4 OR YDLO47W OR D2693.
                                                                                                                                                                                                                                                                                                                                                                                                                            Paulin L., Saren A.M., Laamanen P.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000934; Ser_thr_phosphtse.
Pfam; PF00149; STphosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
115
164
238
35537 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00114; STPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00156; PP2Ac;
                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW PROTEINS.
                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY.
```

ò 셤

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOR WENT THE STATE OF STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. 'Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Portale A.A.;

"Cloning of human 25-hydroxyvitamin D-1 alpha-hydroxylase and mutations causing vitamin D-dependent rickets type 1.";

"Cloning of human 25-hydroxyvitamin D-1 alpha-hydroxylase and mutations causing vitamin D-dependent rickets type 1.";

"Cloning of human 25-hydroxyvitamin D-1 alpha-hydroxylase and mutations causing vitamin D-1997).

"I EUNCTION: CATALYZES THE CONVERSION OF 25-HYDROXYVITAMIN D3 (1.25(OH)2D) PLAYS OF THE CONVERSION OF VITAMIN D3 (1.25(OH)2D) PLAYS OF THE CONVERSION OF VITAMIN D(3) INTO THE ACTIVE FORM (1-ALPHA, 25-DIHYDROXYVITAMIN D(3)).

"I SUBCELLULAR LOCATION: MITOCHORRIAL.

"I DISBASE DEFECTS IN CYP27B ARE A CAUSE OF VITAMIN D-DEPENDENT RICKETS TYPE 1 (VDDR-1), A DISBASE CHARACTERIZED BY MUSCLE WEARNESS AND RICKETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIATRE-98008873; PubMed-9344864;
MONKawa T., Yoshida T., Wakino S., Shinki T., Anazawa H., Deluca H.F.,
Monkawa T., Hayashi M., Saruta T.;
Suda T., Hayashi M., Saruta T.;
"Molecular cloning of CDNA and genomic DNA for human
25-hydroxyvitamin D3 1 alpha-hydroxylase.";
Biochem. Biophys. Res. Commun. 239:527-533(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98075882; PubMed-9415400;
Fu G.K., Lin D., Zhang Y.H., Bikle D.D., Shackleton C.H., Miller W.L.,
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
25-HVDROXXVITAMIN D-1 ALPHA HYDROXYLASE, MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (25-OHD-1 ALPHA-HYDROXYLASE) (25-HYDROXYLTAMIN D3 1-ALPHA-HYDROXYLASE) (V93 1A HYDROXYLASE) (P450C1 ALPHA) (P450VD1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98089075, PubMed-9428799;
Fu G.K., Portale A.P., Miller W.L.;
"Complete structure of the human gene for the vitamin D lalpha-
                                                                                                                               ö
                                                            Length 311;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 508 AA
                                                            Score 42; DB Pred. No. 12; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Cell Biol. 16:1499-1507(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYP27B1 OR CYP27B OR CYP1ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF027152; AAC51854.1; -.
                                                            45.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxylase, P450clalpha.
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                  11:1: || || 205 AWQVSPRGAGWL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                           3 AWRVAHRGIRWL 14
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IISSUE-Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    CP2B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA)
                                                                                                                                                                                                                                                                                                                                                              RESULT 4
CP2B_HUMAN
                                                                                                                               Matches
```

```
FROSTIE; PS00086; CYTOCHROME P450; 1.

Electron transport; Oxidoreductase; Monooxygenase; Membrane;
Heme; Mitochondrion; Transit peptide.
TRANSIT 1 ? MITOCHONDRION (POTENTIAL).
2 25-HOROXYVITAMIN D-1 ALPHA HYDROXYLASE.
BINDING 455 455 HEME (BY SIMILARITY).
SEQUENCE 508 AA; 56504 MW; 7F0611EFAD1B5CIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINI:=97330655; PubMed=9187114;
Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuba C.,
Kodana T., Takao M., Yasui A., Yamanoto K., Asano M., Fukasawa K.,
Yoshinari T., Inoue H., Otsuka E., Nishimura S.;
"Cloning and characterization of mammalian 8-hydroxyguanine-specific
DNA glycosylase/apurinic, apyrimidinic lyase, a functional mutm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=97342862; PubMed=9197244;
Lu R., Nash H.M., Verdine G.L.;
A maminalian DNA repair enzyme that excises oxidatively damaged quanines maps to a locus frequently lost in lung cancer.";
Curr. Biol. 7:397-407(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA GLYCOSYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C3H/HEN;
MEDINE-98096582; Pubmed-9434942;
Tani M., Shinmura K., Kohno T., Takenoshita S., Nagamachi Y.,
Yokota J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97352815; Pubmed-9207108;
Rosenquist T.A., Zharkov D.O., Grollman A.P.;
"Cloning and characterization of a mammalian 8-oxoguanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGGI_MOUSE STANDARD; PRT; 345 AA.
OGGI_MOUSE STANDARD; 035617; 00876; 008991; 035915; 035617; 00876; 008910; Q9QXEB;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
N-GLYCOSYLASE/ONA LYASE [INCLUDES: 8-OXOGUANINE DNA GLYC
(EC 3.2.2.-); DNA-(APDRINIC OR AFYRIMIDINIC SITE) LYASE
(EC 4.2.99.18) (AP LYASE)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer Res. 57:2151-2156(1997).
     . . . . . .
                                                                                                                                                                          InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.6%;
                     EMBL; AB005989; BAA22656.1;
EMBL; AB005990; BAA22657.1;
EMBL; AB006987; BAA23418.1;
EMBL; AF020192; AAC51853.1;
AB005038; BAA23416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                          PRINTS; PR00408; MITP450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
9; Conserve
                                                                                                                           P00189; 1SCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylase.
                                                                                                                                                       MIM; 264700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
OGG1_MOUSE
                                                                                                                              HSSb;
```

ij

us-09-485-571-33.rsp

```
2 YAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INST_ECOLI
                                                                                     9
                                                                                                   OGG1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                   δλ
                                         Op
              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified anorphical institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                             Johnsen B., Luna L., Rognes T., Seeberg E.;
Johnsen B., Luna L., Rognes T., Seeberg E.;
Toomplete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
Toomplete genomic DNA sequence of the Mus musculus 8-oxoguanine DNA
Toomplete Gnomic DNA sequence of the Mus musculus 8-oxoguanine DNA
Toomplete Gnomic DNA SEPATE BENEVIEW THAT INCISES DNA AT 8-OXOG RESIDUES.
TOTALY EPONATION THAT ENTRY THAT INCISES DNA AT 8-OXOG RESIDUES.
TO SECTIVE THAT NINCES DNA 3' TO THE LESION.
TASE ACTIVITY THAT NINCES DNA 3' TO THE LESION.
TO CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE NEAR APURINIC OR APVENTIONING SITES TO PRODUCTS WITH 5' PHOSPHATE.

TO SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS.

TISSUE SPECIFICITY: HIGHEST EXPRESSION IN TESTIS.
"Genomic structure and chromosomal localization of the mouse Oggl gene
that is involved in the repair of 8-hydroxyguanine in DNA damage.";
                                                                                                                         Seeberg E.; "Opposite base-dependent reactions of a human base excision repair "Opposite base-dependent reactions"; enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites."; EMBO J. 16:6314-6322(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Nuclease; Endonuclease; DNA repair; Glycosidase; Multifunctional enzyme; Nuclear protein.

ACT SITE 249 249 BY SIMILARITY.

CONFLICT 10 10 57 WAS -> Q IN REF. 2).

CONFLICT 239 239 A -> G (IN REF. 2).

CONFLICT 299 299 L -> S (IN REF. 5).

CONFLICT 329 299 L -> S (IN REF. 6).

CONFLICT 329 329 S -> F (IN REF. 6).

CONFLICT 336 336 R -> H (IN REF. 5 AND 7).

SEQUENCE 345 AA; 38883 MW; 75BBODDBO84E4947 CRC64;
                                                                                                     Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 345;
                                                                                                                                                                                                                 STRAIN=C57BL/6J;
Radicella J.P., Reille F., Dherin C., Boiteux S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , AF000669; AAB63151.1; -., AF012916; AAB94512.1; -., AF012912; AAB94512.1; -., AF012913; AAB94512.1; JOINED., AF012914; AAB94512.1; JOINED., AF012915; AAB94512.1; JOINED.
                                                                                  TISSUE=Lung;
MEDLINE=98026907; PubMed=9321410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF003596; AAB61289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ001307; CAB65240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U96711; AAB94512.1;
EMBL; V11247; CAA72117.1;
EMBL; Y113479; CAA73883.1;
EMBL; AJ001307:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AAB68616.1;
                                  Mamm. Genome 9:32-37(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00478; ENDO3c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogg1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1097693;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         STRAIN=129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its weby non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           historocal percentage (N. J. Laval F.);

Prieto-Alamo M.J., Laval F.);

Prieto-Alamo M.J., Laval F.);

"Cloning and characterization of a rat 8-oxoguanine-DNA-glycosylase.";

"Cloning and characterization of a rat 8-oxoguanine-DNA-glycosylase.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-i. FUNCTION: DNA REPAIR EWEXME THAT INCIEES DNA AT 8-OXOG RESIDUES.

EXCISES 7, 8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-METHYLPORAMIDOPPREMIDINE (RAPY) FROM DAMAGED DNA. HAS A BETA-INTASE ACTIVITY THAT NICKS DNA 3' TO THE LESION.

-i. CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE NEAR APURINIC OR APPERMIDINIC SITES TO PRODUCTS WITH 5'-PHOSPHATE.

-i. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSI_ECOLI STANDARD; PRT; 370 AA.
1NSI_ECOLI STANDARD; P77426; P76952;
01-AUG-1988 (Rel. 08, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last sequence update)
PUTATIVE TRANSPOSASE INSI FOR INSERTION SEQUENCE ELEMENT IS186A/B/C.
(INSI] OR B0016) AND (INSIZ OR B0582) AND (INSIZ OR B2394).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Nuclease; Endonuclease; Lyase; DNA repair; Glycosidase; Multifunctional enzyme; Nuclear protein.

ACT_SITE 249 249 BY SIMILARITY.
                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last sequence update)
N-GLYCOSYLASE/DNA LYASE (INCLUDES: 8-OXOGUANINE DNA GLYCOSYLASE
(EC 3.2.2.-); DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE
(EC 4.2.99.18) (AP LYASE)].
Rattus norwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%; Score 41; DB 1; Length 345;
41.7%; Pred. No. 20;
Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B7FDF8C782644C41 CRC64;
                                                                                                                                                                           345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF029690; AAC77525.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003265; Endo_3c.
Pfam; PF00730; HhH-GPD; 1.
SMART; SM00478; ENDO3c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 AA; 38711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 HVWQIAHRDYGW 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YAWRVAHRGIRW 13
: |::||| |
270 HVWQIAHRDYGW 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Hepatoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                           OGG1_RAT
070249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID DI DI DI OS OS
```

ö

ö

Gaps

.; 0

4; Indels

Score 41; DB Pred. No. 20; 3; Mismatches

44.18; ilarity 41.78; Conservative

Query Match Best Local Similarity Matches 5; Conserv

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lew H., Lin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Construction of a contiguous 874 kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-68.8 min region on the linkage map
and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                               MEDLINE-86030702; PubMed-2996940;
Chong P., Hui I., Loo T., Gillam S.;
"Structural analysis of a new GC-specific insertion element IS186.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakada S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S.,
Tagami H., Takehashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                               MEDLINE-86033672; Pubmed-2997142;
Kothary R.K., Jones D., Candido E.P.M.;
"IS186: an Escherichia coli insertion element isolated from a cDNA
                                                                                                                                                                                                                                                                                                  of
Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                    Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.; Systematic sequencing of the Escherichia coli genome: analysis the 0-2.4 min region...; Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (B2394).
Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
Federsplel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., L
Namath A., Oeffner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE IS186.
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (B0016; B0582 AND B2394).
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
                                                                                                                                                                                                                                                         MEDLINE-92334977; PubMed-1630901;
                                                                                                                                                                                                    Bacteriol. 164:957-959(1985).
                                                                                                          FEBS Lett. 192:47-52(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (B2394).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 4:91-113(1997)
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mau B., Shao Y.;
                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> G (IN REF. 2).
S -> T (IN REF. 2).
OPSLOFPPRAGSEKKN -> SHRWISPPEVPDPKRRINSL
WRITKKWYIWSLQVAIRGTVSCITAYKTOLKNARHRLNEAPRR
RILQWVQPLS (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPSLDFPPRSAGSEKKN -> SHRWISPPEVRIRKEELTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transposable element; Transposition; DNA-binding; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato S., Nakada Y., Shiratsuchi A.;
"ISAI, a new insertion sequence in Escherichia coli.";
FEBS Latt. 249:21-26(198)
-i- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1; Length 370;
Pred. No. 21;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN REF. 2).
FDD2041F5F3D7F03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 AA.
                                                                                                                                                                                                                              EMBL; M11300; AAA25030.1; --
EMBL; D10483; BAA01293.1; --
EMBL; AE000112; AAC73127.1; --
EMBL; AE000103; AAC73683.1; --
EMBL; AE000327; AAC73683.1; --
EMBL; AE000327; AAC73683.1; --
EMBL; D80598; AAA840781.1; ALT_INIT.
EMBL; D90700; BAA1524.1; ALT_INIT.
EMBL; D90700; BAA35223.1; --
EMBL; D90700; BAA35223.1; --
EMBL; ASA31; OCCC47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene, EG40012; inst.
InterPro, IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89252065; PubMed=2542093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40908 MW;
                                                                                                                                                                                                            EMBL; X03123; CAA26900.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.18;
61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 61.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
126
370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 YIVRVHWRGLRWL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQTR31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
CONFLICT 121
CONFLICT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG40012;
InterPro; IPR0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
126
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A25031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T421_FCOLI
P11901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T421_ECOLI
```

ဖ

ö

Gaps

;

Indels

ij

Mismatches

5;

```
6; Conservative
                                                                                                                                                                                            CHS2_CANAL P30572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                          CHS2_CANAL
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                               SOW WE REPRESENT TO THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                              ŏ
                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000940; PEP_Utilizers; 1.
PROSITE; PS00370; PEP_ENZYMES_PHOS_SITE; FALSE_NEG.
PROSITE; PS0042; PEP_ENZYMES_1; PALSE_NEG.
PROSITE; PS0042; PEP_ENYMES_2; FALSE_NEG.
PROSITE; PS0542; PEP_ENYMES_2; FALSE_NEG.
PROSIDE SPACEN; Transferase; Kinase; Sugar transport;
Phosphorylation; Complete protecome.
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY). 73EBFEEE7C457067 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOENOLPYRIVATE-PROTEIN PHOSPHOTRANSFERASE (EC 2.7.3.9)
(PHOSPHOTRANSFERASE SYSTEM, ENZYME I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 571; Pred. No. 32;
                                           InterPro; IPR02559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
Pypothetical protein; Transposable element; Transposition; DNA-binding; DNA recombination.
SEQUENCE 371 AA; 40995 MW; 2BD731641192DF38 CRC64;
                                                                                                                                                                                                 44.1%; Score 41; DB 1; Length 371; 61.5%; Pred. No. 21;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                571 AA
                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001306; AAC67931.1; -. Interpro; IPR000121; PEP_utilizers. Pfam; PF00391; PEP-utilizers; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=D/UW-3/CX;
MEDLINE=99000809; Pubmed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.18;
66.78;
         EMBL; Y07501; CAA68802.1; -. PIR; S04880; S04880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis.";
Science 282:754-759(1998)
                                                                                                                                                                                                          Query Match 44.1
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                      · 191 YIVRVHWRGLRWL 203
                                                                                                                                                                                                                                                                                             2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTSI OR CT336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT1_CHLTR
084340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                              PT1_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                    à
                  DR
DR
DR
SO
SO
SO
```

Best Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                       GLUCOSAMINYL)](N+1).
-1- SUBCELLUIAR LOCATION: PLASMA MEMBRANE-BOUND.
-1- DEVELOPMENTAL STAGE: VERY HIGH LEVELS OF CHS2 IN CELLS UNDERGOING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                01-NPR-1993 (Rel. 25, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHITIN SYNTHASE 2 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Glycosyltransferase; Transmembrane; Cell wall; Multigene family SEQUENCE 1009 AA; 115585 MW: 182PKANATBRADERO CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 1009;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPHAL OUTGROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 10, Created)
(Rel. 15, Last sequence update)
                                                                                                                                            1009 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycos_transf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001173; Glycos_transı_
Pfam; PF01644; Chitin_synth; 1.
ProDom; PD002998; Chitin_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  гик; мэвцэг; мэвцэг.
InterPro; IPR002923; Chitin_synth.
InterPro; IPR001173; Glycos_trans1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M82937; AAB59308.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.1%;
illarity 72.7%;
Conservative
                                                                                                                                                                                                                                                                                                                    Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 VAKRGCNWLLR 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S20538; S20538.
PIR; A38192; A38192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 8; Conserv
                      :|| :||||
364 SHRSVRWLL 372
7 AHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                              IRANSFERASE 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US31_HCMVA
P09707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US31_HCMVA

ID US31_H

AC P09707

DT 01-MAR

DT 01-AUG
```

```
STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                  YC35_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPCC962.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             014061
                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
YC35_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     QQ
                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                            MEDINE-87169717; PubMed-3031311;
Weston K., Barrell B.G.;
"Sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.";
J. Mol. Biol. 192:177-208(1986).
                                                                                                                                                                                                           Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169."; Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 182 N-LINKED (GLCNAC. . .) (POTENTIAL) 197 AA; 22935 MW; 2B3CBA7DE42EAD5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 40; DB 1; Length 197; 44.4%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davison A.J.;
"Channel catfish virus: a new type of herpesvirus.";
Virology 186:9-14(1992).
                                                     Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
GENE 16 PROTEIN KINASE (EC 2.7.1.-).
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                 Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X17403; CAA35263.1; -. EMBL; X04650; CAA28342.1; ALT_INIT
                                                                                                                                                                                      COMPLETE GENOME.
MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 KFTWWKRLRHSTRRWLFR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYAW--RVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; F27216; QQBED6.
PIR; S09945; S09945.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AUBURN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davison A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KR16_HSV11
Q00098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KR16_HSVI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris D., Wood V., Rajandream M.A., Barrell B.G.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                  ..
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 40; DB 1; Length 536; 46.2%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.0%; Score 40; DB 1; Length 387, 40.0%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 61.9 KDA PROTEIN C962.05 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61852 MW; A994D72219662F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizcsaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizcsaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL031323; CAA20437.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YAWRVAH-----RGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 40.0
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | : | | 379 WNLPHRLVLWTLR 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 WEVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 536 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizcsaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
```

```
808 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search com
Job time:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
ОD
                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                           "First steps from a two-dimensional protein index towards a response-
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- INDOCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
-!- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y14082; CAA74498.1; -.
EMBL; Z99109; CAB12792.1; -.
HSSP; P23457; 1LMI.
Subtlicist; BG13020; yhdN.
Pfam; PF00248; aldo_ket_red; 1.
Oxidoreductase; Heat shock; Complete proteome.
ACT_SITE 125 HORNGEN-BOND DONOR (PROBABLE).
GONFLICT 25 25 G -> K (IN REF. 2).
SEQUENCE 331 AA; 37312 MW; 82BC24D46E4994D0 CRC64;
                                                                                                                                                                                              Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                   Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 331;
Pred. No. 39;
3; Mismatches 6; Indels
                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987 (Rel. 04, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                GS69_BACSU STANDARD; PRT; 331 AA. P80874; 007583; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GENERAL STRESS PROTEIN 69 (GSP69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                             MEDLINE=97443988; PubMed=9298659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| | :||:|
255 RYGKSVIHLAVRWIL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYAWRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOCHROME B.
COB OR CYTB.
Zea mays (Maize).
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                             [2]
SEQUENCE OF 1-25.
                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYB_MAIZE
P04165;
                                                                                                                                                                                       STRAIN-168;
                                                                                                                                                                                                                                                     STRAIN-IS58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYB_MAIZE
                                                                                                 YHDN.
         GS69_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

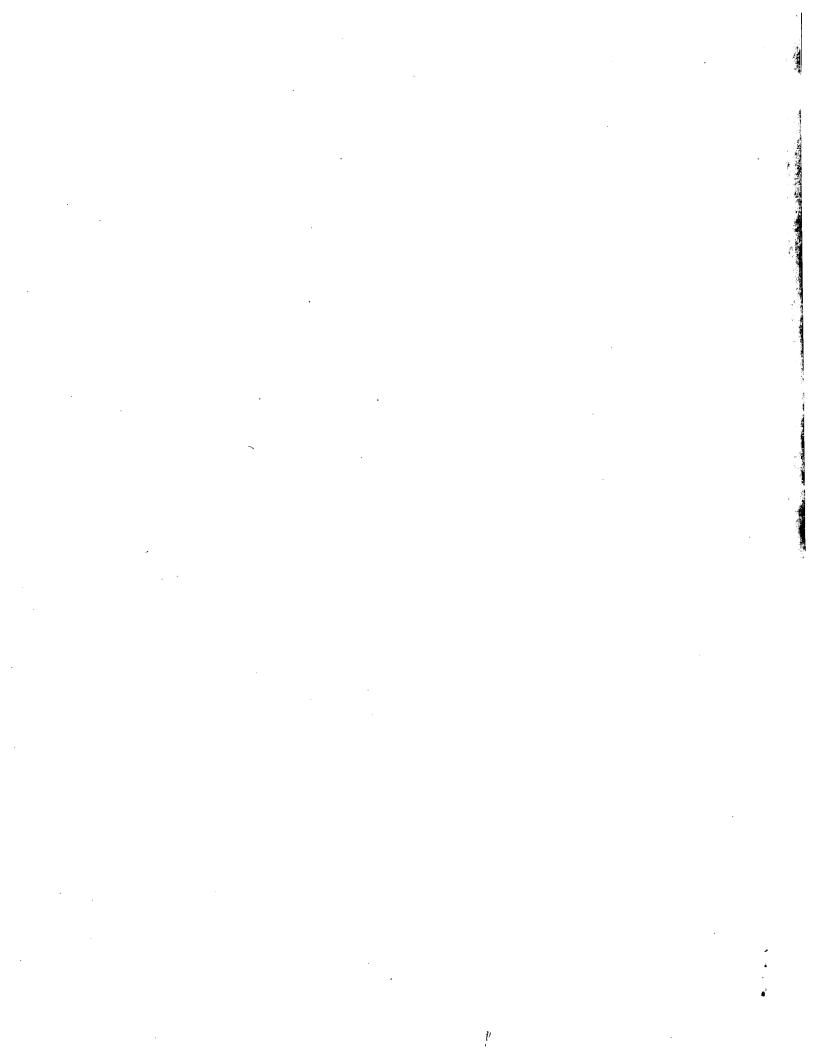
```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                COUPLED TO ATP SYNTHESIS.

-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.

-!- SUBGUIT: THE MAIN SUBGUITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A00156; CBZM.
MaizeDB; 6927; -.
Mendel, 2200; ZEAMa; cob; 1.
InterPro; IPR000179; Cyt.b_b6.
Pfam; PF00032; cytochrome_b_C; 1.
Pfam; PF00033; cytochrome_b_N; 1.
PROSITE; PS00192; CYTOCHROME_B_N; 1.
PROSITE; PS00193; CYTOCHROME_B_OO; 1.
Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
                                  Dawson A.J., Jones V.P., Leaver C.J.;
"The apocytochrome b gene in maize mitochondria does not contain introns and is preceded by a potential ribosome binding site.";
EMBO J. 3:2107-2113(1984).
-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRON 1 (HEWE B562 AXIAL LIGAND)
IRON 2 (HEWE B566 AXIAL LIGAND)
IRON 2 (HEWE B562 AXIAL LIGAND)
IRON 1 (HEWE B566 AXIAL LIGAND)
S6CF734C2B62B3F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 46;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: February 12, 2002, 12:39:55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.9%; 53.8%; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00789; CAA25367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
102
189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323 SFRPIHOGIFWLL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AWRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
102
189
203
388 AA;
[1]
SEQUENCE FROM N.A.
```

us-09-485-571-33.rsp



```
February 12, 2002, 12:38:44; Search time 232.64 Seconds (without alignments) 10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                          473505
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                           US-09-485-571-33
93
1 KYAWRVAHRGIRWLLRX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_arches:*
sp_bacteria:*
sp_human:*
sp_human:*
sp_nammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_phage:*
sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPTREMBL_17:*
                                                                                                                                                            Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                            Searched:
                                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	Q9jmj9 mus musculu	Q60997 mus musculu	Q9ha69 homo sapien	Q9afzl shigella fl	Q9z0f5 mus musculu	Q9urg3 penicillium	080923 arabidopsis	Q9hxu2 pseudomonas	Q9vyp6 drosophila	002175 caenorhabdi		••	Q9v3u3 drosophila	Q9p4w5 kluyveromyc	Q9kbx9 bacillus ha	Q9up42 homo sapien	Q9kny0 vibrio chol	Q9eqk5 mus musculu	069575 mycobacteri
SOFFERENCES		ID	Q5/M79	060997	Q9HA69	Q9AF21	Q9Z0F5	Q9URG3	080923	Q9HXU2	Q9VYP6	002175	Q9C025	Q9AFQ8	Q9V3U3	Q9P4W5	Q9KBX9	Q9UP42	O9KNYO	Q9EQK5	069575
		DB	11	11	4	7	11	~	10	~	'n	S	m	~	Ŋ	m	7	4	7	11	7
		Query Match Length DB	1957	2083	125	133	298	481	125	183	213	221	378	133	293	309	313	65	622	861	144
	æ	Query Match	48.4	48.4	47.3	47.3	47.3	47.3	46.2	46.2	46.2	46.2	45.7	45.2	45.2	45.2	45.2	44.6	44.6	44.6	44.1
		Score	45	45	44	44	44	44	43	43	43	43	42.5	42	42	42	42	41.5	41.5	41.5	41
		Result No.	-	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19

Q91395 klebsiella Q9x2v8 escherichia	Q91cs0 arthrobacte	O35405 mus musculu		Q9n6e9 leishmania	Q9vs49 drosophila			Q9ruk4 deinococcus	Q9nc93 trypanosoma	095992 homo sapien	Q9kyh2 streptomyce	Q9a559 caulobacter	Q9d3w8 mus musculu	Q9nuj5 homo sapien	Q9snv0 antirrhinum		Q9jpb4 rhodocyclus	Q9pp78 campylobact	P72272 rhizobium f	Q53032 rhodospiril	Q66434 dengue viru	P79078 cryptococcu	Q9f3q6 streptomyce	Q9uhd2 homo sapien
204 2 Q9L3G5 208 2 Q9X2V8	0	488 11 035405	711 5 Q9TXJ2	833 5 Q9N6E9	162 5 Q9VS49	178 2 Q9L1Y0	7	256 2 Q9RUK4	'n	272 4 095992	288 2 Q9KYH2	7	310 11 Q9D3W8	316 4 Q9NUJS	361 10 Q9SNV0	7	~	~	~	480 2 053032	545 12 Q66434	555 3 P79078	629 2 Q9F3Q6	729 4 Q9UHD2
41 44.1	41 44.1	41 44.1	41 44.1	41 44.1	40.5 43.5	40.5 43.5	40.5 43.5	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0	40 43.0
20	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

ŏ g

```
112 YLWRCSHRG--WL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiqella flexneri.
                      2 YAWRVAHRGIRWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9AFZ1;
                                                                                                                                                                                                                                                                       Q9HA69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9AFZ1
                                                                                                                                                                                                                                      09HA69
                                                                                                                                                                               m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                               RESULT
Q9HA69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9AFZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                             δλ
                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATA BADDELLO GUCCES.";

ANAL. REC. 244:327-343(1996).

C. -1 - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C. -1 - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (CRP-ALPHA AND CRP-CEC II- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (CRP-ALPHA AND CRAFT ENGLISH OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF CRP-ALPHA.

C. -1 - TISSUE SPECIFICITY: INTESTINE AND PANCREAS. IN THE COLON,

C. -1 - TISSUE SPECIFICITY: INTESTINE AND PANCREAS. IN THE COLON,

C. -1 - TISSUE SPECIFICITY: INTESTINE AND PANCREAS. IN CRAFT CALLS BUT NOT MATURE VILLUS CELLS. MOST HIGHLY

C. -1 - TISSUE SPECIFICITY: OUCTS.

C. -1 - TISSUE SPECIFICITY: INTESTINE AND PANCREAS. IN EPITHELIUM LINING

EXPRESSED IN MID-CRYPT. ALSO.

C. -1 - TISSUE SPECIFICITY: OUCTS.

C. -1 - TISSUE SAME SPERACTROPTR.

DR. PÉTAN: PRO00202: SR: 8.

DR. SMART; SMO0202: SR: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVEDVKKPASSQAVYPTAAIFGGVFLAMVLAVAAFTLGRR
THIDRGQPPSTKL -> PELSSQSQGPSSH (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheng H., Bjerknes M., Chen H.; "CRP-ductin: a gene expressed in intestinal crypts and in pancreatic and hepatic ducts.";
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 11; Length 2083;
Pred. No. 1.8e+02;
1; Mismatches 2; Indels
Length 1957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6D8B21C7737B4A0A CRC64;
                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SMC241; ZP; 1.
SMART; SM00241; ZP; 1.
SMART; SM00241; ZP; 1.
PROSITE; PS00420; SRCR_1; 8.
PROSITE; PS00682; ZP_DOMAIN; UNKNOWN_1.
SM Signal; Transmembrane; Alternative splicing.
AIGNAL
29 2083 CRP-DUCTIN.
CRP-DUCTIN
Score 45; DB 11;
Pred. No. 1.7e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THR-RICH.
PRO/THR-RICH.
PRO/SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                 2083 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRP-BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-JEJUNUM;
MEDLINE-96362470; PubMed-8742698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%;
milarity 61.5%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2083 AA; 226734
            48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 04, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997 (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRP-DUCTIN PRECURSOR (CRP) CRPD OR CRP OR CRP-DUCTIN.
      Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                        | || :||| ||
| 123 YLWRCSHRG--WL 133
                                                                                                                                 2 YAWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                       RESULT . 2
060997
AC 060997
DT 01-JUL-
DE CRE-DG
CC ENKARY
CO C ENKARY
CR STRAIN
RA MEDLIN
RA MEDLIN
RA MEDLIN
RA MEDLIN
RA ANA N-
CC - I - AL
CC - I 
                                                                                                                                                                                                                                                                                                                                                        060997
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete DNA Sequence and Analysis of the Large Virulence Plasmid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                 TISSUE-MAMMARY GIAND;

TARABA T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai IV., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

"NEDO human GIAND Sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK022213; BAB1987.1;

SEQUENCE 125 AA, 13762 MW; 37C386B66AC51B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plašmid virulence pWR501.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 4; Length 125;
Pred. No. 15;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 AA; 15379 MW; 759A64406ACA4F20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
                                               01-NAR-2001 (TrEMBLrel. 16, Created)
01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FLJ12151 FIS, CLONE MAMMA1000431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.3%; Score 44; DB
37.5%; Pred. No. 16;
Live 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AA
125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigella flexneri.";
Infect. Immun. 0:0-0(2001).
EMBL; AF348706; AAK18330.1;
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.3%;
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 WKICHLGFNWIRR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS91 ORFB, FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
```

ö

.,

us-09-485-571-33.rspt

Length 481;

3

g

```
DB 3;
59;
                                                                                                                                                                                                 125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 AA
                  Score 44; DB
Pred. No. 59;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.2%;
47.1%;
                 47.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KYAWRVAH--RGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| |||:|: |||:
460 QYQPRVAYRHLEWLLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                 Conservative
                                                                                 1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
Query Match
Best Local Similarity
8, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               01-JUN-2001 (TrEM)
F13M22.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iron-sulfur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudonionas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                              080923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09HXU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA3698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                               i~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q9HXU2
                                                                                                                                                                 RESULT
                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2001 (TrEMBLrel. 17, Last annotation update)
CARBOXYPEPTIDASE S3, PENICILLOPEPTIDASE S3, CPD-S3.
CARBOXYPEPTIDASE S3, PENICILLOPEPTIDASE S3, CPD-S3.
Enclishium janthinellum (Penicillium vitale).
Eukaryota; Fungi: Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Tritchocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Svendsen I., Day E.S.;
A Svendsen I., Day E.S.;
A Svendsen I., Day E.S.;
The primary structure of carboxypeptidase S3 from Penicillium
Tanthinellum IBT 3991";
EEBS Lett. 371:1-3(1995).
R HSSP; P10619; 11YY.
R InterPro; IPR001369; Est_lip_thioest_actsite.
R InterPro; IPR001369; Est_lip_thioest_actsite.
R InterPro; IPR001369; Serine_carbpept.
R Pfam; PF00450; serine_carbpept.
R PROSTIE; PS00560; CARBOXYPEPT_SER_HIS; UNKNOWN_I.
R PROSTIE; PS00560; CARBOXYPEPT_SER_HIS; UNKNOWN_I.
R PROSTIE; PS00131; CARBOXYPEPT_SER_SER_; I.
C SEQUENCE 481 AA; 54591 MW; 55A313E28E06885A CRC64;
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN—C57BL6/129 MIXED STRAIN, 129SVEV;
MEDLINE—99069428; PubMed—9852097;
Lund E.G., Kerr T.A., Sakai J., Li W.P., Russell D.W.;
Lund E.G., Kerr T.A., Sakai J., Li W.P., Russell D.W.;
CDNA cloning of mouse and human cholesterol 25-hydroxylases,
polytopic membrane proteins that synthesize a potent oxysterol
regularor of lipid metabolism.";
J. Blol. Chem. 273:34316-94327(1998).
EMBL: AF059213; AAC97480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 44; DB 11; Length 298;
40.0%; Pred. No. 36;
Live 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR001541; Sterol_desat.
Pfam: PF01598; Sterol_desat; 1.
PROSITE; SC00070; ALDEHYDR.CYS; UNKNOWN 1.
SEQUENCE 298 AA; 34672 MW; BBCE4A97A20284CG CRC64;
                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 AA
                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                  PRT;
                                                                                                                             01-MAY 1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17, CHOLESTEROL 25-HYDROXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| : | : || |
140 FAWHLLHHKVPWLYR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                 78 RFSWHVADKGFRMVIR 93
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1333869; Ch25h
                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-5079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9URG3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09URG3
                                                                                               Q920F5
```

Best Loc Matches

õ g RESULT Q9URG3

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNIA PROJECT STATE THE STATE STATE STATE STATE THE STATE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;

SURAIN-CV. COLUMBIA;

Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,

Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,

Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,

Somerville C.R., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-1- COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).

EMBL. ACOMG644, ACC23624.1;

ELINEL'S COROSTE; PSO0197; 2FE2S_ferredoxin.

PROSITE; PSO0197; 2FE2S_ferredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 10; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AA; 13953 MW; 0B60805BC5B18C2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA3698.
```

Ξ;

24384 MW; 3F3AF879C11704A0 CRC64;

RE DR SO

q

ŏ

```
213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                           158 HRGIRWL 164
                                                                                                                                                               8 HRGIRWL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9C0Z5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W05H7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                                                                                                                                                                                                                                                                              002175;
                                                                                                                                                                                                                                                                                                                                  002175
                                                                                                                                                                                                                                                                                    RESULT 10
002175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q9C0Z5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DI DE
                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                  Оp
     S
                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC STRAIN-BERKELEY;

RA Amantides PG., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,

RA Amantides PG., Scherer S.E., Holf R.A., Evans C.A., Galle R.F.,

RA Amantides PG., Scherer S.E., Holf R.A., Elband R.A., Galle R.P.,

RA Amantides PG., Scherer S.E., Holf R.A., Shaburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X.,

RA Ballaw R.M., Doyle C., Baxter E.G., Hella C., Nelson C.R., Miklos G.L.G,

RA Ballaw R.M., Basu B., Baxendale J., Bayraktaroglu L. Beasley E.M.,

Ballaw R.M., Basu B.P., Bemors P.V., Bernand B.P., Bhandari D. Bolshakov S.,

RA Berkova D. Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Geboon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Glodek A., Goabriellan A.E., Garg N.S., Gelbart W.M., Classer K.,

RA Glodek A., Goabriellan A.E., Garg N.S., Gelbart W.M., Classer K.,

RA Harris N.L., Harvey D., Heiman T. J., Hernandez J.R., Houck J.,

RA Abalai M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Kalush M., Kalush F., Kalure C.D., Kraft C., Morris J., Moshreii A.,

RA Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,

RA Spier E., Spradin Kiamos I. Simpson M., Stupski M.P., Smith T.,

RA Sher B., Spradin Kiamos I. Simpson M., Stupski M.P., Smith H.O.,

RA Sher B., Spradin Kiamos I. Simpson M., Stupski M.P., Smith H.O.,

RA Harls S.M., Wodege I., Wurlpy K., Wull, Weilsenbach C., Theng L., Sheng X.H., Bond G., Chong C., Charler E., Wassarman D.A., Weiler E., Wassarman D.A., Weiler E., Spradin K., Shong R., Sheng X.H., Zhong F
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                      ;
0
                                                                                                                                                     Length 183;
                                                                                                                                                                                                        Indels
          Nature 406:959-964(2000).

EMBL: AE004789; AAG07086.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 183 AA; 20351 MW; OCF452AB5251FEE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA
                                                                                                                                                        Score 43; DB
Pred. No. 32;
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003488; AAF48146.1; -.
FlyBase; FBgn0030375; CG11356.
                                                                                                                                                               46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                              Query Match
Best Local Similarity 50...
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                           2 YAWRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                            | : |:|:| || |
80 YGFTVSHQGKRWYL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9VYP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VYP6
                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q9VYP6
                                                                                                                                                                                                                                                                                                                                                                                                                                   DD T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T T D T
```

```
Ĥ
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Anderson, Coppey T., Cooper J., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Graxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lidhtning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thherry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRATH-BRISTOL NJ.
Wohldmann P. Le T.T.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APR-1997) to the EMBL/GenBank/DDBJ databases
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 45.0 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                            ;
0
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 5 pred. No. 38; 3; Mismatches
DB
37;
                                                                                                                                                                                                                                     221 AA
                                            0; Mismatches
      46.2%; Score 43; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.28;
                                                                                                                                                                                                                                                                                04,
04,
08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 KYGGTWKLRHLGMRW 72
        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KY--AWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. COSMID W05H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1997) to EMBL; U97552; AAB52865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
```

```
:: | ::|:|: |
EHGWGLSHKGVLW 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KYAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SP555 OR CG14041.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                      "Complete DNA Sequence and Analysis of the Large Virulence Plasmid of Shigella flexneri.";
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                           Plasmid virulence pWR501.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                          Ä
                                                                                                                                                      Score 42.5; DB 3; Length 378; Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 133;
                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                            Saunders D., Harris D., Wood V., Rajandream M.A., Barre Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AL590562; CAC36890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 133 AA; 15361 MW; 759A64452FDE1B20 CRC64;
                                                                                                                           378 AA; 45008 MW; CBAFFE191F8B93E2 CRC64;
        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                        133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AA
                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 0:0-0(2001).
EMBL; AF348706; AAK18494.1; -.
                                                                                                                                                       45.78;
57.18;
                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, C
(TrEMBLrel. 17, I
(TrEMBLrel. 17, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 45.2%;
Similarity 37.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                       IS91 TRANSPOSASE, FRAGMENT
                                                                                                                                             Query Match
Best Local Similarity 57.14
Conservative 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::| || :| | ::|
78 RFSWHVADKGFRIVIR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                      4 WRVAHRGI-RWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conservi
                                     Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                       Shigella flexneri.
                                                             SEQUENCE FROM N.A.
                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG14041 PROTEIN
                                                                      STRAIN-972H-;
                                                                                                                                                                                                                                                                           1-JUN-2001
1-JUN-2001
                                                                                                                                                                                                                                                                                              I-JUN-2001
                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                         Q9AFQ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09v3u3
                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                         ò
ò
```

```
RX STARAH-BERKELEY;
RAMAN-BERKELEY;
RAMAN-BERKEN,
RAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Serano T.L., Pendleton J.D., Rubin G.M.;
"A reverse genetic screen for genes involved in Drosophila eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6102146A0054D999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 5;
Pred. No. 73;
6; Mismatches
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003608; AAF52206.1; -.
EMBL, AR721038; AAF4807.1; -.
FYybass; FBgn0040280; FS555.
InterPro; IPR001870; Gamma_carbxylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001496; SOCS.
InterPro; IPR003877; SPRY.
InterPro; IPR003878; SPRY_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The genome sequence of Dros
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00253; SOCS; 1.
SMART; SM00449; SPRY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00622; SPRY; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM
SEQUENCE
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the alkaliphilic bacterium Bacillus "Complete genome sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:431-4331(2000).

EMBL, APO01513; BAB05514.1; -
InterPro; IPR003348; ArsA_ATPase.

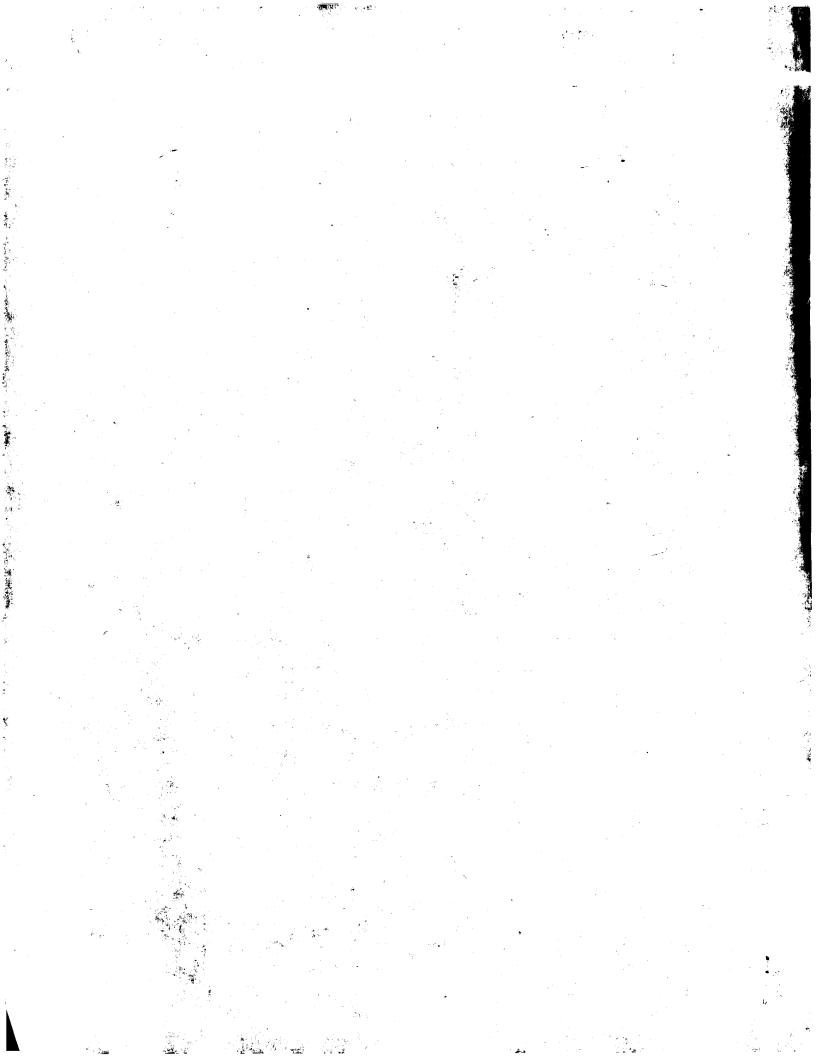
Pfan, PF0274; ArsA_ATPase; 1.

Complete proteome.

SEQUENCE 313 AA; 35531 MW; B530B49414F70376 CRC64;
                                                                                                                                                                                                                                                                                             MEDIATE-2359/152;
MEDIATE-2370185; PubMed=10809730;
MEDIATE-2070185; PubMed=10809730;
MEDIATE-2070185; PubMed=10809730;
Then X.J., Bauer B.E., Kuchler K., Clark-Walker G.D.;
Positive and negative control of multidrug resistance by the Sit4
protein phosphates in Kluyveromyces lactis.";
J. Biol. Chem. 275:14865-114872(2000).
I- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)0 = A PROTEIN +
ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
PPP) FAMILY: TO SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE (OR PPP) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Tukami F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
HOTIKOSHI K.;
                                                                                                                                                    Kluyveromyces lactis (Yeast).
Eukaryota; Fungi: Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.2%; Score 42; DB 3; Length 309; 58.3%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Iron; Manganese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CN-2001 (TrEMBLrel. 17, Last annotation update)
ARSENICAL PUMP-DRIVING AFFASE.
                                                          01-007-2000 (TrEMBLrel. 15, Created)
01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROTEIN SERINE/THREONINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X87624; CAA60955.1; -.
InterPro; IPR000934; Ser thr_phosphtse.
Pfam; PF00149; STphosphatase; 1.
PRINTS; PR00114; STPHPHTASE.
SMART; SM0115; PP2Ac; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 313 AA
                 309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.2'
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|: || ||
205 AWQVSPRGAGWL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 AWRVAHRGIRWL 14
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Q9P4W5
DD Q9P4W5
DT COUT-:
DT 01-CCT-:
DT 01-CCT-:
DE PROTEIN
GN NORI.
GN NORI.
GN NORI.
GN CENARYOI
CC CARUENCI
RY MEDLINE:
RX MEDLINE:
RX MEDLINE:
RX MEDLINE:
RY PROTEIN
RT PROTEIN
RY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KBX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9KBX9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KBX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
```

```
Ouery Match
45.2%; Score 42; DB 2; Length 313;
Best Local Similarity 57.1%; Pred: No. 78;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 YAWRVAHRGIRWLL 15
Db 27 FAWRCAERGEKTLL 40

Search completed: February 12, 2002, 12:38:45
Job time: 758 sec
```



7

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:39:49; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec Run on:

US-09-485-571-20 33 1 XGGXXXXXXXXXXXG 18

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum.Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P41778 mus musculu	O14649 homo sapien	P40424 homo sapien	Q60429 cricetulus	P02400 saccharomyc	P07183 drosophila	Q06650 streptomyce		_		_		Q9uuz6 aspergillus					Q08369 mus musculu	O00458 homo sapien		-		-	P14328 dictyosteli		-	P18540 agrobacteri	_	_	P07663 drosophila	_	53553	P20659 drosophila
SUMMARIES	Ω	PBX1_MOUSE	CIW3_HUMAN	PBX1_HUMAN	SRE2_CRIGR	RLA4_YEAST	CH38_DROME	BLAC_STRCE	PBX2_HUMAN	PBX2_MOUSE	PAX7_HUMAN	SGG_DROME	MSP1_PLAYO	RLA2_ASPFU	19KD_MYCIT	CH18_DROME	BASI_RABIT	EXD_DROME	GAT4_MOUSE	IFR1_HUMAN	GATA_RICPR	MEF2_DROME	SP70_DICDI	DSX_DROME	SP96_DICDI	ELS_BOVIN	ELS_CHICK	VIRA_AGRT5	ELS_MOUSE	PER3_MOUSE	PER_DROME	NRG_DROME	YZ08_MYCTU	TRX_DROME
	DB	-	7	Н	П	-		Н	-	~	-	-	-	-	-	-	-	-	Н	Н	-	-	-	-	-	-	-	Н	-	-	Н	-	Н	
	Query Match Length	347	394	430	1139	110	306	311	430	430	520	1067	1772	111	162	172	270	376	440	451	493	515	537	549	900	747	750	833	860	1113	1224	1302	1901	3726
de	Query Match	48		48.5		45.5	45.5		45.5	45.5	45.5	45.5	45.5	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4		42.4	42.4	42.4	42.4	42.4	42.4
	Score		16	16	16	15	15	15	15	15	15	15	15	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
	Result No.	-	7	m	4	S	Q	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26.	27	28	29	30	31	32	33

P34527 caenorhabd1	P02449 dromaius no	P42037 alternaria	P05389 drosophila	Q50418 methylobaci	P05782 xenopus lae	002786 bos taurus	P13346 mus musculu	Q12837 homo sapien	Q63934 mus musculu	P46152 rattus norv	Q11067 caenorhabd1
YM66_CAEEL	KRFT_DRONO	RLA2_ALTAL	RLA2_DROME	MAUF_METFL	K1C3_XENLA	HMX1_BOVIN	FOSB_MOUSE	BR3B_HUMAN	BR3B_MOUSE	GAT4_RAT	PDA6_CAEEL
1	٦,	7	-	-		Н	7	-	_	-	1
84	102	113	113	153	280	297	338	410	411	440	440
39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4	39.4
13	13	13	13	13	13	13	13	13	13	13	13
34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

TO NOV-1995 (Rel. 32, Created)  OT NOV-1995 (Rel. 32, Last sequence update)  OT NOV-1995 (Rel. 34, Last sequence update)  OT NOV-1995 (Rel. 36, Last sequence update)  OT NOV-1995 (Rel. 36, Last sequence update)  OT NOV-1995 (Rel. 36, Last sequence update)  OT STATE RELEAGURANT TRANSCRIPTION FACTOR 1 (HOMEOBOX PROTEIN PBX1).  ON RELEAGURANT PREAZEST (Christoff Sciurognathi; Muridae; Murinae; Mus.  ON RELL TAXID-10090; TARABNASH Y. Last sequence (CRSI) of CYP17 is a cellular target for TRABANATI ROBOTION PARTIAL SEQUENCE.  ON RELLIAND-201019; PROMEGA-791346; TARABNASH Y. LVANNECH RECHAPTON OF CYP17 (R. 17) (R	RESULT PBX1_M	RESULT 1 PBX1_MOUSE	i di	ģ	E			
	ع ڊ	PBXI_MOUSE	STANDAR	ë;	PKT;	34/	AA.	
	2 E	01-NOV-1995 (	Rel. 32,	Created)				
	E	01-NOV-1995 (	Rel. 32,	Last seq	neuce r	ıpdat	(e)	
	<u>t</u> :	15-JUL-1998 (	Rel. 36,	Last ann	otation	pdn (	ate)	
	i :	PRE-B-CELL LE	CUKEMIA TE	KANSCRIPT	ION FAC	TOK-	I (HOMEOBOX PI	ROTEIN PBXI).
	<u>.</u> .	Mis misculus	· ·					
	ס כ	Firkaryota Mo	(MOUSE).		Craniat	V . e	ortohrata. Find	toloostomi.
	ي ر	Mammalia: Fut	heria: R		Sciuro	na, v	i Muridae M	reicoscomit,
	<b>≥</b> ×	NCBI TaxID=10	0000:				in (appropriate (a)	
	z	[1]						
	ď.	SEQUENCE FROM	1 N.A., AN	ID PARTIA	L SEQUE	SNCE.		
	ပ္က	TISSUE.*Adrena	l gland;					
	×	MEDLINE-94308	1119; Pubh	4ed=79134	64;			
	≴	Kagawa N., Og	o A., Tak	ahashi Y	., Iwan	natsu	A., Waterman	
	턴	"A cAMP-regul	atory sec	nence (C	RS1) of	CYP	17 is a cellu	rget
	E :	the homeodome	in protei	In Pbx1."				
	J 5	J. Blot. Chen	1. 269:18/	716-18/15	(1994)	9		5
	ې د		PLAIS A	KOLE IN	THE CA	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	PENDENT REGULA	
	ې د	SENE EAPT	CESSION VI	A LIS CA	MP-KEGU	JLATO	NI SECUENCE (C	(KSI)
	ع ڊ	HAVE A PC	TN CTE	PROPERTY	FCTC AN	1 2	BSECIENTLY SE	KIDI.
	ر بر بر	DEVELOPME	IN AND DI	FFERENTI	ATTON			
	<u> </u>		AR LOCATI	ON: NUCL	EAR.			
	ပ္ပ		VE PRODUC	TE: TWO	ISOFOR	4S AR	E PRODUCED BY	ALTERNATIVE
	ູບ	SPLICING						
	ပ္		ECIFICITY	C: WIDELY	DISTR	IBUTE	D IN STEROIDO	GENIC AND NON-
	ပ္ (		ENIC CELI	S.				
	ပ္ (	-!- SIMILARI	Y: BELONC	S TO THE	TALE	PBX F	AMILY OF HOME	DBOX PROTEINS.
	و ر					:		
	و ب	A-SSIMS STUI	Cor entry	1s copyr	ignt.	LT 18	produced three	ough a collaboration
	ې د	the Furnisher	SWISS INS	stitute c	I BIOIL	mioit	Hatics and the	e EMBL OUTSTATION .
	۽ ر	the European	Bloinform	maries ir	Stitute		nere are no	restrictions on lts
	ې ر	modified and	thic ctat	oment is	מין לכני		d IIcado hy	and for comparetal
	ָטַ אָ	entities requ	ires a li	cense ad	reement	Se (Se	e http://www.	isb-sib.ch/announce/
	ي د	or send an en	nail to li	censedis	b-sib.	, q		
	<u> </u>							
	æ	EMBL; L27453;	AAA21832	2.1;				
TRANSFAC; T02088; MGD; MGI:97495; Pbx1. InterPro; IPR001047; HTH_repressr. InterPro; IPR001365; Homeobox. Pfam; Pf00046; homeobox; 1. PRINTS; PR00031; HTHREPRESR. SMART; SM0389; HOX; 1. PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	æ	HSSP; P01366;	1AKH.					
MGD; MGI:97495; PbxJ. InterPro; IPR000047; HTH_repressr. InterPro; IPR001356; Homeobox. Pfam; PP60046; homeobox; 1. PRINTS; PR00031; HTHREPRESSR. SMART; SM00389; HOX; 1. PROSITE; PS00027; HOWEOBOX 1; 1. PROSITE; PS00077; HOWEOBOX 2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	뽔	TRANSFAC; TO	'880'					
InterPro; IPR000047; HTH_repressr. InterPro; IPR0000356; HOmeobox. Pfam; PF00046; homeobox; I. PRINTS; PR00031; HTHREPRESSR. SMARY; SM00389; HOX; II. PROSITE; PS50007; HOMEOBOX_1; I. PROSITE; PS50071; HOMEOBOX_2; I. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	<u>ب</u>	MGD; MGI:9749	15; Pbx1.	;				
InterPro; IPR001356; Homeobox. Pfam; PF00046; Homeobox. 1. PRINTS; PR00031; HTHREPRESSR. SMART; SM00389; HOX; 1. PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	<u>ب</u>	InterPro; IPF	2000047; E	TH_repre	ssr.			
PRIMIS; PROUGAS; INDMEDDOX; 1. PRIMIS; PROUGAS; INTHREPRESSR. SMART; SM00389; HOX; 1. PROSTIE: PSO0027; HOMBOBOX_1; 1. PROSTIE: PSS0071; HOMBOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	¥ ;	InterPro; IP	1 1925100	lomeopox.				
SMARY; SMO389; HOX; 1. PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135 POLY-ALA.	¥ 0	DEINT PEODO	); nomeob(	JX; I.				
PROSITE: PS00027; HOMEOBOX_1; 1. PROSITE: PS50071; HOMEOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135 POLY-ALA.	; œ	SMART: SMOO3F	19: HOX: 1					
PROSITE: PS50071; HOMEOBOX_2; 1. Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation.  DOMAIN 127 POLY-ALA.	<u>د</u> د	PROSTTE: PSO(	1027 HOME	COROX 1:	_			
Transcription regulation; DNA-binding; Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135.	<u> </u>	PROSITE; PS5(	0071; HOME	30BOX 2;				
Homeobox; Alternative splicing; Steroid Sexual differentiation. DOMAIN 127 135 POLY-ALA.	ß	Transcription	n requlati	ton; DNA-	binding	N. K	clear protein	; Activator;
	3	Homeobox; Alt	ernative	splicing	; Ster	Sidog	enesis;	
DOMAIN 127 135	3	Sexual differ	rentiation	· .		•		
	Ē	DOMAIN	135		OLY-ALA	نہ		

ö

```
CARBOHYD
SEQUENCE
                                                   IRANSMEM
                                                                                         TRANSMEM
                                                                                                                               IRANSMEM
                                                                                                                                                                 PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PBX1_HUMAN
                                                                                                             DOMAIN
                                                                       DOMAIN
                                                                                                                                               DOMAIN
                                                                                                                                                                                    DOMAIN
                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pima
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HERE RESERVED TO THE SERVED T
                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                          δλ
KKK
FITE FITE FITE STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M., "Inhalational anesthetics activate two-pore-domain background K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SHEFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
                                                                                                                 0;
                                                                             Length 347;
                                                                                                                   14; Indels
       HOMEOBOX (TALE-TYPE).
C4A2BDDD4A410C20 CRC64;
                                                                             Score 16; DB 1; Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                        394 AA.
                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR0013280; 2poreK_channel.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR001309; TASK_channel.
InterPro; IPR000309; TWIK_channel.
Ffan; PP02034; TWIK_channel.
Pfan; PP02034; TWIK_channel.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99254548; PubMed-10321245;
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue=Kidney;
medLine=97459932; pubmed=9312005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF006823; AAC51777.1; -.
         295 H
38427 MW;
                                                                                 48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                near physiological pH.";
EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                124 GGSAAAAAAAAASGGAG 140
                                                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
           233
347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                     Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603220;
                                                                                                                                                                                                                                                                                                                                                                                                                           KCNK3 OR TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTIVATION
                                                                                                                                                                                                                                                                                            CIW3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 channels."
             DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                014649
                                                                                                                                                                                                                                                                          CIW3_HUMAN
                                                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                  g
             FT
```

```
Kamps M.P., Murre C., Sun X.-H., Baltimore D.;
"A new homeobox gene contributes the DNA binding domain of the t(1;19) translocation protein in pre-B ALL.";
Cell 60:547-555(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A. (ISOFORM PBX1A).
MEDLINE-21167395; PubMed-11267683;
Thanneem F., Wolford J.K., Bogardus C., Prochazka M.;
"Analysis of PBX1 as a candidate gene for type 2 diabetes mellitus in
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van Dijk M.A., Voorhoeve P.M., Murre C., "Pbx1 is converted into a transcriptional activator upon acquiring the N-terminal region of E2A in pre-B-cell acute lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The t(1;19)(q23;p13) results in consistent fusion of E2A and PBX1 coding sequences in acute lymphoblastic leukemias."; Blood 77:687-693(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
PAGE-2001 (Rel. 40, Last annotation update)
PRE-B-CELL LENERMIA TRANSCRIPTION FACTOR-1 (HOMEOBOX PROTEIN PBX1)
(HOMEOBOX PROTEIN PRL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

BEDLINE-22049345, bubMed=1682799;
Monica K., Saltman D., Nourse J., Galill N., Cleary M.L.;
Monica A., Saltman D., Nourse Je, Galill N., Cleary M.L.;
"PBX2 and PBX3, new homeobox genes with extensive homology to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91129319; PubMed=1671560;
Hunger S.P., Galili N., Carroll A.J., Crist W.M., Link M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE OF 89-430 FROM N.A., AND CHROMOSOMAL TRANSLOCATION. MEDLINE-90150282; PubMed=1967983;
                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (F
9FF4C8266F615FB7 CRC64;
                                                                                                                                                                                        PORE-FORMING (POTENTIAL).
                                                                          POTENTIAL.
PORE-FORMING (POTENTIAL)
                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                               CYTOPLASMIC (POTENTIAL):
                                                                                                                                                                                                                                                                                                                                             Score 16; DB 1; Pred. No. 2.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 1518:215-220(2001).
                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                           POTENTIAL.
                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human proto-oncogene PBX1.";
Mol. Cell. Biol. 11:6149-6157(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=93317624; PubMed=8327485;
                                                                                                                                                                                                                                                                                   X.
                                                                                                                                                                                                                                                                                                                                                  48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHROMOSOMAL TRANSLOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GGSAHTTDTASSTAAAG 292
                                                                                                                                                                                                                                                           53
43518
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                    8
29
101
128
158
179
207
243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                  78
108
129
159
184
223
                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PBX1_HUMAN P40424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PBX1 OR PRL.
```

ISOFORM PBX1B)

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE B AND T LINEAGE.

DISEASE: A FORM OF PRE-B-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (B-ALL)

25% OF HUMAN PEDIATRIC CASES) IS CHARACTERIZED BY A CHROMOSOMAL

TRANSLOCATION T(1:19) (023:913:3) WHICH INVOLVES PEX1 AND E2A

GENES. E2A-PBX1 TRANSFORMS CELLS BY CONSTITUTIVELY ACTIVATING

TRANSCRIPTION OF GENES REGULATED BY PBX1 OR BY OTHER MEMBERS OF
                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 233-319 IN COMPLEX TO HOXB1. MEDLINE-99159825; PubMed=10052460; Piper D.E., Batchelor A.H., Chang C.-P., Cleary M.L., Wolberger C.; "Structure of a HoxB1-Pbx1 heterodimer bound to DNA: role of the hexapeptide and a fourth homeodomain helix in complex formation."; cell 96:587-597(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THIS NONACTIVATING PROTEIN WHICH COULD BE A REPRESSOR; BINDS THE SEQUENTED INTO A POTENT PRINGS THE SEQUENTED INTO A POTENT TRANSCRIPTIONAL ACTIVATOR BY THE (1,19) TRANSCACATION. MAY HAVE A ROLE IN STEROIDOGENESIS AND SUBSEQUENTLY SEXUAL DEVELOPMENT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: 2 ISOFORMS; PBX1A (SHOWN HERE) AND PBX1B; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT IN CELLS OF
                                                                                                                                                 Lu Q., Wright D.D., Kamps M.P.; "Fusion with E2A converts the Pbx1 homeodomain protein into a constitutive transcriptional activator in human leukemias carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; DNA-binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
HOMEOBOX (TALE-TYPE).
BREARPOINT FOR TRANSLOCATION TO FORM
CAA67062A-PRI ONCOGENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSFNMSNSGDLF -> GYPSPCYQPDRRIQ (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repressor; Homeobox; Proto-oncogene; Chromosomal translocation; Alternative splicing; Steroidogenesis; Sexual differentiation;
                            Proc. Natl. Acad. Sci. U.S.A. 90:6061-6065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PBX1A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the t(1;19) translocation.";
Mol. Cell. Biol. 14:3938-3948(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : M31522; AAA36764.1; ALT_INIT
1B72; 19-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
                                                                                                                     MEDLINE-94254851; PubMed-7910944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M86546; AAA60031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE PBX PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135
295
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01481; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIFFERENTIATION
                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 176310;
   leukemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
THE REAL AND DEATH AND DEA
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (TRUNCATED FORMS SRD-1 TO SRD-3).
BEDLINE-29263566; Pubmed-714865;
Yang J., Brown M.S., Ho Y.K., Goldstein J.L.;
"Three different rearrangements in a single intron truncate sterol regulatory element binding protein-2 and produce sterol-resistant phenotype in three cell lines. Role of introns in protein evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BHLH PROTEIN.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANES OF THE NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                  Cricetulus griseus (Chinese hamster).
Eukarycta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 270:12152-12161(1995).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE STEROL
REGULATORY ELEMENT 1 (SRE-1) (5'-ATCACCCCAC-3') FOUND IN THE
FLANKING REGION OF THE LDRL AND HMG-COA SYNTHASE GENES (BY
                                                                                                       ;
0
                                                                                                                                                                                                                                          SRE2_CRIGR STANDARD;
060427; 060418; 060428; 060427;
15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
20-EDG (Rel. 40, Last annoctation update)
REGULATORY ELEMENT BINDING PROTEIN-2 (SREEP-2) (STEROL REGULATORY ELEMENT BINDING TRANSCRIPTION FACTOR 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND TRUNCATED FORM SRD-1.
MEDLINE=95047343; PubMed=7958866;
Yang J., Sato R., Goldstein J.L., Brown M.S.;
"Sterol-resistant transcription in CHO cells caused by gene rearrangement that truncates SREBP-2.";
Genes Dev. 8:1910-1919(1994).
                                                                         Length 430;
            MISSING (IN ISOFORM PBX1B).
AD3FFACBC5A9E715 CRC64;
                                                                                                      14; Indels
                                                                         Score 16; DB 1;
Pred. No. 3e+03;
0; Mismatches 1.
                            46626 MW;
                                                                         48.5%;
                                                                                                                                                                  GGSAAAAAAAASGGAG 140
                                                                                                                                      GGXXXXXXXXXXXX 18
                                                                         Query Match 48.5
Best Local Similarity 17.6
Matches 3; Conservative
                            430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                     SREBF2 OR SREBP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                   Cricetulus.
              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                            SRE2_CRIGR
                                                                                                                                      7
                                                                                                                                                                    124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>;</u>
                                                                                                                                                                                                               RESULT
                                                                                                                                                                  g
SOFT
                                                                                                                                      ð
```

```
ö
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     Transcription regulation; DNA-binding; Nuclear protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (BY APOPAIN AND CASPASE-7) (BY
                                                                                                                                                                                                                                                                                                                      BASIC DOMAÍN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
LEUCINE-ZIPPER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
60S ACIDIC RIBOSOMAL PROTEIN P-SBETA (L45) (KL44C) (YPA1) (L12EIA).
RPP2B OR RPLA4 OR L12EIA OR RPL45 OR YDR382W.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                      BREAKPOINT FOR TRANSLOCATION TO FORM SREBP-2 FUSION PROTEINS IN SRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-88243786; PubMed=2837476;
Remacha M., Saenz-Robles M.T., Vilella M.D., Ballesta J.P.G.;
"Independent genes coding for three acidic proteins of the large ribosomal subunit from Saccharomyces cerevisiae.";
J. Biol. Chem. 263:9094-9101(1988).
                                                                                                                                                                                                                                                           TRANSCRIPTIONAL ACTIVATION (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                             Endoplasmic reliculum, Polymorphism; Chromosomal translocation. DOMAIN (YTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                               TO STEROL REGULATORY ELEMENT-1 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> N (IN 50% OF THE MOLECULES). E81C2778EBF02653 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 1; Length 1139;
Pred. No. 6.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                      LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newton C.H., Shimmin L.C., Yee J., Dennis P.P.;
                                                                                                                                                                                                                                                                      GLY/PRO/SER-RICH.
                                                                                                                                           SMART; SM00353; HLH; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                               POLY-ALA.
                                   EMBL; U12330; AAA74141.1; -.
EMBL; U12329; AAA74140.1; ALT_TERM.
EMBL; U22819; AAA85719.1; ALT_TERM.
EMBL; U22818; AAA85718.1; ALT_TERM.
HSSP; P36956; 1AM9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SR26-12C;
MEDLINE=90130289; PubMed=2404943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.5%;
17.6%;
                                                                                                     InterPro; IPR003015; HLH_Myc.
InterPro; IPR001092; HLH_dim.
Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               123655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 GGSSGSSSSSNSSSSG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                      531
552
1139
                                                                                                                                                                                                                                                                                                                        341
379
399
593
860
461
                                                                                                                                                                                                                                                                                                                                                                                                                                                      493
                                                                                                                                                                                                                                                          50
124
244
421
                                                                                                                                                                                                                                                                                                                                                                                                                            467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    493
1139
                                                                                                                                                                                                                                                              1
52
125
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                            589
857
460
                                                                                                                                                                                                                                                                                                                                                                                                                            466
                                                                                                                                                                                                                      501
532
553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLA4_YEAST
P02400;
                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                          DNA_BIND
                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
RLA4_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: PHOSPHORYLATED (BY SIMILARITY)
-!- MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SWALL RIBOSOWAL A PROTEINS (RRA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-S28G / AB972;
Johnston M., Ab972;
Johnston M., Androw S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Follon L., Gattung S., Greco T., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Treyaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae. Isolation and characterization of peptides and the complete amino acid sequence."; Blochim. Blophys. Acta 6/116-24 (1981).
Blochim. PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
"A family of genes encode the multiple forms of the Saccharomyces cerevisiae ribosomal proteins equivalent to the Escherichia coli L12 protein and a single form of the L10-equivalent ribosomal protein."; J. Bacteriol. 172:579-588(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN SYNTHESIS.
-!- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of an acidic ribosomal protein YPAl from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1; Length 110; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R., Waterston R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGUS SOURCETON THE TRANSFORM STATE OF THE PROPERTY OF THE PROPERTY OF THE PROSECULATION OF THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82069169; PubMed=7030402; Itoh T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, J03761, AAA34972.1; -.
EMBL, MA26305, AAA34732.1; -.
EMBL, U38373, AAB64818.1; -.
EMBL, U32274; AAB64824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GGASSAAAGAAGAAGG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07,
07,
40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPP2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A35109; R5BYA1
SGD; S0002790; RPP21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH38_DROME STAN
P07183, Q9W3E5;
01-APR-1988 (Rel. 0
01-APR-1988 (Rel. 0
20-AUG-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KESULT 6
CH38_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H H H H H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
```

us-09-485-571-20.rsp

```
ă
                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D. Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
B. Bradon R.C., Rogers Y. H.C., Blazej R.G., Change M., Henderson S.N.,
R. Andron R.C., Rogers Y. H.C., Blazej R.G., Change M., Pielifer B.D.,
R. Ballew R.W. Basu A., Baxendale J., Bayerkataclub B.D., Basiey B. M.,
Ballew R.W. Basu A., Baxendale J., Bayerkataclub L., Beasley E.M.,
Ballew R.W., Bouch B. B., Buller H., Cadlew E., Center A., Chandra I.,
R. Borkova D., Butchen M.R., Buutler H., Cadlew E., Center A., Chandra I.,
R. Burtis K.C., Busam D.A., Buller H., Cadlew E., Center A., Chandra I.,
R. Buttis K.C., Busam D.A., Buller H., Cadlew E., Center A., Chandra I.,
R. Buttis K.C., Busam D.A., Buller H., Cadlew E., Center A., Chandra I.,
R. Buttis K.C., Busam D.A., Buller H., Cadlew E., Center A., Chandra I.,
R. Buttis K.C., Busam D.A., Buller H., Gaz, Guan P., Harris M.
R. Buttis K.C., Garg W.S., Gelbart W.M., Glasser K.,
R. Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Harris M.L.
All IM., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
All IM., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
All IM., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
All IM., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
All IM., Marlin N.V., Mobarry C., Morris J., Woshrefi A.,
Mount S.M., Moy W., Murphy B., Murphy L., Liang Y., Lin X.,
Relazzolo M., Pittman G.S., Pan S., Pollard J., Purt V., Readel F.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Stusse B.,
Spier E., Spradling A.C., Stapleton M., Stusng R., Shang Y.,
Walls B.C., Wassarman D.A., Weller D.C., Scheeler F., Wassarman D.A., Worley K.C.,
When S. Shang C.Y., Wassarman D.A., Weller W., Weller S., Shang Y.,
Wellson R.A., Wood S., Wood S., Weller W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              CP38 OR S38 OR CG1121.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                    Kalfayan L.J., Cooley L.;
"Amplification of the X-linked Drosophila chorion gene cluster requires a region upstream from the $38 chorion gene.";
EMBO J. 6:1045-1053(1987).
                                                                                                                                                                                                                               Spradling A.C., de Cicco D.V., Wakimoto B.T., Levine J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 AA; 30448 MW; 2F51C96F9F82DF83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87246506; Pubmed=3036489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE003444, AAF46383.1,
PIR, S08607, S08607.
HSSP, P04002, 1ATF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0000360; Cp38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X05245; CAA28871.1;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chorion.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINO ACID.
SINILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. THIS IS
CONTRARY TO THE RESULT EXPECTED FROM ITS SUBSTRATE SPECIFICITY AND
ITS PROPERTY OF BINDING BLUE DEXTRAN AND NADP+.
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: HYDROLYZES BENZYLPENICILLIN AND CLOXACILLIN (AT 10% OF THE RATE OF BENZYLPENICILLIN)
-i- CAMALYTIC ACTIVITY: A BETA-LACTAM + H(2)O - A SUBSTITUTED BETA-
                                                                                                                                                                                                                                                                                     Streptomyces cellulosae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of a gene encoding beta-lactamase from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 1; Length 311; Pred. No. 3.9e+03;
 Length 306;
                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
SUBSTRATE (BY SIMILARITY)
F3578EBEEA92A3FB CRC64;
                                                                                                                                                                                                    01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BETA-LACTAMASE PRECURSOR (EC 3.5.2.6) (PENICILLINASE).
Score 15; DB 1; 1
Pred. No. 3.9e+03;
); Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Antibiotic resistance; NADP; Signal. SIGNAL 1 33 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BETA-LACTAMASE.
                                                                                                                                                                           311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS00146, BETA_LACTAMASE_A; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D12653; BAA02176.1; -.
PIR; JN0520; JN0520.
HSSP; P00810; ITEM.
InterPro; IPR001466; Beta_lactam.
InterPro; IPR0000871; Beta_lactam.A.
Pfam; PF00144; beta-lactamase; 1.
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN ** KCC S0127;
MEDLINE = 93178958; Pubmed = 7916705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33136 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00118; BLACTAMASEA.
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                              2 GGXXXXXXXXXXX 18
                                                                                            39 GGADAASAAAAAGGAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGALALGSTTASAASAG 37
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               cellulosae.";
Gene 124:111-114(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 AA;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1968;
                                                                                                                                                                                                                                                                                                                                                                                                                   Ogawara H.;
                                                                                                                                                                        BLAC_STRCE
Q06650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                         BLAC_STRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                               Matches
                                                                                          g
                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
interPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                    ð
     DR
DR
DR
DR
DR
DR
DR
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Three genes in the human MHC class III region near the junction with the class II: gene for receptor of advanced glycosylation end products, PBNZ homeobox gene and a notch homolog, human counterpart of mouse mammary tumor gene int-3."; defenomics 23:408-419(1994).
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-95137587; Pubmed-7835890;
Sugaya K., Fukagawa T., Matsumoto K., Mita K., Takahashi E., Ando A.,
Inoko H., Ikemura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUTAR LOCATION: NUCLEAR (PROBABLE).
-1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
-1- SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lu Q., Wright D.D., Kamps M.P.;
"Fusion with E2A converts the Pbx1 homeodomain protein into a constitutive transcriptional activator in human leukemias carrying the t(1:19) translocation.";
Mol. Cell. Biol. 14:3938-3948 (1994).
-i- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS THE SEQUENCE 5'-ATCAATCAA-3'.
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95278934; PubMed-7759099;
Aguado B., Campbell R.D.;
The novel gene G17, located in the human major histocompatibility complex, encodes PBX2, a homeodomain-containing protein."; Genomics 25:650-659(1995).
                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-2 (HOMEOBOX PROTEIN PBX2)
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDILINE-22049345; MEDILINE-22049457; PubMed-1682799; Monica K., Gallii N., Nourse J., Saltman D., Cleary M.L.; Monica R., Gallii N., Nourse J., Saltman D., Cleary M.L.; PEXZ and PEXZ and PEXZ and PEXZ and PEXZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.
Banta A., Spies T., Hood L.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                   430 AA
                                                                                                                                                                                                                                                                    human proto-oncogene PBX1.";
Mol. Cell. Biol. 11:6149-6157(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000047; HTH_repressr.
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94254851; PubMed=7910944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X59842; CAA42503.1; --
EMBL; X80700; CAA56717.1; --
EMBL; D28769; BAA05957.1; --
EMBL; U89336; AA847490.1; --
PIR; S19009; S19009
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01366; 1AKH.
MIM; 176311; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                       NCBI_TaxID=9606;
                                      PBX2_HUMAN P40425;
           RESULT 8
PBX2_HUMAN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S., Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrone K., Hood L.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS THE SEQUENCE 5'-TONCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS THE SEQUENCE 5'-TONCTION: TRANSCRIPTION NUCLEAR (PROBABLE).
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: BELONGS TO THE TALE/PBX FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-2 (HOMEOBOX PROTEIN PBX2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                         PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
Transcription regulation; DNA-binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                            Score 15; DB 1; Length 430; Pred. No. 5e+03;
                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Liu Y., Macdonald R.J.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                             POLY-ALA.
M -> I (IN REF. 1).
: EF2FFA158C4DAF68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMEOBOX (TALE-TYPE)
                                                                                                                                                                   HOMEOBOX (TALE-TYPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Æ.
                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01366; 1AKH.
MGD; MGI1341793; Pbx2.
Interpro; IPR000047; HTH_repressr.
Interpro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF020198; AAB71193.1; -. EMBL; AF030001; AAB82006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                              45881 MW;
                    PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                                                 45.5%;
ilarity 17.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 GGGSAAAAAAAAAGGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306
                                                                                                                                                                        306
145
393
                                                 SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00389; HOX;
                                                                                                                                                                        244 3
137 1
393 3
430 AA;
                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PBX2_MOUSE
035984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox.
DNA_BIND
DOMAIN
                                                                                                                                                                                                  DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                           DNA BIND
                                                                                                                                                      Homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PBX2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                          Matches
```

SOT

ð 윱

```
TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NF42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
SGG_DROME
                                                                           EMBL;
EMBL;
EMBL;
                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                      EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                  EMBL;
                                     EMBL;
EMBL;
                                                                                                                                EMBL;
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DISEASE: RHABDOWYOSARCOMA-2 (RMS2) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(1;13) (P36;014) WHICH INVOLVES PAX7 AND FOXOIA. THE RESULTING PROTEIN IS A TRANSCRIPTIONAL ACTIVATOR.
-!- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
-!- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89305521; PubMed-2501086;
Burri M., Tromvoukis Y., Bopp D., Erigerio G., Noll M.;
Conservation of the paired domain in metazoans and its structure it three isolated human genes.";
EMBO J. 8.1183-1190(1899).
-I- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaefer B.W., Czerny T., Bernasconi M., Genini M., Busslinger M.; "Molecular cloning and characterization of a human PAX-7 cDNA expressed in normal and neoplastic myocytes.";
Nucleic Acids Res. 22:4574-4582(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genomic organization and full coding region of the human PAX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBDNIT: CAN BIND AS A HETERODIMER WITH PAX3.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vorobyov E., Mertsalov I., Dockhorn-Dworniczak B., Dworniczak B.,
                                                                                                              ö
                                                               Score 15; DB 1; Length 430;
Pred. No. 5e+03;
                                                                                      5e+03;
Thes 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
               CB6B71A6FE207E8D CRC64;
                                                                                                                                                                                                                                                                                                                      01-NoV-1991 (Rel. 20, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MAG-2001 (Rel. 40, Last annotation update)
PAIRED BOX PROTEIN PAX-7 (HUPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=97480728; PubMed=9339373;
                                                                                                                                                                                                                                                                                    520 AA
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 30-195 FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-467 FROM N.A. (LONG FORM).
 POLY-ALA
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95075634; PubMed-7527137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG FORM).
               45809 MW;
                                                                         45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X96743; CAA65520.1; -.
                                                                                                                                                                                       133 GGGSAAAAAAAAAGGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 45:168-174(1997).
                                                                                                                                                  2 GGXXXXXXXXXXX 18
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                 430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                   PAX7 OR HUP1.
                                                                                                                                                                                                                                                                                    HUMAN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horst J.;
                                                                                                                                                                                                                                                                  PAX7_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.
```

```
Ruel L.: Pantesco V., Lutz Y., Simpson P., Bourouis M.; "Functional significance of a family of protein kinases encoded at the shaggy locus in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0027; HOMEOBOX_1; 1.
PROSITE; PSO0021; HOMEOBOX_2; 1.
PROSITE; PSO0034; PAIRED_BOX; 1.
Transcription regulation; Homeobox; DNA-binding; Nuclear protein; Developmental protein; Paired box; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGG_DROME STANDARD; PRT; 1067 AA.
P18431; P23646; Q27603; Q27605; O76881; Q9U094; Q9W4X3; Q27604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTEIN KINASE SHAGGY (EC 2.7.1..) (PROTEIN ZESTE-WHITE 3).
SGG OR XW3 OR BG:BACR7C10.8 OR EG:155E2.3 OR CG2621.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 1; Length 520;
Pred. No. 5.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN SHORT ISOFORM) 3B0F8CC99D65699C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proto-oncogene: Alternative splicing.
DOMAIN 34 161 PAIRED BOX.
NNA RIND 217 276 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-ALA.
                                                                                                                                        X96744; CAA65522.1;
X15242; CAA65522.1; JOINED.
X15250; CAA65522.1; JOINED.
X12251; CAA65522.1; JOINED.
X96745; CAA65522.1; JOINED.
X96746; CAA65522.1; JOINED.
X96747; CAA65522.1; JOINED.
X96748; CAA65522.1; JOINED.
X15042; CAA65521.1; JOINED.
X15250; CAA65521.1; JOINED.
X15251; CAA65521.1; JOINED.
X96745; CAA65521.1; JOINED.
X86747; CAA65521.1; JOINED.
X86747; CAA65521.1; JOINED.
X96748; CAA65521.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001356; Homeobox.
Interpro; IPR001523; Paired_box.
Pfam; PP00046; homeobox; 1.
Pfam; PF00292; PAX; 1.
PRINTS; PR00027; PAIREDBOX.
SMART; SM00389; HOX; 1.
SMART; SM00351; PAX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDLINE=93223707; PubMed=8467811;
                                                                                                                                                                                                                                                                                                        CAA16432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 M
56896 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 GGLAAAAAAADTSSAYG 353
                                                                                                                                                                                                                                                                                                        AL021528; CAA16432.1
Z35141; CAA84513.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276
346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 1
520 AA;
                                                                                                                                                                                                                                                                                                                                                     S06959; S06959
                                                                                                                                                                                                                                                                                                                                                                                       T00396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                         P06601;
                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 167410;
```

ö

```
RC STRAIN-BERKELEY,
RA AGMAIN-BERKELEY,
RA AMMARIGES P.C., CAIDER R.A., EVANS C.A., GOCAYNE J.D.,
AGMARIA N.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.E.,
AGMARIA N.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.E.,
GOCTGE R.A., Lewis S.E., Kichards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Brandon R.C., Raxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apdayani A., An H.-J., Andraws-frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxehale J., Bhandari D., Bolshakov S.,
RA Ballew R.M., Basu A., Baxehale J., Barkstein P., Beasley E.M.,
Ballew R.M., Doyle C., Davenport L.B., Davies P.,
RA Borkwa D., Botchan M.R., Bouck J., Brokstein P., Brokstein P., Brokra P.,
Borkwa D., Botchan M.R., Bouck J., Brokstein P., Brokstein P.,
Burtis K.C., Busam D.A., Dalke C., Davenport L.B., Davies P.,
RA Borkwa D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Ac Pablics B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Borkwa D., Botchan M.R., Gary N.S., Gelbart W.M., Glasser K.,
RA Borkwa D., Botchan A.E., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Hehman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Hehman T.J., Weil M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mentel B.E., Kodira C.D., Kraft C., McLeod M.P., Morbison D.L.,
RA Mentel B.E., Moyl M., Murphy B., Murphy L., Mursy D.M., Neblson D.K.,
Rabon D.R., Pittman G.S., Pan S., Pollard J., Puri, Weilsen B.K.,
Rolen Kinnos I., Suden Kinnos I., Sunger P., Smith T.,
Raber B.C., Spradling A.C., Stapheton M., Strong R., Sun E.,
RA Wang Z. Y., Weilsen D.A., Weinstock G.W., Weilsenbach J.,
RA Wang Z. Y., Wessenbach J., Sulphy R., Weilsenbach J.,
RA Wang Z. Y., Weilsenbach J., Sulphy R., Weilsenbach J.,
RA Wang Z. Y., Rapsarman D.A., Weinstock G.W., Weilsenbach J.,
RA Weilliams S.M., Woodage T., Worley C., Whu D., Sanger P., Sang
                                                                                                                                                                                                                                                                                                                                                  PERTAIN-OREGON-R:
MEDLINE-20196011; PubMed-10731137; Murphy L., Harris D., Agneline-20196011; PubMed-10731137; Murphy L., Harris D., Cadieu E., Benrell B.G., Perraz C., Vidal S., Brun C., Demailles J., Borkova D., Dreano S., Gloux S., Lelaure V., Mortier S., Galibert F., Borkova D., Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S., Madueno E., de Pablos B., Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schoefer U., Jaeckle H., Bucheton A., Ballister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., Momillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                    EQUENCE OF 193-1067 FROM N.A. (ISOFORMS SGG46 AND ZYGOTIC).
TISSUE-Embryo, and Ovary,
MEDLINE-90294930; PubMed-2113617;
Siegfried E., Perkins L.A., Capaci T.M., Perrimon N.;
Putative protein kinase product of the Drosophila segment-polarity
gene zeste-white3.";
Nature 345:825-829(1990).
                                  SEQUENCE FROM N.A. (ISOFORM ZYGOTIC), AND CHARACTERIZATION. STRAIN-DP CN BW; TISSUE-Embryo;
MEDLINE-90361000, PubMed-2118107,
MEDLINE-90361000, PubMed-2118107,
MEDLINE-90361000, PubMed-2118107,
MEDLINE-9036100, PubMed-2118107,
Facilial Moore P., Ruel L., Grau Y., Heitzler P., Simpson P.;
An early embryonic product of the gene shaggy encodes a serine/threonine prodein kinase related to the CDC28/cdc2+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \ensuremath{\text{\textit{P}}}\xspace_{\text{\tiny{$}}}\xspace_{\text{\tiny{$}}} for the X chromosome of D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:2220-2222(2000).
          EMBO J. 12:1657-1669(1993)
                                                                                                                                                   subfamily.";
EMBO J. 9:2877-2884(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glover D.M.;
```

```
A Zheng X.H., Zhong E.N., Zhong E.N., Zhong W. Zhou, X., Zhu X., Smith H.O.,

Chibbs R.A., Where we'n thosophilia melanogaster.;

The genome and a state of the chipsophilia melanogaster.;

The genome and a state of the chipsophilia melanogaster.;

The genome and a state of the chipsophilia melanogaster.;

The genome and a state of the chipsophilia melanogaster.;

Hughes K., Wheelaali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Wholakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Plyte S.E., Totty N.F., Woodgett J.R.;

Hughes K., Micolakali E., Woodgett J.L.;

Hughes K., Micolakali K., Woodgett J.L.;

Hughes Repulses Allocated J. Woodgett J.L.;

Hughes Repulses Allocated J. Woodgett J. J. Woodgett J. Woodgett J. J. Woodgett J. Woodgett J. J. Woodgett J.
```

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR

(FOTENTIAL)

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> GSQSNSALNSSGSGGSGNGEAAGSGSGSGSGSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-8812489; PubMed-2448778;
Burns J.M. Jr., Daly T.M., Vaidya A.B., Long C.A.;
The 3' portion of the gene for a Plasmodium yoelii merozoite surface
antigen encodes the epitope recognized by a protective monoclonal
antibody.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis upstream of the gene encoding the precursor to the major merozoite surface antigens of Plasmodium yoelii."; Mol. Blochem. Parasitol. 39:285-288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DS -> GSQSNSALNSSGSGGSGNGEAAGSGSGSGSGSGGG
NGGDNDAGDSGAIASGGGAAETEAAASG (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN ISOFORM ZYGOTIC AND ISOFORM
                                                                                                                                                                                                                                                  Serine/threonine-protein kinase; ATP-binding; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSPI_PLAYO STANDARD; PRT; 1772 AA.
P13828;
01-JAN-1990 (Rel. 13, Last sequence update)
01-JSPI-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                     SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS001019; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Developmental protein; Segmentation polarity protein; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFAEGNKQSPSLVLGGVKTCS (IN ISOFORM ZYGOTIC AND ISOFORM SGG39).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R -> A (IN REF. 4).
T -> I (IN REF. 3).
MISSING (IN REF. 3).
MISSING (IN REF. 4).
AD -> RI (IN REF. 4).
C -> R (IN REF. 1; CAA50214).
V -> I (IN REF. 1; CAA50214).
G -> D (IN REF. 1; CAA50214).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 1; Length 1067;
Pred. No. 9.9e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENVKTAKLARTQSCVSWTKVVQKFKNILG
                                                                                                                                                                                                                                                                                                                           GLY/ALA/SER-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 85:602-606(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORY LATION.
                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
     InterPro; reynu003371; sgg.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam; PF00069; pkinase; 1.
PRMRT; SM00220; S_TKC: 1
PROSTURE. F.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGG39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-90205979; PubMed-2320061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1093-1772 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 GGAGAATAAATATGAIG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium berghei yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                    891
1067
621
636
732
767
553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
2559
2559
2559
750
750
797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PMMSA) (230 KDA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alvec
NCBI_TaxID=5862;
                                                                                                                                                                                                                                                                               Phosphorylation |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-17XL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis A.P.;
                                                                                                                                                                                                                                                                                                                           DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ARSPLIC
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSP1_PLAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND COOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
60S ACIDIC RIBOSOMAL PROTEIN P2 (ALLERGEN ASP F 8).
Aspergillus fumigatus (Sartorya fumigata).
Eukaryoża; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NIBI_TRXID=5085;
                        THE MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT.
-!- PTM: PHOSPHORYLATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 42202 / AF-102;
Hemmann S., Crameri R.;
Highly conserved ribosomal proteins binding to serum IgE of Aspergilus funigatus sensitized individuals.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                               Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> V (IN REF. 2).
9A6291658EB0F45D CRC64;
                                                                                                                                                                                                                                                                                                           PROTEIN
                                                                                                                                                                                                                                                                                                     MEROZOTTE SURFACE PI

N-LINKED (GLCNAC.)

N-LINKED (GLCNAC.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 1; 1
Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                    EMBL; J03612; AAA29762.1; -. EMBL; J04668; AAA29702.1; -. PIR; A28121; A28121. PIR; A45532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA; 197230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGSSASGTSSSGQASAG 317
                                                                                                                                                                                                                                                                                GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                      54
406
646
1018
1018
1090
11408
1154
11680
11680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            1408
1446
1541
1629
1680
1521
                                                                                                                                                                                                                                                                                                                                                                                1018
                                                                                                                                                                                                                                                                               Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLA2_ASPFU
Q9UUZ6;
                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLA2_ASPFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
ප්
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ö

Gaps

ö

14; Indels

0; Mismatches

3; Conservative

Score 14; DB 1; Length 162; Pred. No. 4e+03;

42.48;

N -> S (IN REF. 2). TRRLAPG -> SASASTGG (IN REF. 2). A38EC8100D8870C5 CRC64; 19 KDA LIPOPROTEIN ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
N -> S (IN REF. 2).

21 PH 162 15 22 N-37 N-48 TR 15517 MW;

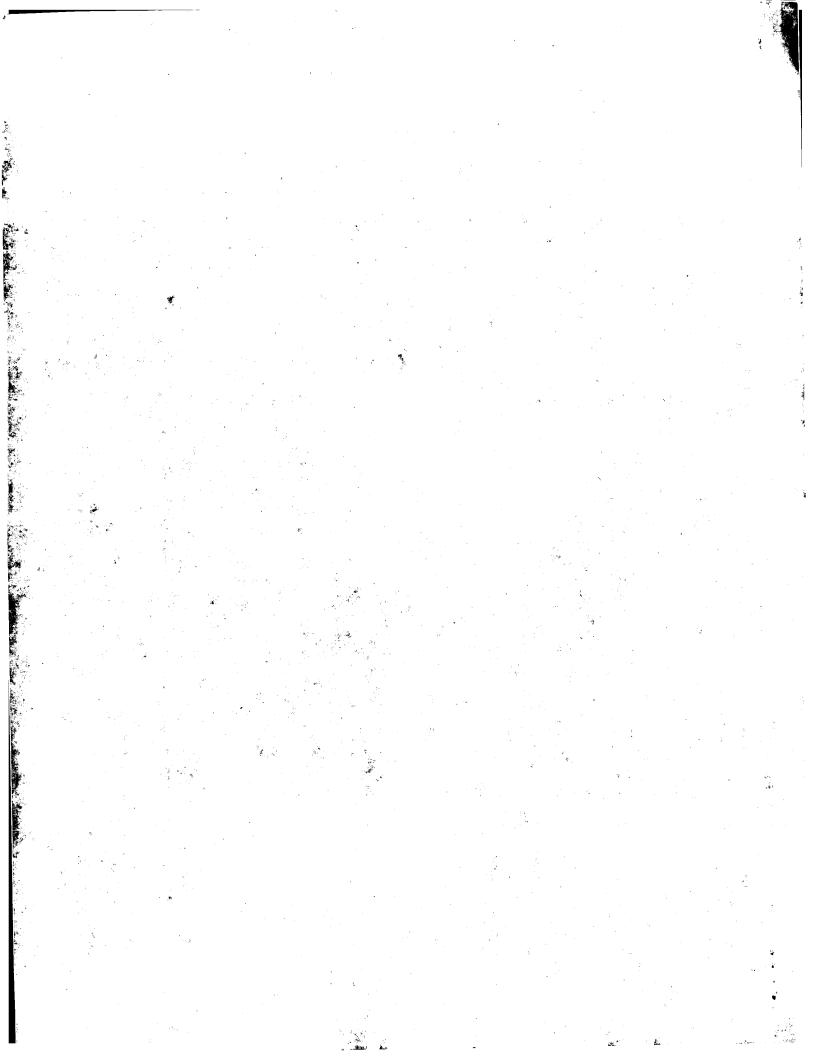
22 22 37 42 162 #

AA;

```
Search completed: February 12, 2002, 12:39:50
Antigen; Membrane; Lipoprotein; Signal.
SIGNAL 1 21 PROBABLE.
                                                                                                                                                            2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                     24 GGNKSGTSASSSANSSG 40
                                                                                                                 Query Match
Best Local Similarity
                        CHAIN
LIPID
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                           RESULT 15
CH18_DROME
                                                                                                                                         Matches
                                                                                                                                                                                                                                                    δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                         g
     KW
FT
FT
FT
SO
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               ó
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Booth R.J., Williams D.L., Moudgil K.D., Noonan L.C., Grandison P.M., McKee J.J., Prestidge R.L., Watson J.D.; Almondogs of Mycobacterium leprae 18-kilodalton and Mycobacterium tuberculosis 19-kilodalton antigens in other mycobacteria."; infect. Immun. 61:1509-1515(1993).
                                                                                                                                                                                                                                                                                                                                                                   01-UUL-1993 (Rel. 26, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
19 KDA LIPOPROTEIN ANTIGEN PRECURSOR (22 KDA LIPOPROTEIN ANTIGEN)
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                      Score 14; DB 1; Length 111; Pred. No. 3e+03;
                                                                                                                                                                                                                                14; Indels
                                                                                              EMBL; AJ22433; CAB64688.1; -
InterPro: IPR001813; GOS_ribosomal.
InterPro: IPR001815; Ribosomal_P2.
InterPro: IPR00428; CoS_ribosomal; 1.
PRINTS; PR00456; RIBOSOMALP2.
Ribosomal protein; Phosphorylation; Allergen.
Ribosomal III AA; 11136 MW; 0FCDE3F6023994A7 CRC64;
                                                                                                                                                                                                                                                                                                                                             162 AA
                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-DARDEN / SEROVAR 19;
MEDLINE-93202760; Pubmed=8454357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
STRAIN-SEROVAR 14;
MEDLINE-92326626; PubMed-1445568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L12238; AAA25344.1; -. EMBL; X65483; CAA46469.1; -. PIR; S22630; S22630.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium intracellulare.
                                                                                                                                                                                                           42.48;
17.68;
                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                   68 GGAAAAPAAAGAAAGG
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1767;
                                                                                                                                                                                                                                                                                                                                                                                                                       (MI22 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                              19KD_MYCIT
P31502;
                                                                                                                                                                                                                                                                                                                        RESULT 14
19KD_MYCIT
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                               g
              οŽ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neotera; Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-85229804; PubMed=2988878;
Wong Y.-C., Pustell J., Spoerel N., Kafatos F.C.;
Wong Yand potential regulatory sequences of a cluster of chorion genes in Drosophila melanogaster.";
Chromosoma 92:124-135(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-85229805; PubMed=3924529;
Levine J., Spradling A.;
"DNA sequence of a 3.8 kilobase pair region controlling Drosophila chorion gene amplification.";
Chromosoma 92:136-142(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 1; Length 172;
Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928405D34360D0CE CRC64;
                      01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHORION PROTEIN S18.
172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 AA; 17269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X02497; CAA26328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.48;
17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase, FBgn0000357; Cp18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXX 18
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 GGSAAAAASSVAAGKKG
     CH18_DROME
P07184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
```

Job time: 803 sec



Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
07621 mytilus edu
044367 mytilus edu
094x21 drosophila
099x21 drosophila
099ub5 galleria me
099ub5 galleria me
09114 leishmania
091444 candida alb
094x40 drosophila
099xb5 homo sapien
094x40 drosophila
094x40 drosophila
094x40 drosophila
094b6 brachydanio
094b6 drosophila
094b6 drosophila
094b6 drosophila
O9r1q2 rattus norv
O9ar00 lycopersico
                  Q9tyl3 caenorhabd1
Q9st59 triticum ae
Q9biu3 dolomedes t
                                                                                                                                                                                                                Q9bit9 latrodectus
Q9zny6 oryza sativ
Q9bmt6 ciona intes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99398697; Pubmed=10468597;
Venkatesh B., Ning Y., Brenner S.;
"Late changes in spliceosomal introns define clades in vertebrate evolution.";
proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
EMBL; AF137232; AAD53455.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 13; Length 286; Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 AA; 29687 MW; BE724A520927BD8A CRC64;
                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MIXED LINEAGE LEUKEMIA-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 AA.
                                                                                                                                                                                                                                                                                                             286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VXV2 PRELIMINARY; PRT; Q9VXV2; 01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                              Created)
                                           0.900.33
0.900.33
0.900.33
0.900.36
0.900.09
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
0.900.00
                                                                                                                                                                                              Q9BTW4
Q9BIU0
Q9BIT9
Q9ZNX6
Q9BMT6
                  Q9TYL3
Q9ST59
                                                                                                                                                                                                                                                                                                            PRT;
                                     Q9BIU3
                                                                                                                                                                                                                                                                                                                                                                             Gadus morhua (Atlantic cod).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
17.6%;
                                                                                                                                                          113
 111
110
110
113
113
                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 GGNAAAAAAAAAAAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
Query Match
Best Local Similarity
NCBI_TaxID=8049;
 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                           Q9PUX6
Q9PUX6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VXV2
                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9vxv2 drosophila
Q9vxv2 drosophila
Q9vxi6 drosophila
Q9vxi6 drosophila
Q9vxi0 oryza sativ
Q9z2w7 rattus norv
Q922w7 rattus norv
Q024Q2 princtada fu
Q15Q2 homo sapien
Q9v5u8 drosophila
Q9urs5 kluyveromyc
Q99188 mus musculu
Q9csz3 mus musculu
Q9csz3 mus musculu
Q9csz3 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9ibl4 gallus gall
Q9ci25 lactococcus
Q9lb15 gallus gall
Q80890 herpesvirus
Q9uk58 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9pux6 gadus morhu
                                                                         (without alignments)
11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                               ; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                  473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                               February 12, 2002, 12:38:37
                                                                                                                                                                                                                                                    summaries
                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PUX6
Q9VXV2
Q9VKR9
Q9VII6
Q9AWIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99LS8
Q9CSZ3
Q9VKR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91B15
Q80890
Q9UK58
                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P70581
002402
                                                                                                                     1 XGGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9IB14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9V5U8
Q9URS5
                                                                                                                                                                                                                                                                                                                                                                                                      sp_unclassified:*
                                                                                                                                                                                                                                                                                                           sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                     sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 sm
                                                                                                                                                                                                                                                                                                                                               sp_organelle:*
                                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
                                                                                                US-09-485-571-20
33
                                                                                                                                                                                                       seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
113
113
113
113
114
115
                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:*
                                                                                                                                                                                                                                                                                                                              sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
                                                                                                                                                                                                                                                                                                   sp_fung1:*
                                                                                                                                                                                                                                                                       SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                           sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
```

Query Match 1

Score

Result Š. 118 117 117 117 116 116 116 116 116 116

```
RECEINGARD SERVELEY;

RAMANDENERIELEY;

RAMAD REDENELEY;

RAMAD RECEINGER S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAMAD RECEINGER S.E., Filands S., Ashburner M., Henderson S.N.,

RAMAD George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMAD R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RAMAD R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RAMAD R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Malklos G.L.G.,

RAMAD R.M., Basu A., Barcadale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Barcadale J., Bayraktaroglu L., Beasley E.M.,

RAMAD R.C., Bocher R., Bouck J., Brokstein P., Brottler P.,

RAMAD B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RAMAD B., Delcher R., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RAMAD B., Delcher R., Gonner R., Garbiellan A.E., Garp N.S., Celbart W.M., Classer R.,

RAMAD B., Delcher R., Gonner R., Garbiellan A.B., Ramad R.J., Ramad R., Ramad R.J., Ramad R., Ramad R.,
                                                                                            Drosophila melanogaster (Fruit fly).

Drosophila metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.5%; Score 17; DB 5; Length 127; 17.6%; Pred. No. 2.6e+03; ive 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11014 MW; CBFDEC3362C2560F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CG7294 PROTEIN. CG7294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0032284; CG7294.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 13, TremBLrel. 13, (TremBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GGGAASASSSSASAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003629; AAF52991.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00341; PRION SEQUENCE 127 AA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   911760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA LA LA
                   DDT

SOOCC

SOCC

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                       RC STRAIN-BERKELEY.

RX ANINE-ERKELEY.

RX Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. Celniker S.E., Holt R.A. Evans C.A., Gocayne J.D., RA Adams M.D. Celniker S.E., Holt R.A. Baberier S.E., Changer R.A., Galle R.F., Reton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.

RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen E.X., Radon R.C., Rogers Y.H.C., Blazej K.G., Change M., Pfelifer B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendala J., Bayakaracglu L., Basaley E.M., Beson K.Y., Baros P.V., Barman B.P., Bhandari D., Bolshakov S., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Raderier R., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Burtis K.C., Busam D.A., Dahlke C., Davaphort L.B., Davies P., RA Burtis K.C., Busam D.A., Dahlke C., Davaphort L.B., Davies P., RA Goson K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Goson K., Doup LE., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Bostin D., Harvey D., Heiman T.J., Herrey S., Gelbart W.M., Glasser K., A Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L., Harvey D., Heiman T.J., Herrang D., Lai Z., R. Andell M., Ralush F., Karpen G.H., Re Z., Kennison J.A., Retching M., Ralush F., Karpen G.H., Re Z., Kennison J.A., Netchum R.A. Allal M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Netchum R.A. Basko P., Lei Y., Levitsky A.A., Li J., Li Z., Ling Y., Lin X., Matteri B., McIntosh T.C., Morise D., Lei Y., Levitsky A.A., Li J., Li Z., Ling Y., Will M. R., Rainer K., Pentington K.A., Mixon K., Muspky D.M., Nebschool J., Moshrefi A., Rainer K., Pentington K., Stunders R.D.C., Scheeler F., Shen H., R. Spradling A.C., Studen F., Wallsenbach J.C., Shen H., Walliams S.M., Woodage T., Worley K.C., Wu D., Yu Y., Walliams S.M., Woodage T., Worley K.C., Wu D., Yu Y., Walliams S.M., Woodage T., Worley K.C., Wu D., Yu Y., Resee M. H., Peneg M., H., Peneg M., Peneg M., Walliams S.M., Woodage T., Worley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidee; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 5; Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00142; ZINC_PROTEÀSE; UNKNOWN_1.
526 AA; 58657 MW; 2DFF254910BADF1F CRC64;
                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; Zn_MTpeptdse.
PROSITE; PS00142; ZINC_PROTEASE; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0030640; CG6294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 GGSSSSSTSSSSSAG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003499; AAF48456.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
                                                                                                           CG6294 PROTEIN.
```

ö

Gaps

.; 0

SEQUENCE

Q9VKR9; Q9VKR9 ٣

RESULT Q9VKR9

á

186 AA.

3

ö

```
Hu T., Guan T., Gerace L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOPORIN P58.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (
01-MAY-1999 (
01-MAY-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1.997
01-NOV-1.998
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P58/P45.
                                                                                                                                                                                                                                                                                                                                                                                                            Q922W7
                                                                                                                                                                                                                                                                                                                                                                                                                             0922W7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P70581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                       Adams M.D. Celnis Fubmed-10/3113/1.

RA Adams M.D. Celnis Fubmed-10/3113/1.

Ranantides P.G. Scherer S.E. Li P.W., Hoskins R.A., Galle R.F.,

Ranantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Freiffer B.D.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Freiffer B.D.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Freiffer B.D.,

Randon R.C., Baxen B.P., Baxendal J., Baylaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendal J., Baylaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendal J., Baylaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendal J., Baylaktaroglu L., Beasley E.M.,

Ballew R.M., Baurler H., Cadlew E., Center A., Chandra I.,

Ranckova D., Botcham M.R., Bouck J., Baylaktaroglu L., Belshakov S.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

Randoson K., Lasto G.C., Ferraz C., Ferraz C., Ferrar S.,

Rodek A., Gong F. Gorrell J.H., Wel M.-H., Ibegwan C.,

Jalali M., Kalush F., Karpen G.H., Wel M.-H., Ibegwan C.,

Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lux Mattel B., Morincoh T.C., McLeod M.-H., Moshrefi A.,

Mourt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nalson D.L.,

Randorn E.M., Morincoh T.C., Stapleton M., Stung Y., Lin X.,

Randorn E.M., Work M. Murphy B., Murphy L., Muzny D.M., Nalson D.L.,

Randorn E.M., Work Remington K., Saunet E., Wang A., Wang Z.Y., Wassarman D.A., Wellshim S., Yen R., Wooden T., Sungson M., Stung G., Shen H.,

Spier E., Spradling A.C., Stapleton M., Stung G., Zhon Q., Shen Y.,

Mulliams S.M., Wooden S.M., Wooder J., C., C., Wooden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 5; Length 186;
Pred. No. 3.7e+03;
); Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21236 MW; D847BE4817AA7C79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE ZINC-FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 AA.
                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0032893; CG14404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003668; AAF53933.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GGATTTTTTTTTTSG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 AA;
                                                                                                                   SEQUENCE FROM N.A.
CG14404 PROTEIN.
CG14404.
                                                                           Ephydroidea; Dr
NCBI_TaxID-7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AWIO
Q9AWIO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9AWIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

```
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu T., Gerace L.; derace L.; coning and analysis of the expression of nucleoporin p45."; cone 221:245-253(1998). EMBL; ARC000900; AAC08218.1; SEQUENCE 513 AA; 51820 MW; C70EC7465F5AAD0B CRC64;
Bukarycta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0489A05.";
                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 10; Length 357;
Pred. No. 7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 11; Length 513; Pred. No. 1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                               Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                357 AA; 37090 MW; 32F6C145E4823760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=96326666; PubMed=8707840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 99013879; PubMed = 9795236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; (Rodentia;
                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 51.5%;
Best Local Similarity 17.6%;
Matches 3; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TremBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 10, TrEMBLrel. 10, (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1.997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                     EMBL; AP003105; BAB32997.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 GGRSSSSSSSSAAAAG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GGTSAGTTATTSASTTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                 SEQUENCE FROM N.A. STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
```

Gaps

0

Score 17; DB 4; Length 803; Pred. No. 1.6e+04; 0; Mismatches 14; Indels

51.5%; 17.6%;

803 AA; 89963 MW; CDFB901A35F29A7C CRC64;

```
113 GGSYSASSSSSAAAAAG 129
                                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                    3; Conservative
                                                           Query Match
Best Local Similarity
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    CG9080
                                                                                                                                                                                                                                                                                         09V5U8
                                                                                                    Matches
                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                      09V5U8
                                                                                                                                                                                                                                                                                                               S
                                                                                                                                              ŏλ
                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97320490; PubMed=9177341;
Sudo S., Fujikawa T., Nagakura T., Ohkubo T., Sakaguchi K., Tanaka M.,
Nakashima K., Takahashi T.;
"Structures of mollusc shell framework proteins.";
Nature 387:563-564(1997).
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IV.
by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96127530; PubMed=8590280; Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.; Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.; Prediction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced analysis of cDNA clones from human cell line KG-1."; DNA Res. 2:167-174(1955).

EMBL: D63881; BAA09931.1; -...
InterPro: IPRO00822; Znf-CZH2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
"Molecular and functional characterization of the p62 complex, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Pterioida;
Pterioidea; Pteriidae; Pinctada.
NCBL_TaxID=50426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                     ;
                                                                                                                                           51.5%; Score 17; DB 11; Length 585; 17.6%; Pred. No. 1.1e+04; Live 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 5; Length 738;
Pred. No. 1.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, D86074; BAA20466.1; -. SFOUENCE 738 AA; 61723 MW; FDF984139BF3BA59 CRC64;
                   assembly of nuclear pore complex glycoproteins.";
J. Cell Blol. 134:589-601(1996).
EMBL; UG3838, AAC52789.1; -.
SEQUENCE 585 AA, 59264 MW; 4D5F5C2744A75C3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) INSOLUBLE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   803 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                      04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GGSAAAAAAAAAAGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                      77 GGTSAGTTATTSASTTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                               Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinctada fucata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORF (FRAGMENT)
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q15022
Q15022;
                                                                                                                                                                                                                                                                                                                                                                            002402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT OF STATE OF ST
                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
Q
                                                                                                                                                                                                                                                                                                                                                                            á
  δ
```

```
RG STRAIN—BERKELEY.

RA Adams M.D., Celniker S.E., Li P.M., Hoskins R.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.M., Hoskins R.A., Galle R.F., Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F., B. Amanatides P.G., Scherer S.E., Li P.M., Woskins R.A., Galle R.F., R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Worthan J.R., Yandell M.D., Zhang O., Chefilt R. B. Ditton G.G., Worthan J.R., Pall G., Change M., Miklos G.L.G., Apbayani A., An H.-J., Andrews-Fennicoh C., Baldwin D., Ballew R.M., Basu A., Barandala J., Bayraktaroglu L., Basalay E.M., Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P. Brottier P. Conter Y., Cavley S., Dalike R. B. Davies P. C., Buller H., Cadleu E., Center A., Chandra I., Rattis K.C., Buangelista C., Ways A.D., Dow I.D. Ditto S., M., Achery J.M., Cavley S., Dalike R. Dowles B., Delciner A., Dang Z., Mays A.D., Dow I.D. Doug L.E., Downes M., Dugan-Rocha S., Plukov B.C., Dunn P., R. Dough I.E., Downes M., Dugan-Rocha S., Plukov B.C., Dunn P., R. Dough I.E., Downes M., Dugan-Rocha S., Plukov B.C., Dunn R. A. Garielian A.E., Garg N.S., Gelbart W.M., Gasser K., Alalia M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McInten G.H., Ke Z., Kenison J.A., Ketchun K.A., Hallian N.V., Moberry C., McIrison J.A., McIrch B., McInten G.B., Murphy L., Muzny D.M., Nelson D.L., A. Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K., Rander B., McInten G.S., Pan S., Pollard J., Puri, Wang X., A. Spier E., Spradling A.C., Stepleton M., Stupk R., Sin E., Spier E., Spradling A.C., Stapleton M., Stupk R., Sin E., Spier E., Spradling A.C., Stapleton M., Stupk S., Shu M., Wang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Pan R., Mang Z.-Y., Wassarman D.A., Worley K.C., Wu D., Yang S., Pan M., Marphy E., Murphy E., Murphy
                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                   UL-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) CG9900 PROTEIN.
121 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE03826; AAF58699.1; -.
FlyBase; FB9n0033593; CG9080.
SEQUENCE 121 AA; 11690 MW;
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
```

qq

ö

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/GJ; TISSUE-EMBRYO;

MEDLINE-21085660; PubMed-11217851;

MEDLINE-2108560; PubMed-11217851;

A arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishil Y.,

A hazawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A hazawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl F., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl F., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Ruehl B., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Whyshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Masseria V., V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-EERKELEY;
MEDLINE-20196006; PubWed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatices P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George F.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
Mature 409:685-695-5000.
MGI:192264; 2610030623Rik.
InterPro, IPR000553; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 11; Length 309;
Pred. No. 1.1e+04;
); Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AA; 34255 MW; CEE35068FC302E7A CRC64;
                    09CSZ3 PRELIMINARY; PRT; 309 AA.
09CSZ3:
10JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
2610030E23RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequ 01-JUN-2001 (TrEMBLrel. 17, Last and CG17108 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.5%;
ilarity 17.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00385; CYCLIN; 2.
NON_TER 309 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 GGSSSGTTTTTTTGG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
'-hes 3; Conserve
                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                      2610030E23RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VKR8
Q9VKR8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG17108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29VKR8
                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bao W.G., Huo K.K., Li Y.Y., Fukuhara H.;
"Protein distultide isomerase genes of Kluyveromyces lactis.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243960; CAB51777.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 11; Length 242; Pred. No. 8.4e+03; 0; Mismatches 14; Indels
                    Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 3; Length 178;
Pred. No. 6.2e+03;
0; Mismatches 14; Indels
                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002244; AAH02244.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      099LS8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 178 AA; 18698 MW; C3D8EB079CE4661A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244; AAHU2244.1; -.
242 AA; 26995 MW; BBB062AA144ABE62 CRC64;
                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                  Score 16; DB 5; I
Pred. No. 4.3e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                    48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.58;
                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                        103 GGSASASASASSSWG 119
                                                                                                                                                                                                                                                                                                                                        CRN1 HOMOLOGUE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GGAAGAAAAAGAAAAG 122
                                                                                                   2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GGSAAAAAAAASGGAG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 17.6
Matches 3: Conservative
                                                           Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-2359/152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                       Q9URS5
Q9URS5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
```

RESULT 12 099LSB AC 099LSB AC 099LSB DT 01-JUN-DT 01-JUN-DT 01-JUN-DE SIMILAP OC Mammaly OC Mammaly OX NCBL_TE RN [1] RP 5EQUENC RR STRAUSK RR STRAUSK

RESULT 09CSZ3

g

ð

887660

g

ð

ö

Gaps

us-09-485-571-20.rspt

```
q
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Aril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center P.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Plakovis P.C.,

RA Dodson K., Doup L.E., Downes M., Harvis M.,

RA Horstin D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Horstin D., Houston K.A., Howland T.J., Well M.-H., Ibeqwam C.,

RA Alanial M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalali M., Aattei B., Morincsh T.C., Morison J.M., Nelson D.L.,

RA Alancko P., Lei T., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Anteris M., Nelson K.A., Whomarry C., Morris J., Moshrefi A.,

RA Balazolo M., Pitman G.S., Pan S., Pollard J., Puriv V., Reese M.G.,

RA Shine B.C., Siden-Kammon K.A., Weinsern D.R., Pacleb J.M.,

RA Shine B.C., Siden-Kammon C., Turner R., Venter E., Wang X.,

RA Shine B.C., Siden-Kammon D.A., Weinscock G.M., Weissenbach J.,

RA Shine B.C., Savaleur J.S., Zahan M., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,

RY Penner R., Reparence of Drosophila melanogaster.";

Physiologaster.";

Ry Parker R., Parker R., Shong M., R., Parker R., Parker R., Parker R., R., Parker R., R., R., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.5%; Score 16; DB 5; Length 342; 17.6%; Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamagishi A., Kuroiwa A.;
"chicken PBX1A mRNA, complete cds.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26813 MW; E98DD0407300F7AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BREED WHITE LEGHORN; TISSUE-LIMB BUD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0032285; CG17108.
InterPro; IPR002952; Eggshell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9IB14;
01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 GGGSGASASASASAG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003629; AAF52992.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 3; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9IB14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PBX1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091B14
091B17
00 DT
00 D
```

οg

ŏ

```
ö
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              ö
                                                                                                                                                                                            Length 347;
                                                                                                                                                                                                                            14; Indels
                                                                                          PROSITE; PS00027; "CM," HOMEDBOX_1; 1.
PROSITE; PS50071; HOMEDBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEOUENCE 347 AA; 38540 MW; F01F96FC41287854 CRC64;
                                                                                                                                                                                             48.5%; Score 16; DB 13;
17.6%; Pred. No. 1.2e+04;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                            Search completed: February 12, 2002, 12:38:38 Job time: 751 sec
EMBL; AB043620; BAA96136.1; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_repressr.
                                              Pfam; PF00046; homeobox; 1.
PRINTS; PR00031; HTHREPRESSR.
                                                                                                                                                                                                                                                                                               124 GGSAAAAAAAAAGGAG 140
                                                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                Conservative
                                                                                  SMART; SM00389; HOX; 1
                                                                                                                                                                                                                Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                   Query Match
```

* ·Ţ.		
*		· •
<b>ķ</b>		
€ ST Se		
		+ 1 + 1 - N
*		
-		
S.		
į.		
		· .
4		
À.		
*		
	보는 사람들은 사람들이 되었다. 그는 사람들은 사람들은 사람들은 사람들은 사람들이 되었다. 그는 사람들은 사람들은 사람들은 사람들은 사람들이 되었다. 그는 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은 사람들은	
ia		•
n		
*		. * ·
	rando de la companya	•.
io.		
CD-W		
÷		•
		Y +-
		•

```
(without alignments)
5.497 Million cell updates/sec
                                                                                                                                                                                  February 12, 2002, 12:30:31; Search time 242.57 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDSB/gcgdata/geneseq/geneseqp/AA1989.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1984.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS8/gcgdata/geneseq/geneseqp/AA1980.
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                        US-09-485-571-21
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                         Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
		æ				
Result		Query				
Q	Score	Match	Match Length DB ID	DB	ID	Description
-	74	92.5	18	20	AAW99408	Protegrin derivati
7	54	67.5	18	20	AAW99406	Protegrin derivati
М	44	55.0	•	21	AAY49438	M. tuberculosis ar
4	4.2	52.5	18	20	AAW99403	Protegrin derivati
ហ	42	52.5		21	AAY93616	Peptide which may
9	40	50.0		16	AAR78768	Protegrin peptide
7	40	50.0	18	16	AAR78776	Protegrin peptide
æ	40	50.0	٠,	20	AAY39927	T. roseum DNA poly
6	39	48.8		16	AAR78778	Protegrin peptide
10	39	48.8		20		Protegrin derivati
11	39	48.8		21		Protegrin-like pep

Protegrin-like pep Peptide which may Human ORFX ORF33 Amino acid sequenc Cystelne protease Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Peptide #2271 enco Peptide #2271 enco Peptide #2284 enco Peptide #2105 enco Peptide #8113 enco Peptide #8110 co Peptide #8113 enco Peptide #91205 enco Human orphan G protein co Human G-protein co Human LTB4 recepto Human HGO7 protein Human HGO7 protein Human LTB4 recepto Mycobacterium tube An antigen from de	a-sheet; secondary structure; itumour agent; antiviral; passive transport; cytoplasm; k M;
21 AAY93179 22 AAX93179 22 AAX840568 22 AAX867065 22 AAX867065 22 AAX86729 23 AAX818151 24 AAX818151 25 AAX818152 22 AAX8377 22 AAX8377 22 AAX837798 22 AAX837993 22 AAX8379769 22 AAX8379769 22 AAX837477	ALIGNMENTS  18 AA.  antibiotic; beta ; ribozyme; anti cell membrane; pr.  alifiers  alifiers  .
48.88.88.88.88.88.88.88.88.88.88.88.88.8	standard; peptide;  99 (first entry) derivative peptid rotegrin; peptide entidody ammatory; antibody ammatory; manmal; blood-brain barrie  . Location/Qu site 0.10 /label- Nle site 14 /label- Nle site 9.10 /label- Nle 99. 99. 99. 97; 97FR-0010297 YNT:EM SA. Chavanieu A, Gra
7.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.2.10.9.8.4.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3	1 MW99408 s MW99408; 3-JUN-199 Cotegrin Linear; pr Linear; pr Cotegrin Anti-linear; pr Anti-linear; pr An
	RESULT LID AAN 994CH LID AAN 994CH A

```
eprosv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sim E,
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                      AAY49438
                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                       g
888888888888
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                        This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used
                                                 - nseq
                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                             Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Score 74; DB 20; 1 Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaczorek
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protegrin derivative peptide SM2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                              92.5%; Scor
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99406 standard; peptide; 18
                                                                                                Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-190034/16
                  WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99406;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW99406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

g ò

```
ö
agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein from M. tuberculosis, M. smegmatis and Salmonella typhimurium. The methods and products can be used for the detection of mycobacterium and for the treatment of mycobacterial infections. They can also be used for the design of compounds for treating mycobacterial infections, e.g. tuberculosis. Administration of ligands of mycobacterial arylamine NAT, together with isoniazid may increase its effectiveness against other pathogenic mycobacteria, such as M. leprae which causes leprosy of M. bovis which infects cattle. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptides used to develop products for the detection and treatment of mycobacterial infections e.g. tuberculosis, leprosy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a novel arylamine N-acetyltransferase (NAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arylamine N-acetyltransferase; NAT; mycobacterium; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. tuberculosis arylamine N-acetyltransferase (NAT) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 283;
                                                                                                                                                                                                                                                                                                Score 54; DB 20; Length 18;
Pred. No. 0.0061;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB pred. No. 4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis arylamine NAT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49438 standard; Protein; 283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Payton M, Sinclair J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-0011407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB01692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                 61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         | || || || || |||| |||| 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                       1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                    Local Similarity 61.1 nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-072627/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ46695
                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cattle disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9961625-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49438;
                                                                                                                                                                                                                                                                                                         Query Match
```

ò g

```
The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, machanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                   New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                  Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 21; Length 18;
Pred. No. 0.71;
); Mismatches 9; Indels
Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                           Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US08305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0093926
                                                                                                                                                                                                   99WO-FR02939
                                                                                                                                                                                                                                     98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 rggrlsysrrrfsvsvgr 18
                                                                                                                                                                                                                                                                                                           Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
The 9; Conserve
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-412166/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78768 standard;
                                                                                                                                                                                                                                                                         (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                         WO200032237-A1
                                                                                       Unidentified
                                                                                                                                                                                                 26-NOV-1999;
                                                                                                                                                                                                                                     30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                      cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and non-liver active agents to consist the derivative agents including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                   Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.5%; Score 42; DB 20; Length 18; 50.0%; Pred. No. 0.71; 1ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaczorek M;
                                                                                                                                                                                                                                     Protegrin derivative peptide SM1738
                                                                                                                       AAW99403 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93616 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.0
Matches 9; Conservative
3 ARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calas B, Chavanieu A,
                  | |||| || ||
82 aelgyrvrrfaarv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 AA;
                                                                                                                                                                                                 08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                  WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93616;
                                                                                                                                                           AAW99403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW99403
```

a

ð

ö

Gaps

;; 0

```
Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections {\sf var}
                                                                            and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-579612/49.
N-PSDB; AAZ27471.
             WPI; 1995-075188/10
                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ettwiller L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5962296-A.
                                                                                                                                                                                                                                                                                                                                                                    analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY39927;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY39927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                     New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced combinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino Carlo C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                              Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 16; Length 16;
Pred. No. 1.4;
0; Mismatches '5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kokryakov VN, Lehrer RL;
                                                                                                Lehrer RL;
                                                                                                                                                                                                                             Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR78776 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0093926.
93US-0095769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US08305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0182483.
               94US-0182483.
94US-0243879.
 93US-0095769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protegrin peptide sequence
                                                                                                Harwig SSL, Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 61.5 nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |||| |||
| rggrlgygrrrfg 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFG 13
                                                                                                                                                                                               and as preservatives
                                                                                                                              WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1993;
26-JUL-1993;
13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1994;
                13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9503325-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR78776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

```
New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g., cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino and research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is a specific example of the protegrin logues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the Thermomicrobium roseum (ATCC 27502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pure thermostable DNA polymerase providing high fidelity DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA polymerase I; thermostable enzyme; PCR enzyme; 3' to 5' proof reading activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 16;
Pred. No. 1.6;
2; Mismatches 8;

    roseum DNA polymerase I protein sequence.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39927 standard; Protein; 917 AA
Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0028361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0028361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ratrisfsrrrfsvsvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermomicrobium roseum.
```

; 0

```
ó
                    5' proof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in beth animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. portine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acytation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino
thermostable DNA polymerase I of the invention. The polymerase is useful in the polymerase chain reaction (PCR). The polymerase has 3' to 5' prooreading activity and therefore provides high fidelity amplification.
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiblotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                     protegrin; antiblotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                        ő
                                                                                                        Score 40; DB 20; Length 917;
Pred. No. 56; 6; Indels
); Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note- "D-form residue'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                           AAR78778 standard; peptide; 18 AA.
                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0093926.
93US-0095769.
94US-0182483.
94US-0243879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid residues can be present
                                                                                                        50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US08305,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                       Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                        Conservative
                                                                                                                                                                                               789 raaelgyvetlfgrr 803
                                                                                                                                                                    1 RAARLGYRXXRFGXR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-075188/10.
                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                             917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1993;
13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                       08-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                   antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                             Sequence
                                                                                                                                                                                                                                                                                                        AAR78778;
                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                             AAR78778
                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                             8×3333
                                                                                                                                                                      ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and ono-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                   Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; uucleus; blood-brain barrier
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - nsed
The present sequence is a specific example of the protegrin analogues in which Cys(6, 13) have been replaced by Val and Gly.
                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB.20; Length 18;
Pred. No. 2.3;
                                                                                    DB 16; Length 18;
                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                    Mismatches
                                                                                    Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                        Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                  AAW99412 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 28; 37pp; French.
                                                                                    48.88;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97FR-0010297.
                                                                                                                                              1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                               1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 rggrisysrrrfststgr 18
                                                                                                                                                                                                                                                                                                          08-JUN-1999 (first entry)
                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYNT-) SYNT: EM SA.
                                                                                                   Best Local Similarity
Matches 9; Conserv
                                          18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09907738-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-3997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                               AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                            Sequence
                                                                                       Query Match
                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                        оp
                                                                                                                                                                                                                                                                               q
SXCC
                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

studying drug behaviour in BBB models.

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1- X16; (b); BXXBXXXXBBXBXXXXBBXB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is an acontaining a side chain that includes a basic group; be Trp; each B is an acontaining a side chain that includes a basic group; card each X is an aliphatic or aromatic as. The linear peptide may be retro forms of (a)-(c) containing D = and/or 1-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, tachyplesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. corropins and maganins; (ii) peptides with alpha-helices, with no major structure but containing bends due to the presence of the normal are actericins and PR39. The peptides of the invention fall into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the based on tachyplesins; this and based on tachyplesins, the passed on the presence of protegrins; and (c)-peptides are based on the based on the antibiotic categories defined above: (a)-peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protegrins, and (c)-peptides are based on tachyplesins. This sequence represents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a doxorubicin molecule by a succinate linker. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                   neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                               _note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                          blood-brain barrier; diagnostic; central nervous system; protegrin;
Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                           cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                         Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temsamani J;
                                          AAY93177 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example I; Page 13; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98FR-0015074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-FR02938
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by a glycoamide linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-422871/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1999;
                                                                                                                                                                                                                                        Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                           AAY93177;
RESULT 11
```

```
agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1- X16; (b); BXXBXXXXBBXBXXXXXBBXBB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is an containing a side chain that includes a basic group; and each X is an aliphatic or aromatic an The linear peptide may be retro forms of (a)-(c) containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 6 peptides able to cross the BBB include protegrins, Antennapedia, categories absed on their structure: (i) peptides with alpha-halices, e.g. cecropins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tackplbesins, (iii) peptides with no major structure but containing bends due to the presence of
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood'brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a molecule of dalargin via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                ;
                                               Length 18;
                                                                                Indels
                                                                                10;
                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disulphide linker"
                                                                                                                                                                                                                                                                                                                                        Protegrin-like peptide antibiotic Dal-SynBl.
                                             Score 39; DB 2
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "cross-links to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temsamani J;
                                                                                                                                                                                                                                    AAY93179 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example II; Page 20; 54pp; French
                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-FR02938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98FR-0015074
                                               48.88;
                                                                  44.48;
                                                                                                                  1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                 1 rggrlsysrrrfststgr 18
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT:EM SA.
                                                                 Best Local Similarity
18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200032236-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1998;
                                                                                                                                                                                                                                                                                                       06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-links
                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clair P,
                                                                                                                                                                                                                                                                     AAY93179;
 Sequence
                                                 Query Match
                                                                                                                                                                                                    12
                                                                                Matches
                                                                                                                                                                                                                    AAY93179
                                                                                                                                                                                                                                                       g
                                                                                                                    δλ
```

us-09-485-571-21.rag

48.88;

Query Match

```
.,
Pro residues, e.g. bactericins and PR39. The peptides of the invention fall into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on protegrins; and (c)-peptides are based on tachyplesins. This sequence represents a synthetic linear peptide designed on peptides able to cross the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                    48.8%; Score 39; DB 21; Length 18;
44.4%; Pred. No. 2.3;
Live 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93615 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                     1 rggrlsysrrrfststgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-2000
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93615
   88888888888888888
                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                     qq
```

Ą

18

Sequence

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antiperiatic; antipartinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunosuppressant; antidatabetic; hypotenaive; dermatological; immunosuppressive; antidiabetic; hypotenaive; dermatological; immunosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                             vulnerary; antipsoriatic; antiarthritic; immunosuppressant; cardiant; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; cogulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressave; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; carcer; proliferative disorder; hypertension; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunoeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                       ö
Score 39; DB 21; Length 18;
Pred. No. 2.3;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; detection; cytostatic;
                                                                                                                                                                                                                                                                                                                                         Human ORFX ORF332 polypeptide sequence SEQ ID NO:664.
                                     10;
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 774; 5507pp; English.
                                                                                                                                                                                                                   AAB40568 standard; Protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                    44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127607
                                                                              1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                               08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis; contraceptive.
                                       Conservative
                                                                                                                 rgarlsysrrrfststgr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
N-PSDB; AAC74777.
                Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-2000.
                                                                                                                                                                                                                                                          AAB40568;
                                                                                                                                                                                                AAB40568
                                                                                                                                                                                                                                        ò
                                                                                                                 qq
```

```
g
                                                                                                                                                                      ;
0
        graft vs host disease, cardiovascular disease, diabetes mellitus, hyporthension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
 proliferative disorders, neurodegenerative disorders, osteoarthritis,
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               shy-brager Syndrome; Guamanian parkinsonism dementia complex, amyotrophic lateral sclerosis; memory impairment; neuronal disorder; neuropathy; ischemic stroke; acute brain injury; acute spinal cord injury; nervous system tumour; multiple sclerosis; neurotoxin exposure; metabolic disease; diabetes; renal dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                  cerebral ischemic neuronal damage; traumätic brain injury;
peripheral neuropathy; Alzhaimer's disease; Huntington's disease;
Parkinson's disease; Parkinson-Plus syndrome;
progressive Supranuclear Palsy; Olivopontocerebellar atrophy;
                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a human neublastin neurotrophic factor.
                                                                                                                                            Score 39; DB 21; Length 184;
Pred. No. 19;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                      Neurotrophic factor; neublastin; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "glycosylated residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                           AAY68705 standard; Protein; 200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hansen C;
                                                                                                                                           48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0092229.
98DK-0001048.
98US-0097774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DK-0000904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98DK-0001265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0347613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-DK00384
                                                                                                                                                                                                                                                                                                                       05-MAY-2000 (first entry)
                                                                                                                                                                     Conservative
                                                                                                                                                                                          2 AARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                  40 aarkgirtamvgsrig 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35..101
39..103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NEUR-) NEUROSEARCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blom N,
                                                                                                                                Query Match
Best Local Similarity
'.hes 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-171013/15.
                                                                                                           184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ60561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200001815-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johansen TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eye disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1999
                                                                                                                                                                                                                                                                                                 AAY68705;
                                                                                                           Seguence
                                                                                                                                                                                                                                                              AAY68705
8
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                            à
```

```
New isolated polypeptides, used for treating e.g. neurodegenerative disease or disorder, neuronal damage or neuronal disorder of the disease or disorder, neuronal damage or neuronal disorder of the preparation of the ginal cord - the peripheral nervous system, the medulla or the spinal cord - the present sequence represents a neurotrophic factor sub-class of the transforming growth factor-beta corporation factor sub-class of the transforming growth factor-beta superfamily of neurotrophic factors. The polypeptides can be used cor the GRR-alpha3.RET receptor complex. The polypeptides can be used for treating a neurodegenerative disease or disorder, cerebral ischemic computant damage, tranmatic brain injury, peripheral neuropathy. Alzheimer's disease, Huntington's disease, Parkinson's disease, Parkinson's disease, Parkinson's memory computance of the peripheral nervous system, anyotrophic lateral sclerosis, memory impairment, or a neuronal disorder of the peripheral nervous system, the medulla or the spinal cord injury, nervous system tumours, coute brain injury, acute spinal cord injury, nervous system tumours, multiple sclerosis, exposure to neurotoxins, metabolic diseases such as classed or various disorders in the eye.

Squence 200 AA;
```

Query Match

Best Local Similarity 69.2%;
Matches 9; Conservative (

1 RAARLGYRXXRFG 13 |||||| | | | 1 85 raarlggraarsg 97

ö

Gaps

.; 0

Indels

4;

0; Mismatches

Score 39; Pred. No.

DB 21; Length 200;

Search completed: February 12, 2002, 12:30:31 Job time: 364 sec

		* **	And the second s	
Ļ				
				,
<b>5</b>				
A-				
(32°)				
*				•
j.				
		•		
		en de la companya de La companya de la co		
		•		
į.				
<b>F</b>			$\frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) \right) = \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \right) + \frac{1}{2} \left( \frac{1}{2} \left( \frac{1}{2} \right) + $	
É				
7				
		• • • • • • • • • • • • • • • • • • •	en Timoria de la companya de la company	
<b>X</b>				
	van de v			•
•				
				en de
2				1
345 2 *				
e.	and the second of the second o			
2				**************************************
<b>1</b>	S. A.			
ř				
<b>90</b> 0			v.	
2				
di a i				
4				
Ď.				
t.				
			## N - 3	
e E			**************************************	en e
3				va.
15		9.		
Ì.				Ÿ
		artinia di Maria. ⊯artinia		*
e de La companya de la companya de l				
				74.1
A.		in the state of t	$\frac{d}{dx} u^{\alpha}$	
4	State of the state			

Appli Appli

Sequence 7, Al Sequence 7, Al Sequence 7, Al Sequence 27, Sequence 1, Al Sequence 1, Al Sequence 6, Al Sequence 18, Sequence 38, Sequence 38, Sequence 38, Sequence 5, Al

Sequence

```
COMPUTE: ...

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION: 435
ATYCRNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08182483A
Fatent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORNISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CONTROLLY: Washington
            US-08-964-127-4
US-08-964-127-4
US-08-57-959A-9
US-09-357-014-9
US-09-357-014-7
US-09-1357-014-7
US-09-105-537-27
US-09-105-537-27
US-09-105-537-6
US-09-105-537-6
US-08-182-483A-18
US-08-182-483A-18
                                                                                                                                                                                                                                                US-08-499-523-38
US-09-128-345-38
US-08-499-523-65
US-08-984-294-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1;
Pred. No. 0.17;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
61.5%;
18 4
526 4
520 4
905 905 1135
1135 1135
336 349
3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 16 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLGYGRRRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
'-has 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAARLGYRXXRFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-08-182-483A-20
 STATE:
οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appl
Appl
Appl
Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      February 12, 2002, 12:32:23; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-182-483A-20
US-08-243-879A-19
US-09-128-34-40
US-09-128-34-40
US-08-182-483A-28
US-08-499-523-63
US-08-499-523-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-08-499-523-58
US-08-128-345-59
US-09-128-345-59
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-499-523-62
US-09-128-345-57
                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                               1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                            US-09-485-571-21
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                  Scoring table:
                                                                                     OM protein
                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
No.
```

ö

Gaps

ö

Length 16;

```
DB 1; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/09/128,345 FILING DATE: 03-806-1998 CLASSIFICATION: 514
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1;
Pred. No. 0.17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ITILE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/09128345 Patent No. 6159936
                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNBARE: 29,959
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEFROME (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura, A. REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                             APPLICATION NUMBER: US/0
FILING DATE: 07-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |||| ||||
1 RGGRLGYGRRRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RAARLGYRXXRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                     FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-40
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-499-523-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-128-345-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 40; DB 1; Length 16; 61.5%; Pred. No. 0.17;
                                                                                 Sequence 19, Application US/08243879A
Fatent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
COLITY: WEARINGTON, DC
                                                                                                                                                                                                                                                                                                                                                                ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
FILLING APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILLING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-0540.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISCRATION NUMBER: 29,599
REFRENCE/CDCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 887-1500
TELEAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RAARLGYRXXRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-08-243-879A-19
                                                                       US-08-243-879A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-499-523-40
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
```

Gaps

```
Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EBAPE Compatible
COMPUTER: IBM PC COMPUTER: ISM PS APPLICATION NUMBER: US/08/243,879A
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/COCKET NUMBER: 29,959
REFERENCE/COCKET NUMBER: 29,959
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
TELEPHONE: CANANO SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
FEWTHER: IB amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-0540.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-499-523-48; Sequence 48, Application US/08499523; Petent No. 5804558; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/DOCKET NUMBER: 2000.
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RAP.RLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match.
Best Local Similarity 44.41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                   Washington, DC
                     CLTI.
COUNTRY: USA
7TP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLCGY:
US-08-243-875A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ដ្ឋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                         ö
              Score 40; DB 4; Length 16;
Pred. No. 0.17;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OFFICENT PAPELICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-304-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
SEGISTRATION NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-0763
TELEFEX: 90-4030
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 main acids
                                                                                                                                                                                                                                                                                              APPLICANT: LEHER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: MANENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania AVE. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB Pred. No. 0.2; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08243879A
Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                               RESULT 5
US-08-182-483A-28
S-08-182-483A-28
S-08-182-483A-38
Patent No. 5693486
GENERAL INFORMATION:
              50.0%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                      1 RGGRLGYGRRRFG 13
                                                                                           1 RAARLGYRXXRFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                               g
                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

0; Gaps

```
ö
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a cother information: small, or a large polar amino acid"
US-08-499-523-63
                                                                                                                                                             Length 18
                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: MORRISON & FOERSTER 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1;
Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-0540.24
                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROFECRINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                Sequence 63, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERA: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                        50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLXYXRRFFXVXVGR 18
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERLSTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALDANA
STREET: ZUUU
TTY: Washington
                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                     ; TOPOLOGY:
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                          Matches
                                                                                                                                                                                                                            οy
                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: group(6, %, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 18;
Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEHEER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-0540.24
                                                       GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDUIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.09-128-345-48
Sequence 48, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
US-08-499-523-67; Sequence 67, Application US/08499523; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLXYXRRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 887-076.
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                      STATE:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                         NAME/KEY: Modified-site
| LOCATION: group(6, 8, 13, 15)
| COTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "X is a hydrophobic, a small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 4; Length 18;
Pred. No. 0.2;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                           Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345 FILING DATE: 03-4UG-1998 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ATILLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY ACENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 806
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.03
Matches 9; Conservative
                         18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.0
Best Local Similarity 50.0
Matches 9; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLUGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-128-345-67
                         LENGTH:
                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: U3/09/128,345
FILING DATE: U3/09/128,345
FILING DATE: U3/09/128,345
FILING DATE: U3/03-1098
CLASSIFICATION: 514
ATTONREY/AGENT INFORMATION:
NAME: COCULZI, LAURE: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COLUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (6141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/09128345
Sequence 63, Application US/09128345
Sequence 66, Application US/09128345
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
CORRESPONDENCE New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No.
                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                       ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RATRISFSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 44.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-128-345-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-63
```

q ò

õ

```
Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                  COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC Compatible
OMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION NUMBER: 20,08/499,523
FILING DATE: 07-JUL-1995
ATTON NUMBER: 20,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
REGISTRATION NUMBER: 20,000-0540.24
TELEFRA: (202) 887-0763
TELEFRA: (202) 887-0763
TELEFRA: (202) 887-0763
TELET ON FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LYPE: AMINO acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site;

LOCATION: group(9, 18)

CHER INFORMATION: /note= "D form of amino acids"

US-08-499-523-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFEWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
               2000 Pennsylvania Ave. N.W., Ste. 5500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 1 Pred. No. 0.3; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-9

Squence 50, Application US/09128345

Patent No. 615936

GENERAL INFORMATION:

APPLICANT: LEHREN, ROBERT I.

APPLICANT: HARNIG, SYLVIA S.L.

APPLICANT: ROKRYAKOV, VLADIMIR N.

TITLE OF INVENTION: PROTEGRINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: USA

2IP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RATRIVECRREGUCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0v
- Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                       20006-1812
    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-128-345-50
                                                               STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATION SYSTEM:
OPERATION OF THE PATCHET RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFLATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870-763
TELER: 90,4030
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                        APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
LOCATION: group(9, 18)
OTHER INFORMATION: /note= "D form of amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1;
Pred. No. 0.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-499-523-50
Sequence 50, Application US/08499523
Sequence 50, Application US/08499523
RELEGIT NO. 5804558
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPRRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             ; Sequence 30, Application US/08182483A; Patent No. 5693486; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || |: : ||| |||
| RATRIVECRRREGUCVGR 18
                                 1 RAARLGYRXXRFGXRVGR 18
                                                                            RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY: USA
20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-182-483A-30
                                                                                                                                              RESULT 13
US-08-182-483A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                              g
```

ö

Gaps ; 0

Search completed: February 12, 2002, 12:32:23 Job time: 451 sec

	e s ^{e e} e e			<b></b>		
						or the state of t
					٠.	
				***		
*						4. •
•			•			
	e de la companya de l					
						10
				1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		
		•				
40 A	*					
		1 0				
		2 2				
	Size of	And w			A Company of the Comp	
		ė,	1 1 4 A 1 4 A			
in the second se						
		order (1. <del>4</del> 1 - 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.				
		And the second				
			and the second			
рі Ад эн					, The second se	
						s en
	e e e e					a de la companya de l
*. * * * * * * * * * * * * * * * * * *						
$ \psi_{n,j}  =  \psi_n(L_{n,j}) $						
		•				
		et et e	<b>4</b> * 20			
						e and the second
j.		•				
			1 P			and the second s
					and the second	
		and the second	. · ·		Art.	
						<b>.</b> **
		en e				٤
•		The state of the s	April 1	7		*

ŧ

`

```
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical prote probable nhoA prot cell surface glyco aminomethyltransfe DNA polymerase I V hypothetical prote hypothetical prote probable transposa probable DNA polymeramide neuropep FMRFamide neuropep conserved hypothet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acetylcholinestera
probable SOJ prote
hypothetical prote
nitrite extrusion
hypothetical prote
mismatch DNA recog
probable hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable 6-phospho
Wnt-6 protein - mo
leukotriene B4 rec
early E1B 53K prot
probable murc prot
                                                                                            February 12, 2002, 12:34:38; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical prote L2 protein - human genome polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methionine synthas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                               219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                             1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128805

D70605

D70605

B82364

D011HBC

J0211HBC

J0211HBC

J03176

A23172

A33172

A
                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                      US-09-485-571-21
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                             Searched:
                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ş
```

 10000000000000000000000000000000000000		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	926 942 11192 1451 451 203 203 208 306 413 471 540	000000000000000	T15683 T73624 T73624 140323 140325 H70542 G70516 G70516 G70518 G70518 G36145 G36145 G71089 JN0059	hypothetical prote 6-phosphofructokin 5-methyltetrahydro dermonecrotic toxi hypothetical prote hypothetical prote iron-regulated vir iron-regulated vir probable membrane precorrin-6y-depen hypothetical prote hypothetical prote hypothetical a prote hypothetical prote hypothetical 57.4k DN-directed DNA
				•	ALIGNMENTS	
 RESULT 1 T28805 hypothetical protein C53B7.7 - Caenorhe C; Species: Caenorhabditis elegans C; Date: 29-0:t-1999 #sequence_revision C; Accession: T28805 R; Du. Z.	cal pro Caenc 9-Oct-:	protein C5 enorhabdit tt-1999 #sed T28805	C53B7.7 · Sequence_	gan gan	enorhabditis el ision 29-Oct-19	hange 18-Feb-2000
 submitted A; Descript A; Referenc A; Accessic A; Status:	to the tion: J te numb on: T22 prelir	the EMBL Data Library, in The sequence of C. e umber: 220526 T28805	ata Librar ence of C. 526 translated	orar) f C.	<pre>'y, December 1995   elegans cosmid C53B7. 1 from GB/EMBL/DDBJ</pre>	
A: Molecule type: DNA A: Residues: 1-433 < CUZ> A: Residues: 1-433 < CUZ> A: Cross-references: EMBL: U42830; A: Experimental source: strain Bric, Genetics: A: Genetics: A: Genetics: A: Map position: X A: Map position: X A: Introns: 99/3: 151/3; 260/3; 31	type i. 1-4: iference ii. isp:c5: tion: 99/3;	: DNA 33 <duz> ces: EMB source: : X X X</duz>	L:U4283 strain 260/3;	30; Bri:	PIDN:A	00028; CESP:C53B7.7
Query Match Best Local Matches Qy 1 RAS	Match socal Sir ss 8; 1 RAARLG 1 RAARLG	tch al Similarity 47. 8; Conservative RAARLGYRXXRFGKRVG 1   ::     :  RASKLGYTGTRVGHEIG 2	56.2%; 47.1%; vative XRVG 17 :	28; 7	Score 45; DB 2; Length 4 Pred. No. 1.3; 3; Mismatches 6; Indel	433; els 0; Gaps 0;
 RESULT 2 D70605 probable nhow protein - Mycobacterium tub C; Species: Mycobacterium tuberculosis C; Cate: 17-Jul-1998 #sequence_revision 17 C; Accession: D70605 R; Cole, S.T.: Brosch, R.; Parkhill, J.; G, Connor, R.: Davies, R.; Devlin, K.; Fel Rajandream, M.A.; Rogers, J.; Rutter, S.; Nature 393, 537-544, 1998 A.Authors: Sqares, R.; Sulston, J.E.; Tay A; Title: Deciphering the biology of Mycob A; Title: Deciphering the biology of Mycob A; Reference number: A70500; MUID:98295987 A; Accession: D70605 A; Scatus: preliminary; nucleic acid seque A; Molecule t;pe: DMA A; Residues: 1-332 cCOL> A; Cross-references: GB:29774; GB:AL12345 A; Seperimental source: strain H37Rv C; Genetics:	Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Myco Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob Mycob M	cotein - 1998 #see	Mycobe m tuber quence.; Parl .; Devl .; Devl s, J.; 98 Sulstor e biol E biol mucleic nucleic strain	courte chi. lin Run yy, yy JID H3; G	erculosis (stra- Jul-1998 #text arnier, T.; Chu twell, T.; Gent Seeger, K.; Sk lor, K.; Whiteh acterium tubero nce not shown;	<pre>#text_change 22-Oct-1999 ; Churcher, C.; Harris, D.; Gord Gentles, S.; Hamlin, N.; Holroy .; Skelton, S.; Squares, S. hitehead, S.; Barrell, B.G. uberculosis from the complete ge own; translation not shown 61729; PIDN:CAB07160.1; PID:e129</pre>

```
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, F chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: B82364
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-934 <HEI>
A; Cross-references: GB: AE004101; GB: AE003852; NID: 99654497; PIDN: AAF93286.1; GSPDB: G
A; Experimental source: serogroup 01; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein (gene N internal ORF) - bovine coronavirus (strain Mebus)
N.Alternate names: 10RF protein
C.Species: bovine coronavirus
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C.Date: 31-Mar-1989 B.G.; Brian, D.A.
R.Lapps, W.: Hogue, B.G.; Brian, D.A.
Virology 157, 47-57, 1987
A.Title: Sequence analysis of the bovine coronavirus nucleocapsid and matrix protein
A.Accession: C26347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein (gene N internal ORF) - turkey coronavirus
NyAlternate names: IORF protein
C; Species: turkey coronavirus
C; Species: turkey coronavirus
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
C; Accession: JQ1174
R; Verbeek, A.: Tijssen, P.
J; Gen. Virol. 72, 1659-1666, 1991
A; Title: Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrael A; Reference number: JQ1172; MUID: 91311418
                                                                                                                                                                                                                                                                                                                          A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
                                                                        DNA polymerase I VC0108 [imported] - Vibrio cholerae (strain N16961 serogroup 01)
                                                                                                     C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M16620; NID:9323354; PIDN:AAA66398.1; PID:9807593 C;Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 2
Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 40; DB 50.0%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 1
C;Superfamily: DNA-directed DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:|||
813 RAQLGYVETIFGRRL 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.2
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: genomic RNA A; Residues: 1-207 <LAP>
                                                                                                                                                                   C; Accession: B82364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: VC0108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.M.
Nature 399, 323-329, 1999
Nature 37403

                                                                                                                                                                                                                                                                            RESULT 4
E72403
aminomethyltransferase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72403
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1408 <MTH>
A;Cross-references: GB:AE000911; GB:AE000666; NID:g2622623; PIDN:AAB85988.1; PID:g262263
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1513
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514 A; Accession: H69068 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1408;
      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 364;
                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2;
Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2;
Pred. No. 8.5;
3; Mismatches
      5;
      Score 44; DB 2
Pred. No. 1.5;
0; Mismatches
      55.0%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.2%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|||| :| : ||
| 1319 AKLGYRTFKFTLKPGR 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 RIARKGYEVLKNGERVG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 50.v.
8; Conservative
Query Match 55.0
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.2
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ARLGYRXXRFGXRVGR 18
                                                                                                                               3 ARLGYRXXRFGXRV 16
                                                                                                                                                                                       82 AELGYRVRRFAARV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             í
                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

•

```
FWRFamide neuropeptide precursor - California sea hare C; Species: Aplysia californica (California sea hare) C; Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 21-Jul-2000 C; Accession: A23172 R; Schaefer, M.; Picciotto, M.R.; Kreiner, T.; Kaldany, R.R.; Taussig, R.; Schaller, Call 41, 457-467, 1985 A; Tile: Aplysia neurons express a gene encoding multiple FWRFamide neuropeptides. A; Reference number: A23172; MUID:85176970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M11282; GB:M14957; NID:g155751; PIDN:AAA27751.1; PID:g155752
C;Keywords: alternative splicing; neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The Aplysia FMRFamide gene encodes sequences related to mammalian brain pe A;Reference number: A25790; MUID:87132918 A;Accession: A25790 A;Accession: A25790 A;Molecule type: DNA; mRNA
                                                                                                                                                                                         probable DNA polymerase alpha chain PA0669 [imported] - Pseudomonas aeruginosa (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: ï-1031 <STO>
A; Cross-references: GB: AE004502; GB: AE004091; NID: 99946547; PIDN: AAG04058.1; GSPDB
                                                                                                                                                                                                                   C; Species: Pseudomonas aeruginosa
C, Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: F83561
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ... Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Aplysia californica (California sea hare)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 31-Dec-1993
C;Accession: A25790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - California sea hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB;
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain PAO1
C, Genetics:
A, Gene: PAO669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%; 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
A25790
FMRFamide neuropeptide precursor
   |||||| :| ||||| 55 RLGYRSGHYGRTLITRVGK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.97
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RAÄRLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Taussig, R; Scheller, R.H.
DNA 5, 453-461, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-309 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RAARLGYR 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: F83561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nypothetical protein (gene N internal ORF) - bovine coronavirus (strain F15)
N/Alternate names: 1078 protein
C;Species: bovine coronavirus
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Jul-1999
C;Accession: 806869
B;Cruciere, C.; Laporte, J.
Ann. Inst. Pasteur Virol. i39, 123-138, 1988
A;Title: Sequence and analysis of bovine enteritic coronavirus (F15) genome. I. - Sequence number: 806399; MUID: 89087718
A;Reference number: 806869
A;Molecule type: genomic RNA
A;Residues: 1-207 <CRU>
A;Cross-references: EMBL:M36656; NID:g210700; PIDN:AAA42759.1; PID:g210702
A;Cross-references: Brabi:M36656; NiD:g210700; PIDN:AAA42759.1; PID:g210702
A;Note: the source is designated as bovine enteritic coronavirus
C;Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C;Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A57261
probable transposase - Rhizobium meliloti insertion sequence ISRm5
C;Specias: Rhizobium meliloti
C;Specias: S; Middleton, A1: Wheatcroft, R.
J. Bacteriol. 177, 313-3142, 1995
A;Title: Characterization, nucleotide sequence, and conserved genomic locations of inser
A;Reference number: A57261; MUID:95286494
A;Recession: A57261; MUID:95286494
A;Accession: A57261
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 < LABA

                A; Molecule type: genomic RNA
A; Residues: 1-207 < VER>
A; Residues: 1-207 < VER>
A; Experimental source: strain Minnesota
C; Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C; Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 207;
Pred. No. 5.3;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                    Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                      ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
9.6;
                                                                                                                                                                                                                                                    Score 40; DB 1;
Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2
Pred. No. 9.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                        50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.0%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 RLGYRXXRFG----XRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                      150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                 Query Match 50.0
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                               1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

ö

```
Search completed: February 12, 2002, 12:34:38
Job time: 556 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 RVSRLGQRATMFTRSGKRIG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRF---GXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.09
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                      C. Species: Rhodobacter capsulatus
C. Species: Rhodobacter capsulatus
C. Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C. Accession: T03576
R. Vicek, C.; Pacces, V.; Maltsev, N.; Pacces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A. Feference of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A. Reference number: 214955; MUID:97404404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004671; GB:AE004091; NID:g9948483; PIDN:AAG05828.1; GSPDB:GN001
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A,Reference number: A82950; MUID:20437337
A,Accession: G83340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16229.1; PID:g3128377 C;Genetics:
A;Map position: 1
C;Superfamily: conserved hypothetical protein MJ0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PA2440 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83340
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 320;
                                                                                                                                   DB 2; Length 597; 21;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.5; DB 2;
Pred. No. 14;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.5; DB
Pred. No. 22;
0; Mismatches
                                                                                                                                                                                Mismatches
                                                                                                                                   Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.9%; Scc
Best Local Similarity 47.4%; Pro
Matches 9; Conservative 3;
                                                                                                                                   48.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 RSARFYGLGWLLARFGARI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 266 RAALGRIGYRFA-FGARNG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RAAR---LGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RAA--RLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                  553 RFMRFGKRFMRFGRSVG 569
                                                                                                               Query Match
Best Local Similarity 52.9,
                                                                                                                                                                                                                     1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.23
Matches 12; Conservative
A, Residues: 1-597 <TAU>
C, Genetics:
A, Introns: 37/1
C, Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-194 <VLC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA A; Residues: 1-320 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

```
ij
L2 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
                                                                                 C. Accession: S36519
R. Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A. Description: Primer-directed sequencing of human papillomavirus types.
A. Reference number: S3646
A. Molecule type: DNA
A. Residues: 1-472 < DEL>
A. Residues: 1-472 < DEL>
C. Superfamily: papillomavirus L2 protein
C. Superfamily: papillomavirus L2 protein
C. Keywords: late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 37.5; DB 2; Length 472;
45.0%; Pred. No. 32;
tive 2; Mismatches 6; Indels
```

	*				*	
			•			2
			•			
				*		
		e e e e e e e e e e e e e e e e e e e			*	
		3				
	· *			t sy i		
			4.000 m			
					<b>*</b> - 1	
				***		
		9				÷
	***************************************					d.
그 한다는 사람은 경기가 되었다.						
			e set			
						- ei
						F .
	4.4 4.4					
	a. y					
					and the second s	
	(* (M) - (M)					v'
				V.		
		*		er,	# 	4
	•	Service Control of the Control of th	•			4 · · · · · · · · · · · · · · · · · · ·
	,	1		* .		
					# A	
	i i i i i i i i i i i i i i i i i i i		*			
			6.		* *	
	Programme and the second secon			- 1	e grade e	
	•		**************************************		£,	÷ <u>1.</u>
			र्गे. ज			- 1
			*			

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 12, 2002, 12:39:50 ; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec Run on:

Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		щус		P22654 bovine coro	P10525 bovine coro	P26626 turkey ente	Q52873 rhizobium m		P08021 aplysia cal	mycobs	human	human	t gen		_	Q56215 thermus agu	Q9zix6 thermus aqu	Q56239 thermus agu		_	Q9y6f9 homo sapien	_	O33259 mycobacteri	Q49775 mycobacteri	_	P25543 vibrio chol	P21921 pseudomonas		Q10977 mycobacteri			_		P56346 chlorella v
SUMMARIES	ID	NAT_MYCTU	GCST_THEMA	YIOR_CVBF	YIOR_CVBM	YIOR_CVTKE	TRA5_RHIME	FMR1_APLCA	FMR2_APLCA	MURC_MYCLE	VL2_HPV34	VL2_HPV22	POLG_TVMV	NARK_BACSU	GAA4_MOUSE	MUTS_THEAQ	MUTS_THECA	MUTS_THETH	VL2_HPV23	WNT6_MOUSE	WNT6_HUMAN	MURC_MYCTU	METH_MYCTU	METH_MYCLE	MTRG_METKA	IRGB_VIBCH	COBL_PSEDE	AK11_RAT	PPSA_MYCTU	VL2_HPV32	VL2_HPV42	AAT_METEX	GAR1_SCHPO	MIND_CHLVU
	DB		П														7																	
	Length		364	207	207	207	398	309	552	495	472	524	3023	395	552	811	817	818	519	364	365	494	1192	1206	74	298	413	1129	1876	476	477	93	194	282
d	Query Match	55	51.2	50.0	50.0	50.0	50.0	48.8	48.8	47.5	o	46.9	46.9	46.2	46.2	46.2	46.2	46.2	45.6	45.0	45.0	45.0	45.0	45.0	43.8	43.8	43.8	43.8	43.8	43.1	43.1	(4	42.5	42.5
	Score	4 4	41.	40	40	40	40	39	39	38	37.5	37.5	37.5	37	37	37	37	37	36.5	36	36	36	36	36	32	32	35	32		34.5	4	34	34	34
	Result No.	:	7	m	4	S	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

12 lymnaea sta 11 escherichia 13 homo saplen 10 bradyrhizob 10 drosophila 13 homo papil 15 rhesus papil 16 drosophila 18 drosophila 18 drosophila 14 alcaligenes 12 homo saplen	oacterium.	Harris D., F., F., Holroyd S., hy L., s J.,	white O., Hickey E., Salzberg S.L., J., Mikula A., clinical and	rase genes s: increased SE FAMILY.
P19802 P3571 060231 09rh70 081009 081009 09hk06 09hk06 094518 044518	283 AA. update) n update) 3.1.5). 1.13C. r. Actinobacteridae; Mycobacteriaceae; Mycobacterium	hurcher C. I. Tekaia T. Connor amlin N. B. S., Murg A., Rogers uares R., G.;	enter L., Haft D., Heva M.D., I., Gill erculosis databases	is;  "T., Everitt M., Sim E.; f arylamine N-acetyltransferase d Mycobacterium tuberculosis: in resistance."; 1 resistance."; 19). COLAR DRUG ISONIAZID. COA + ARYLAMINE - COA + 'LASMIC. ARYLAMINE N-ACETYLTRANSFERASE F' FERS FROM THAT SHOWN DUE TO A
FMRF_LYMST CALA ECCLI DDD 16_HUMAN RPOZ_BRAJA RSZ_DROME VLZ_HPV61 VLZ_RHPV1 TRPD THEAC OGGI_DROME OCCC_ALCXX FA10_HUMAN	RT; ence tatic EC 2. Y06G1 teria	230; 1 J. J. 1 J. 1 J. 1 T. M.A. M.A. S.,	, Eisen J.A., con Mr. Gwinn P. (mayam L.A., leidman J., Kho Mycobacterium EMBL/GenBank,	P. P
306 1 380 1 041 1 104 1 104 1 459 1 322 1 327 1 488 1 539 1	RD; Creat Last Last NSFERA 671 OR 10sis.	1978 N. A. 1978. 1978. 1978. 1978. 1982. 1982. 1982. 1982. 1982. 1982. 1982. 1983. 1982. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983. 1983.	the of the	Med=99 Delgc rizati egmati egmati 3-130n 3-130n ANTIT Y: ACF OS TO QUENCE
8 8 9 1 9 4 4 8 8 4 4 R	STANDARD; 1. 40, Cr 1. 40, La 1. 40, La TYLTRANSF OR MT3671 uberculos; Ac cutes; Ac ; Coryneb;	Pulk R. R. K. K. Lor Lor Dio	M N.A. S51 / Oshkos. R.D., Alland DeBoy R., D Nelson W.C Utterback T. e comparison Exains.";	N. Publ 9; Publ ty R., aracte, 1tu sm itu 1tu sm 1tu sm 1tu sm 1tu sm 0ULD H 0ULD H CTIVITE CTIVITE LAMINE LOCAT BELON IN POS
24444444444444444444444444444444444444	S (Rel (Rel (Rel (Rel (Rel (Rel (Rel (Rel	THOM N.A.  =#13.7KV.;  E=96295987;  Pubme  S.V., Elglmeier  S.V., Elglmeier  K.K., Basham D.,  R., Devlin K.,  R., Jaqels K.,  S., Seeger K.,	rROM N.A. 1551 / Oslin R.D., Allin R.D., Nelson F., Utterback Home compari	AATION 138759 1, Aut 1, Aut 1, Aut 1, Cha 1,
	JLT 1  MAT_MYCTU  B96848; 20-AUG-:3001 (Rel. 40, Last sequ 20-AUG-:3001 (Rel. 40, Last sequ 20-AUG-:3001 (Rel. 40, Last ann ARYLAMINE N-ACETYLTRANSFERASE ( MYCOBACIERIUM tuberculosis. Bacteria; Firmicutes; Actinobac Actinomycetales; Corynebacterin [1]	SEQUENCE FROM N.A. STRAIN=H37RV, MEDLINE=+9925987, Cole S.Ç., Brosch Gordon S.V., Eigln Badcock K., Bashan Bavies R., Devlin Hornsby T., Jagels Ollver S., Osborne Rutter S., Seeger Sulston J.E., Tayl, "Deciphering the R., Deciphering the R., Deciphering the R., Deciphering the R., Sulston J.E., Tayl, "Deciphering the R., Deciphering the R., Complete genome se Nature 393:537-54«	mar mar mar mar mar mar mar mar mar mar	193 MEDLINE-99138759; PubMed=99733 MEDLINE-99138759; PubMed=99733 Payron 14 A., Auty R., Delgoda "Cloning and characterization from Mycobacterium smegmatis a expression results in isoniazi J. Bacteriol. 181:1343-1347(1) INACTIVATION: COULD HAVE A ROI INACTIVATION: COULD HAVE A ROI INACTIVATION: CATIVITY: ACETYI N-ACETYLARYLAMINE
	RESULT NAT MY CALL OF			5072444444000000000000000000000000000000

Gaps

; 0

7; Indels

Length 364;

1;

DB 1

Score 41; DB 1 Pred. No. 1.9; 1; Mismatches

51.2%; 52.9%;

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

Pfam; PF01571; GCV_T; 1. Transferase; Aminotransferase; Complete proteome. SEQUENCE 364 AA; 40332 MW; 66F33CC151CC6F1 CRC64;

SWA

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pelaschmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE AMINOMETHYLTRANSFERASE (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCINE (BY SIMILARITY)

-!- CATALYTIC ACTIVITY: (6S)-TETRAHYDROFOLATE +
S-AMINOMETHYLDIHYDROLIPOYLPROTEIN = (6R)-5,10-
METHYLENETRAHYDROFOLATE + NH(3) + DIHYDROLIPOYLPROTEIN.

-!- SUBUNT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:
P, T, L, AND H (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE GCVT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001447; Acetyltransf2.
ProDom; PD002783; Acetyltransf2; 1.
Transferase; Acyltransferase; Complete proteome.
SEQUENCE 283 AA; 31029 MW; 9C8D98E3256D088A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.0%; Score 44; DB 1; 64.3%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                        EMBL; Z92774; CAB07160.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001706; AAD35303.1; -. TIGR; TM0211; -.
                                                                                                                                                                                                                                                                                                                        EMBL; AE007168; AAK48028.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002536; GCV_T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                TubercuList; Rv3566c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AELGYRVRRFAARV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCVT OR TM0211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCST_THEMA
09WY54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCST_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
          HDD BEAR BAND OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                            Bovine coronavirus (strain F15).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine coronavirus (strain Mebus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                          Cruciere C., Laporte J.;
"Sequence and analysis of bovine enteritic coronavirus (F15)
"Sequence of the gene coding for the nucleocapsid protein;
of the predicted protein.";
Ann. Inst. Pasteur Virol. 139:123-138(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 207; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A4E5DE61171BAB50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                            01-AUG-1991 (Rel. 19, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-BCC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                  207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                             MEDLINE=89087718; PubMed=3207501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87151119; PubMed=3029965;
                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
01-DEC-1992 (Rel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein.
207 AA; 23001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
50.0%;
                    | || || : | |||
290 RIARKGYEVLKNGERVG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coronaviridae; Coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M36656; AAA42759.1;
1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | |||:| |: ||
|150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
The 8; Conserve
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI_TaxID=11129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                YIOR_CVBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YIOR_CVBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                 YIOR_CVBF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIOR_CVBM
                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                Вb
 δy
                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
FMR1_APLCA P08020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY.
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        FMR1_APLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@licenserver.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Verbeek A., Tijssen P.; "Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrane protein genes: a close genomic relationship with bovine
                                                                                                                                                                                                                             Gaps
Lapps W.E., Hogue B.G., Brian D.A.; "Sequence analysis of the bovine coronavirus nucleocapsid and matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Turkey enteric coronavirus (TCV).
Yutuses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID-11152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
17-RANSPOSASE FOR INSERTION SEQUENCE ELEMENT ISRMS.
18-RAIZODIUM meliloti (Sinorhizobium meliloti).
18-Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 1; Length 207;
Pred. No. 1.7;
2; Mismatches 6; Indels
                                                                                                                                                                                                      Length 207
                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                       BE76DC4D663DD32A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F69E2D8F2F006F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                                                                                                      DB 1;
1.7;
                                                                                                                                                                                                                                                                                                                         207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 AA
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                      Score 40;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72:1659-1666(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91311418; PubMed-1856695;
                                                                                                                                                                                                                                                                                                                                            (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 protein.
207 AA; 23005 MW;
                                                                                                                                                            ll protein.
207 AA; 23054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                      50.0%;
                                                                                                                                        EMBL; M16620; AAA66398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 157:47-57(1987).
                                                                                                                                                                                                                                                              | |||:| |: ||
150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                      Query Match 50.0
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                 1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JQ1174; JQ1174.
                                                                                                                                                  PIR; C26347; QQIHBC
Hypothetical protei
SEQUENCE 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MINNESOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAS_RHIME
Q52873;
01-NOV-1997 (
01-NOV-1997 (
01-NOV-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                             01-AUG-1992
                                                                                                                                                                                                                                                                                                                          YIOR_CVTKE
P26626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                               YIOR_CVTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRA5_RHIME
                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
 ô
                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEPTER
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                   Laberge S., Middleton A.T., Wheatcroft R.;
"Characterization, nucleotide sequence, and conserved genomic
locations of insertion sequence ISRmS in Rhizobium meliloti.";
J. Bacteriol. 177:3133-3142(1995).
-!- FUNCTION: REQUIRED FOR THE TRANSPOSITION OF THE INSERTION ELEMENT.
-!- SIMILARITY: BELONGS TO THE MUTATOR FAMILY OF TRANSPOSASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: FWRFAMIDE INDUCES CONTRACTIONS IN VISCERAL AND SOMATIC MAGSCULATURE AS WELL AS IN THE HEART.
-i- ALTERNATIVE PRODUCTS: THE DIFFERENT FMRFAMIDE PRECURSORS ARE GENERATED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transposable element; Transposition; DNA-binding; DNA recombination.
SEQUENCE 398 AA; 45695 MW; 0A7AA811C82CFF51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-85176970; PubMed-3838698;
Schaefer M., Picciotto M.R., Kreiner T., Kaldany R.-R., Taussig R.,
Schaeller R.H.;
"Aplysia neurons express a gene encoding multiple FMRFamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
1-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FMRFAMIDE NEUROPEPTIDE PRECURSOR (CLONE FWRF-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001207; Transpo_mutator.
Pfam; P?00872; Transpo_mutator; 1.
PROSITE: PS01007; TRANSPOSASE_MUTATOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                 STRAIN=12450;
MEDLINE=95286494; PubMed=7768811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; So
ilarity 47.4%; Pr
Conservative 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U)8627; AAA81001.1; -.
Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 RLGYRXXRFG----XRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 RLGYRSGHYGRTLITRVGK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41:457-467(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 9; Conserv
                                                                                                   SEQUENCE FROM N.A.
                             NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuropeptides
```

Я.,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                -!- FUNCTION: FARFAMIDE INDUCES CONTRACTIONS IN VISCERAL AND SOMATIC MUSCULATURE AS WELL AS IN THE HEART.
-!- ATTERNATIVE PRODUCTS: THE DIFFERENT FWRFAMIDE PRECURSORS ARE GENERATED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
"The Aplysia FMRFamide gene encodes sequences related to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (G-28 PROVIDE AMIDE GROUP)
(G-112 PROVIDE AMIDE GROUP
(G-119 PROVIDE AMIDE GROUP
                                                          SEQUENCE OF 87-267 FROM N.A.
MEDILINE-89176970; PubMed-3838698;
Schaefer M., Picciotto M.R., Kreiner T., Kaldany R.-R., Taussig
Schaller R.H.;
                                                                                                                       "Aplysia neurons express a gene encoding multiple FMRFamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROVIDE PROVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage on pair of basic residues; Repeat;
de; Alternative splicing.
24 27 FMRFAMIDE.
1108 111 FMRFAMIDE.
115 118 FMRFAMIDE.
153 156 FMRFAMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (G-157
(G-164
(G-179
(G-195
(G-202
(G-218
(G-233
(G-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMREAMIDE
AMIDATION
AMIDATION
AMIDATION
AMIDATION
AMIDATION
AMIDATION
AMIDATION
AMIDATION
AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION
AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION
AMIDATION
AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M14958; AAA27755.1; -. EMBL; M11283; AAB59169.1; -. InterPro; IPR002544; FARP. Pfam; PF01581; FARP; 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuropeptides.";
Cell 41:457-467(1985).
               brain peptides.";
DNA 5:453-461(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amidation; Cle
Neuropeptide;
                                                                                                                                                                                                                                             FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aplysia californica (California sea hare).
Eukaryota, Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                            (G-11 PROVIDE AMIDE GROUP).
(G-42 PROVIDE AMIDE GROUP).
(G-49 PROVIDE AMIDE GROUP).
(G-49 PROVIDE AMIDE GROUP).
(G-65 PROVIDE AMIDE GROUP).
(G-95 PROVIDE AMIDE GROUP).
(G-110 PROVIDE AMIDE GROUP).
(G-142 PROVIDE AMIDE GROUP).
(G-142 PROVIDE AMIDE GROUP).
(G-144 PROVIDE AMIDE GROUP).
(G-158 PROVIDE AMIDE GROUP).
(G-158 PROVIDE AMIDE GROUP).
(G-159 PROVIDE AMIDE GROUP).
(G-206 PROVIDE AMIDE GROUP).
(G-219 PROVIDE AMIDE GROUP).
(G-228 PROVIDE AMIDE GROUP).
(G-238 PROVIDE AMIDE GROUP).
(G-254 PROVIDE AMIDE GROUP).
(G-257 PROVIDE AMIDE GROUP).
(G-277 PROVIDE AMIDE GROUP).
(G-277 PROVIDE AMIDE GROUP).
(G-277 PROVIDE AMIDE GROUP).
(G-277 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GROUP).
GROUP).
GROUP).
GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                         Score 39; DB 1; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FMRFAMIDE NEUROPEPTIDE PRECURSOR (CLONE FMRF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6F268BD6C3F90908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                       EMRFAMIDE.
FMRFAMIDE.
                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                  FMRFAMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87132918; PubMed=3816495; Taussig R., Scheller R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 RFMRFGKRFMRFGRSVG 281
EMBL; M11282; AAA27751.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                       PIR; A23172; A23172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           48
64
79
94
109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMR2_APLCA
P08021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                           PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RES
                                                                                                                                                                                                              PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RES
                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                RES
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
FPMR2_ADLCA
ID PRREZA
AC P08021
DT 01-NUG
DT 01-NUG
DE FWRREAM
OS APJYSi
OC APJYSi
OC APJYSi
CX NCBLTY
RN [1]
RN SEDUEN
RX TEUSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

q δŽ

AMIDE GROUP)

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                              GROUP)
GROUP)
                                                                                                                                                                                                                                                                                                                                                                                         GROUP)
GROUP)
GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP)
GROUP)
                                                                                                                       GROUP)
GROUP)
                                                                                                                                                                                                                                                                                                                 GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: CELL MALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                          AMIDE
                                                                                                                                                                                                  AMIDE
AMIDE
AMIDE
                                                                                                                                                                                                                                                                                                                 AMIDE
AMIDE
AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 1; Length 552;
Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE. PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS. SUBCELLULAR LOCAFION: CYTOPLASMIC (PROBABLE). SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DD-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-RETYLMURAMOYL-L-ALANINE SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                   PROVIDE PROVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROVIDE PROVIDE PROVIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROVIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104E9A4E6EB3E5F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             PROVIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROVIDE
                                           (G-293
(G-308
(G-332
(G-333
(G-385
(G-417
(G-413
(G-449
(G-449
(G-449
(G-449
(G-449
(G-449
(G-449
(G-449
(G-449
(G-465
(G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                           AMIDATION
   AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21128732; PubMed-11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 48.8
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
   2277
2292
3322
3322
3322
3322
3324
4400
4416
4416
4480
4480
4480
5115
5115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519
552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
MURC_MYCLE
ID MURC_MYCLE
AC P57994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
SEQUENCE
MOD_RES
MOD_RE
       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Burspaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;;
                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                       Gaps
                                                                                                                                                                     .;
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94265501; PubMed=8205838;
Delius H., Hofmann B.;
"Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 472;
             Leproma; ML0915; -.
InterPro; IPR000713; Mur_ligase.
Jefan; FF01225; Mur_ligase; 1.
PeptidGglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding; Complete proteome.
                                                                                                                                         Length 495;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 34.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                  122 128 ATP (POTENTIAL).
495 AA; 51588 MW; 46F816A650C847A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50648 MW; 5118928245C63C70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
9
                                                                                                                                         Score 38; DB 1;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MINOR CAPSID PROTEIN L2.
                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                            47.4%; Scor.
47.4%; Pred. No. >,
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.5; DE
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X74476; CAA52559.1; -.
PIR; S35519; S36519;
InterPro; IPR000784; Late_L2.
Pfam; P:700513; late_brotein_L2; 1.
Coat protein; Late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
EMBL; AL583920; CAC31296.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 RVSRLGQRATMFTRSGKRIG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.9%;
                                                                                                                                                                                                                 237 RIAELGIRVLRYGSDDRIG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RANKLGYRXXRF---GXRVG 17
                                                                                                                                                                                                 1 RAARLGYRXXRFGX--RVG 17
                                                                                                                            Ouery Match
Best Local Similarity 47.4*
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      MINOR CAPSID PROTEIN L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10613;
                                                                                                                                                                                                                                                                                                                                                                                                                             Papillomavirus
                                                                                                                                                                                                                                                                                            VL2_HPV34
P36758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VL2_HPV32
P50796;
                                                                                  NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VL2_HPV22
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                 ð
```

```
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POGG_TVMV STANDARD; PRT; 3023 AA.
POGG_TVMV STANDARD; 084901; 084902;
01-MAR-1989 (Rel. 10, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
40-MAY-2001 (Rel. 40, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: N-TEMRINAL PROTEIN (PI); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN 8 (NI-A) (NIA)
(EC 3.4.22.44) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                           э;
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The nucleotide sequence of tobacco vein mottling virus RNA."; Nucleic Acids Res. 14:5417-5430(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domier L.L., Franklin K.M., Shahabuddin M., Hellmann G.M., Overmeyer J.H., Hiremath S.T., Siaw M.F.E., Lomonossoff G.P.,
                                                                                                                                                                                                                                                                                                                                                                            Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                          Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 papillomavirus type 22.
es; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                              Premi Projectivi late protein. 12; 1.

Coat protein; Late protein.

SEQUENCE 524 AA; 57619 MW; E9738FE2C3B19CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1874-1888, AND COVALENT RNA-LINKAGE.
                                                                                                                                                                                                                                                                                                                                                                            Score 37.5; DE Pred. No. 12; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tobacco vein mottling virus (TVMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE~86286553; Pubmed=3737407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 RVSRLGQRASLSTRSGARVG 358
                                                                                                                                                                                                                                                                                                                                                                                46.9%;
50.0%;
                                                                                                                                                                                                                                                                                  InterPro; IPR000784; Late_L2
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RAARLGYR---XXRFGXRVG 17
                                                                                                                                                                                                                                                                    EMBL; U31780; AAA79406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.03
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shaw J.G., Rhoads R.E.;
"The nucleotide sequence
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COAT PROTEIN (CP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=12228;
                                               NCBI_TaxID=37954;
                                  Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potyvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shaw J.G
                                                                                             Delius
```

Ω

ô

```
between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
MAY BE INVOLVED IN REPLICATION.

CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.

CATALYTIC ACTIVITY: NUCLEAR INCLUSION PROTEIN A HYDROLYSES
GLUTAMINYL BONDS, AND ACTIVITY IS FURTHER RESPRICTED BY
PREFERENCES FOR THE AMINO ACIDS IN P6 -P1' THAT VARY WITH THE
SPECIES OF POTYVIRUS, E.G. GLU-KAA-KAA-TYR-AYAA-GAH-(SER OR GLY)
FOR THE ENZYME FROM TOBACCO ETCH VIRUS. THE NATURAL SUBSTRATE IS
THE VIRAL POLYPROTEIN, BUT OFFER PROTEINS AND OLIGOPEPTIDES
CONTAINING THE APPROPRIATE CONSENSIGS SEQUENCE ARE ALSO CLEAVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                              PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEGUTIC
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6. SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4 SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
(BY 49 KDA PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-TERMINAL PROTEIN.
HELPER COMPONENT PROTEINASE.
29 KDA PROTEIN CYTOPLASMIC INCLUSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COVALENT LINKAGE OF VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 KDA PROTEIN.
NUCLEAR INCLUSION PROTEIN A.
NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
299FDED15C0E5B87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anterto, its Notice 1. In Profile 1. Profile 1. Pfam: PF00270; DEAD; 1. Pfam: PF00271; helicase_C; 1. Pfam: PF00851; Peptidase_C6; 1. Pfam: PF00767; Poty_coat; 1. Pfam: PF00767; Poty_Loat; 1. Pfam: PF00680; RNA_dep_RNA_pol; PRINTS; PR00966; NIAPOTYPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicase_C.
Peptidase_C4.
Peptidase_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poty_P1.
Poty_coat.
RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04083; CAA27720.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.9
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1818
2242
2758
3023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR001730; PInterpro; IPR001456; PInterpro; IPR00150; PInterpro; IPR001592; PInterpro; IPR001205; Interpro; IPR001205; PInterpro; IPR001205; PInterpro; IPR001254; TInterpro; IPR001254; TInterpro; IPR001254; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001410;
InterPro; IPR001650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A23647; GNVSTV. MEROPS; C04.001; -. MEROPS; C06.001; -. MEROPS; S30.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNVSTV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11130
1765
2242
2758
1878
1215
3023
```

5 LGYRXXRFGXRVGR 18

ô

```
SIGNAL
                                                                                                                                                          GABRA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                        GAA4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                             "Anaerobic transcription activation in Bacillus subtilis: identification of distinct FNR-dependent and -independent regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Transmembrane; Nitrate assimilation; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISSIMILATORY REDUCTION OF NITRATE.
-1- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE NARK/NASA FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            de la Fuente V., Hullo M., Lelong C., Schleich S., Sekowska A., Song B., Villani G., Kunst F., Danchin A., Glaser P., Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                  Cruz Ramos H., Boursier L., Moszer I., Kunst F., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.2%; Score 37; DB 1; Length 395; Best Local Similarity 58.3%; Pred. No. 11; Masmatches 4; Indels Matches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E41A35C3EC58921F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Presecan E., Moszer I., Boursier L., Cruz Ramos H.,
                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NITRITE EXTRUSION PROTEIN (NITRITE FACILITATOR).
                                                                                 395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                               PRT;
                                                                                                                                                                                                                                                                     STRAIN=168;
MEDLINE=96112813; PubMed=8846791;
                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42956 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z49884; CAA90041.1; -. EMBL; Z97024; CAB09704.1; -. EMBL; Z99123; CAB15760.1; -. SUBLILISE; BG11342; nark.
                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 14:5984-5994(1995).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-171 FROM N.A.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
64
64
1116
1180
1223
223
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
330
357
395 AA;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-168;
                                                                                 NARK_BACSU
                                                                                                                                                                                                                                                                                                                                                           mechanisms
                                                                                                                                                                                                                                                                                                               Glaser P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                  NARK_BACSU
         g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishil Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Relp P., Lowis S., Marsuo Y., Nikaido I., Rochiwa H.,
Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Iyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whyshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wynshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
-!- FUNCTION: GABA, THE MAJOR INHIBITORY NEUROTRANSMITTER IN THE VERIEBRATE BRAIN, MEDIATES NEURONAL INHIBITION BY BINDING TO THE
                                                                                                                                                           20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-4 SUBUNIT PRECURSOR (GABA(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: GENERALLY PENTAMERIC. THERE ARE FIVE TYPES OF GABA(A)
                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DELTA, AND RHO.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GABA/BENZODIAZEPINE RECEPTOR AND OPENING AN INTEGRAL CHLORIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT.
EXTRACELLULAR (PROBABLE)
                                                                                                  552 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-Hippocampus; MEDLINE-21085660; Pubmed=11217851;
                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AX013727; BAB28975.1; -.
MCD; MCI:95616; Gabra4.
InterPro; IPR001175; Neur_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Multigene family.
                                                                                                                                          (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PR00065; neur_chan; 1.
PRINTS; PR00252; NRIONCHANNEL
                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
280
306
340
62 LGYLTNRFGARL 73
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36
259
285
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHANNEL.
                                                                                              GAA4_MCUSE
Q9D6F4;
                                                                                                                                        20-AUG-2001
                                                                                                                                                                                                                        RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                       g
```

PROBABLE

LGYRXXRFGXRV 16

'n

ó

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biswas I., Hsieh P.;
"Identification and characterization of a thermostable MutS homolog from Thermus aquaticus."
If Inom Thermus aquaticus."
1. Biol. Chem. 271:5040-5048(1996).
-I. FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN DNA. IT IS POSSIBLE THAT IT CARRY OUT THE MISMATCH RECOGNITION STEP. THIS PROTEIN HAS A WEAK ATPASE ACTIVITY.
-I. SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
NCBI_TaxID=271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.2%; Score 37; DB 1; Length 811; 53.3%; Pred. No. 22; tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                   Ouery Match 46.2%; Score 37; DB 1; Length 552; Best Local Similarity 50.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                             BY SIMILARITY.
213C16C423D7F97B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43A5E5296A333515 CRC64;
CYTOPLASMIC (PROBABLE). PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U33117; AAC43637.1; -.
InterPro; IPR00043; MutS_C.
InterPro; IPR000438; MutS_N.1
Pfam; PF00488; MutS_C; 1.
Pfam; PF01624; MutS_N: 1.
ProDon; PD001263; MutS_C; 1.
SMART; SM00534; MUTSaC; 1.
SMART; SM00534; MUTSaC; 1.
DNA FP9115; PS00486; DNA_MISMATCH_REPAIR_2; 1.
DNA FP911; ATP-binding; DNA_binding.
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADM MISMATCH REPAIR PROTEIN WUTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 811 AA
                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96214934; PubMed=8617781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90627 MW;
                                                                                                                                                                            60878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          464 RPASIGSASTRPAFGSRLGR 483
                                                                                                                                                                                                                                                                                                                                                                                     1 RAARLGYRXXR--FGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.3'
                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    811 AA;
                                                                                                                                                                            552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTS_THEAQ
Q56215;
                                                    CARBOHYD
CARBOHYD
CARBOHYD
DISULFID
SEQUENCE
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
MUTS_THEAD
IN CALLED
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 20-AUG
DE NOTE:
OC Bacter
OC Bac
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
   FFFFFS
                                                                                                                                                                                                                                                                                                                                                                                        ŏ
```

```
Search completed: February 12, 2002, 12:39:51
Job time: 804 sec
```

us-09-485-571-21.rsp

b .	Andrew State (1997)	•	e e e e e e e e e e e e e e e e e e e	
		a ²		
*				
			4 (1) (4) (1) (2) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4	
			A.	- 1
	in the second of			
				*
			**************************************	
				· · · •
			A.	
		· Saint		

099977 arcopyrum p 099571 homo saplen 09654 gallus gall 09656 synechococc 090657 kluyveromyc 09957 kluyveromyc 09187 streptomyce 09187 streptomyce 09187 humo herpe 065320 unidentifie 09545 humo herpe 066320 unidentifie 09557 mycobacteri 09657 mycobacteri 09657 mycobacteri 09657 mycobacteri 09657 mycobacteri 09657 sycobacteri 09657 sycobacteri

09176 prototheca 09npcl homo sapien 09npcl homo sapien 006053 mycobacteri 053038 rhodococcus 09nx16 pseudomonas 09nx12 leishmania 09sn79 oryza sativ 018284 caenorhabdi

sed

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

t

OM protein

Run on:

Scoring table:

```
Wilson E., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases EMBL; U42830; AAC48280.1; -. InterPro; IPR000718; Peptidase_M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01431; Peptidase_M13; 1.
SEQUENCE 433 AA; 50075 MW; 819E8A1EB676B054 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                               Q9H571
Q9W6S4
Q9R6S6
Q9HQES
Q9Y857
Q9R57
Q9R6F0
Q9R6F0
Q66320
                                                                                                                                                                                                                                                                                                                                                                                                           Q9SM79
Q18284
                                                                                                                                                                                                                                                      09NPE5
P78762
Q9TJR6
Q9NPC1
Q9HM39
                                                                                                                                                                                                                      049785
                                                                                                                                                                                                                                         09xc63
                                                                                                                                                                                                                                                                                                                                          006053
                                                                                                                                                                                                                                                                                                                                                            053038
                                                                                                                                                                                                                                                                                                                                                                            09HWL6
                                                                                                                                                                                                                                                                                                                                                                                             O9NKL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 06, C
(TrEMBLrel. 06, L
(TrEMBLrel. 17, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                    3300
3334
3358
3359
3359
3391
4111
4111
562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature :68:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-FRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE: FROM N.A.
C53B7.7 PROTEIN.
                                                                                                                                                   36.5
36
36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               045311 045311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C53B7.7
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 045311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  045311 caenorhabdi
076267 aplysia cal
02757 methanobact
09kvn3 vibrio chol
09gar7 bovine coro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        091ha4 thermonicro
0915q2 pseudomonas
016663 aplysia cal
016964 aplysia cal
068994 mycobacteri
068139 rhodobacteri
091142 pseudomonas
088925 tobacco vei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine coro
                                                                                                                                   (without alignments)
11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9qaq4 bovine cord
Q9k4v0 alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                  ; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                        473505
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     473505 segs, 146272329 residues
                                                                                                                  February 12, 2002, 12:38:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   045311
076267
027557
0904R7
0904R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q88925
P94950
Q9N3G0
                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9QAQ4
Q9K4V0
                                                                                                                                                                                                                   1 RAARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091502
016963
016964
068994
09CCS8
068139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09RHA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_organelle:*
sp_phage:*
                                                                                                                                                                   US-09-485-571-21
80
                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934
207
207
207
513
917
1031
127
373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
320
3023
224
253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511.2
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
550.0
```

Length 433;

DB 5;

Score 45;

56.2%;

Query Match

P94950 methanopyru Q9n3g0 caenorhabdi

Score

Result Š

```
1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VC0108;
                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                              O9KVN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGE;
                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                  Q9KVN3
                                                                                                                                                                                      g
   δ
                                                                                                                                                                                                                                                        δλ
              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                       Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Aplyaiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keaple P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL SURFACE GLYCOPROTEIN (S-LAYER PROTEIN) RELATED PROTEIN (S-LAYER
                                                                                                                                                                                                                                                                                                          negatively coupled to adenylate cyclase...;
J. Neurosci. 18:5586-5593(1998).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF041039; AAC28786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                              Cloning and functional expression of an Aplysia 5-HT receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 492;
                                                                                                                                                                                                                                                             MEDLINE-98337861; PubMed-9671650;
Angers A., Storozhuk M.V., Duchaine T., Castellucci V.F.,
Desgroseillers L.;
             Indels
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 492 AA; 56261 MW; 24F0044CA94901B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) G-PROTEIN-COUPLED 5-HYDROXYTRYPTAMINE RECEPTOR.
              ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB Pred. No. 14;
              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
 Pred. No.
                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DELTA H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%;
55.6%;
47.18;
                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||::||| | :|
257 RASKLGYTGTRVGHEIG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RAARLGYRXXRFGXRVGR 18
                                  1 RAARLGYRXXRFGXRVG 17
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                01-NOV-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=145262
                                                                                                                                                                                  5-HTAP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN)
                                                                                                               076267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               027557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                       δ
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=EL TOR N16961 / SEROTYPE 01;

MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Meidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: Inctional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                  DB 1; Length 1408;
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 934;
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                         1408 AA; 152736 MW; 294EC7742ABB29F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 934 AA; 103874 MW; B23F2AF96769F1F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 65;
                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Complete proteome.
SEQUENCE 934 AA; 103874 MW; B23F2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 3_5_exonuclease.; 5_3_exonuclease.; DNA_poli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; 1PR002562; 3.5_exonuclea
InterPro; 1PR002421; 5.3_exonuclea
InterPro; 1PR002298; DNA_pol1.
InterPro; 1PR001298; DNA_pol_A.
InterPro; 1PR000513; Exo_N_I.
InterPro; 1PR003583; HHH_1.
InterPro; 1PR003584; HHH_2.
Pfam; PF01612; 3.5_exonuclease; 1.
Pfam; PF01612; 5.3_exonuclease; 1.
Pfam; PF01612; 5.3_exonuclease; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE004101; AAF93286.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.2%;
                                                                                                                                                                                                                                                  53.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                            |:|||| :||
|319 AKLGYRTFKFTLKPGR 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00475; 53EXOC; 1.
                                                                                                                                                                                                                                               Query Match 53.8
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                              3 ARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00868; DNAPOLI
SMART; SM00474; 35EXOC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
Bacteria; Protec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA POLYMERASE
VC0108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00279;
```

ċ

PROTEIN

090AR7 090AR7

RESULT

g

```
Chouljenko V.N., Kousoulas K.G., Lin X., Storz J.;
"Nuclectide and predicted amino acid sequences of all genes encoded by "Nuclectide and predicted amino acid sequences of all genes encoded by the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17:33-42(19.98).
EMBL: AF058944; AAF25526.1;
SEQUENCE 207 AA; 22989 MW; C83903664387E059 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohlmann A., Cramm R., Schmelz K., Friedrich B.;
Pohlmann A., Cramm R., Schmelz K., Friedrich B.;
"A novel NO-responding regulator controls the reduction of nitric soxide in Ralstonia eutropha.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBL_TaxID=11128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; Irrocold; Irroco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NITRIC JIDE REDUCTASE REGULATOR NORR.
                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                        207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alcaligenes eutrophus (Ralstonia eutropha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=OK-0514-3;
MEDLINE=98451808; PubMed=9778786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ278371; CAC00710.1; -.
                                                                                                                       (TrEMBLrel. 13, 1
(TrEMBLrel. 13, 1
(TrEMBLrel. 13, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003593; AAA.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                   bovine coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=H16;
                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TakID=510;
                                                                                                                    01-MAY-2000 (
01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pHG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOM:NIN.
                                                                                                                                                                                                    PROTEIN.
                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ralstonia
                                                                   090AQ4
090AQ4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9K4V0
Q9K4V0;
                                                 090A04
                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-LSU-94LSS-051-2;
MEDLINE-98451808; PubMed=9778786;
MEDLINE-98451808; PubMed=9778786;
Chouljenko V.N., Kousoulas K.G., Lin X., Storz J.;
Micleotide and predicted amino acid sequences of all genes encoded by the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17:33-42(1998)
EMBL; AF058943; AAF25516.1;
SEQUENCE 207 AA: 23012 MW; C84E1F7612C9C3DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chouljenko V.N., Kousoulas K.G., Lin X., Storz J.;
"Nucleotide and predicted amino acid sequences of all genes encoded by the 3' genomic portion (9.5 kb) of respiratory bovine coronaviruses and comparisons among respiratory and enteric coronaviruses.";
Virus Genes 17:33-42[1938].

EMBL: APC58942; AAF25506.1; -
EMBL: APC88942; AAF25506.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                        Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 12;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 40; DB 12;
50.0%; Pred. No. 19;
iive 2; Mismatches 6
                                                                                                                                              207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                         Bovine coronavirus (strain LY-138)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-LY-138;
MEDLINE-98451808; PubMed-9778786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 13, I
                                                                                                                                                                                          (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 16, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||:| |: ||
150 RLFRLGFRLARYSLRV 165
| |||:| |: ||
|150 RLFRLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAARLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine coronavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11128;
                                                                                                                                                                                          01-MAY-2000 (
01-MAY-2000 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-MAY-2000
```

PROTEIN

ð g

090ARO; Q9QAR0

ö a

ö

Gaps

ö

;

12; Length 207; Indels us-09-485-571-21.rspt

SEQUENCE

g

09RHA4;

Q9RHA4

RESULT

qq

ð

```
ALTINIE-ZO43737; PubMed=10984043; Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Sher M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOl, an opportunistic pathogen."; Nature 406:959-964(2000).

EMBL; ABO04502; AAG04058.1; -. InterPro: IPR003141; PHP.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMRRAMIDE (FRAGMENT).
Apjysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
Apjysiidae; Apjysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MISSOB—ABDOMINAL GANGLION;
MEDLINE—87132918; PubMed=3816495;
Taussig R., Scheller R.H.;
Taussig R., Scheller R.H.;
Digit Expressing gene encodes sequences related to mammalian brain peptides ";
DNA 5:453-461(1986).
BNB: L29473; ABS59170.1;
InterPro: IPR002544; FARP.
Pfam; PF01581; FARP; 7.
                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 40; DB 2; Length 1031; 100.0%; Pred. No. 1.1e+02; iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06C6EB22D9F4AD40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3BCCB4421EE1B88E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE DNA POLYMERASE ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1031 AA; 115768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02231; PHP_N; 1.
Pfam; PF01336; tRNA_anti; 1.
SMART; SM00481; POLIIIAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
7
23
39
55
71
887
14697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AA;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RAARLGYR 8
                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuropeptide.
NON_TER
CHAIN
CHAIN
                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              016963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
Q16963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
         δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ettwiller L., Wayne J., Xu S.-Y.;
"Molecular cloning and characterization of a thermostable DNA polymerase from Thermomicrobium roseum: T. roseum DNA polymerase I possesses 3.5' exonuclease activity.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF050678; AAF24859.1;
HSSP; P00582; IRFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Bright N.A. M. S.-Y.; Butwiller L., Xu S.-Y.; Method for cloning and producing Thermomicrobium roseum DNA polymerase I in E.coli."; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Green non-sulfur bacteria; Chloroflexaceae group; Thermomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 917;
                                                                         Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00482; POLAC; 1.
E 917 AA; 103587 MW; 4A7E282F26197CBC CRC64;
         56211 MW; 8A5EF3761D466EAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 95;
); Mismatches
                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1031 AA.
                                                                            Score 40; DB 7
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                917 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002562; 3.5_exonuclease.
InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR002298; NDA_POII.
InterPro; IPR001099; DNA_POII.
InterPro; IPR001099; DNA_POIA.
InterPro; IPR003583; HHH.1.
InterPro; IPR003584; HHH.2.
INTERPRO; IPR003584; HHM.2.
I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  091502;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, DNA POLYMERASE I.
                                                                              50.0%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.v.
                                                         Ouery Match
Best Local Similarity 5b.2.
9; Conservative
                                                                                                                                                                                                     378 ARLGMRSLPVGRRAGR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                        3 ARLGYRXXRFGXRVGR 18
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00279; HhH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RAARLGYRXXRFGXR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermomicrobium roseum
                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00278;
                513
```

SEQUENCE

091502 RESULT 10 Q915Q2

g ò

E S E

SMART;

ö

Gaps

; 0

```
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             068139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9CCS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q9CCS8
SPR
                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=2151;
Eckstein T.W. Lambert M.L., Brennan P.J., Belisle J.T., Inamine J.M.;
Electrication of a gene cluster involved in glycopeptidolipid
blosynthesis and of a gene cluster encoding daunorubicin resistance in
two strains of Mycobacterium avium serovar 2.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC106182; AAC11696.1;
EMBL; ARC106182; AAC14266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EMRFAMIDE (FRAGMENT).
Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-87132918; PubMed-3816495; Taussig R., Scheller R.H.; "The Aplysia FMRFamide gene encodes sequences related to mammalian
                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Length 373;
                                                         Length 127;
                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-1151;
ECKSTein T.M., Silbaq F.S., Inamine I.M., Belisle J.T.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9A309C1514EA8276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE FRANSPOSASE.
                                                         .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB Pred. No. 53; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 AA
                                                   Score 39; DB Pred. No. 16; 0; Mismatches
                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 AA; 43453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brain peptides.";
DNA 5:453-461(1986).
EMBL; M14960; AAA27752.1;
InterPro; IPR002544; FARP.
Pfam; PF01581; FARP; 23.
                                                      48.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 REMREGKREMREGRSVG 345
                                                                                                                                                                         1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                  83 REMREGKREMREGRSVG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RAARLGYRXXRFGXRVG 17
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium avium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conservi
                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
068994
AC 068994, DT 01-AUG
DT 01-AUG
DT 01-JUN
DE PUTATIV
OC ACTINO
OC ACTINO
OC ACTINO
OC ACTINO
RN SEQUEN
RN SEQU
                                                                                                                                                                                                                                                                                                                            RESULT 12
016964
AC 016964
AC 016964
DT 01-NOV
DT 01-NOV
DT 01-JUN
OC APLYSI
OC APLYSI
OC APLYSI
OC APLYSI
COC APLYSI
COC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             068994
                                                                                                                                                                                                                                                                                                                                                                                     016964
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ö
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21128732; PubMed-11234002; MEDLINE-21128732; PubMed-11234002; Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruthers S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 21.3 KDA PROTEIN.
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                        ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                                                                                                                                       Length 415;
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
EMBL; AF143772; AAD44203.1; -.
InterPro; IPR001207; Transpo_mutator.
Pfam: PF00872; Transpo_mutator; 1.
SEQUENCE 415 AA; 45256 WW; 50FF161AA40CA891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AA; 45625 MW; B25B500D075716B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583918; CAC30022.1; -.
SEQUENCE 421 AA; 45625 WW; B25B500D075716B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 421 AA
                                                                                                                                                       DB
90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                        Mismatches
                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
STRAILNE-SB1003;
MEDLINE-97404404; PubMed-9256491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%;
                                                                                                                                                       47.5%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                     1 RAARLGYRXXRFGXRVG 17
                                                                                                                                                                                                                                                                                                      57 RAQRNGYRHRGLDTRVG 73
                                                                                                                                                       Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RANRLGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 RLAKSGYRCRRFADKI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
```

```
1;
                                                                                                                                                                                                                                 Gaps
Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003."; Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
EMBL: ARCHG229.1; --
Hypothetical protein.
SEQUENCE 194 AA; 21263 MW; 73F67C4F9F8A9677 CRC64;
                                                                                                                                                                                                                                 3;
                                                                                                                                                                                    Query Match

46.9%; Score 37.5; DB 2; Length 194;
Best Local Similarity 47.4%; Pred. No. 48;
Matches 9; Conservative 3; Mismatches 4; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 12, 2002, 12:38:39 Job time: 752 sec
                                                                                                                                                                                                                                                                                             |:|| ||: ||| ||:
147 RSARFYGLGWLLARFGARI 165
                                                                                                                                                                                                                                                                       1 RAAR---LGYRXXRFGXRV 16
                                                                                                                                                                                                                                                                                                            QQ
    RA
RT
RL
DR
SQ
                                                                                                                                                                                                                                                                          ŏ
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- protein search, using sw model OM protein February 12, 2002, 12:30:31; Run on:

Search time 242.57 Seconds (without alignments) 3.054 Million cell updates/sec

US-09-485-571-22 49 Title: Perfect score:

1 YRRRFSVSVR 10 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

sed DB DB Minimum I Maximum I

length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_1101:*

/SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:* :: !

| SIDS8/goddata/geneseq/geneseqp/AA1993.DAT:*
| SIDS8/goddata/geneseq/geneseqp/AA1994.DAT:*
| SIDS8/goddata/geneseq/geneseqp/AA1995.DAT:*
| SIDS8/gogdata/geneseqp/AA1996.DAT:*
| SIDS8/gogdata/geneseqp/AA1996.DAT:*
| SIDS8/gogdata/geneseqp/AA1999.DAT:*
| SIDS8/gogdata/geneseqp/AA1999.DAT:*
| SIDS8/gogdata/geneseqp/AA1999.DAT:*
| SIDS8/gogdata/geneseqp/AA1999.DAT:*
| SIDS8/gogdata/geneseqp/AA2000.DAT:*
| SIDS8/gogdata/geneseqp/AA2000.DAT:* 14: 115: 17: 19:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

Arabidopsis thalia Arabidopsis thalia Amino acid sequenc Soybean glutamyl+t Cyclic peptide of Protegrin derivati Peptide which may Protegrin derivati Protegrin derivati Human polypeptide Protegrin peptide Description AAW99409 AAW99411 AAR78776 AAY93616 AAX93616 AAX58075 AAG58075 AAG58074 AAG58074 AAG58074 Ωī DB Length Query 69.4 65.3 65.3 65.3 65.3 Score 440 334 334 334 44 34 34 34 34 10 9 8 7 8 9 3 1 1 Result . 9

Cyclic peptide of Cyclic peptide of Antimicrobial cycl Antimicrobial cycl Antimicrobial cycl Antimicrobial prot Cyclic peptide of Antimicrobial cycl	
AAW52513 AAW52517 AAX17324 AAX17320 AAW52516 AAW52516 AAW52567 AAW52567 AAW52540 AAW52540 AAW52537 AAX17343 AAX17344 AAX17343 AAX17323 AAX17323 AAX17323 AAX17323 AAX17323 AAX17323 AAX17323 AAX17333 AAX17333 AAX17333 AAX17333 AAX17333 AAX17333	AAW5250 AAY1731 AAW10815 AAB1063 AAB1063 AAB1063 AAB5245 AAB1063 AAB1063 AAY3679 AAX3679
13 19 19 19 19 19 19 19 19 19 19 19 19 19	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
$\begin{array}{c} \alpha \alpha$	
11111222222222222222222222222222222222	

## ALIGNMENTS

AAW99409 standard; peptide; 10 (first entry) 08-JUN-1999 AAW99409; AAW99409 

AA

Protegrin derivative peptide SM2194.

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.

Synthetic.

WO9907728-A2

18-FEB-1999

98WO-FR01757 06-AUG-1998; 97FR-0010297 12-AUG-1997;

(SYNT-) SYNT:EM SA

Kaczorek M; Grassy G, Chavanieu A, Calas B,

WPI; 1959-190034/16.

Derivatives of antibiotic peptides lacking disulfide bridges – used as carriers to deliver active agents into cells

~

ö

Gaps

.; 0

0; Indels

Length 15

DB 20; 0.063;

85.7%; Scc. 100.0%; Pred. No. v. 0; Mismatches

15 AA;

```
protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78776 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protegrin peptide sequence.
                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-075188/10.
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1993;
13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR78776;
                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                  ~
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR78776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
             XX
So
                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                     disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                      This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protegrin derivative peptide SM2193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99411 standard; peptide; 15 AA
Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW99411;
Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAW99411
\overset{\alpha}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

Kokryakov VN, Lehrer RL;

93US-0095769. 94US-0182483. 94US-0243879.

94WO-US08305 93US-0093926

(first entry)

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. porcine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino acid residues can be present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a specific example of the protegrin analogues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \int_{-\infty}^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides are disclosed which are designated "protegrins". The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.5%; Score 37; DB 16; 100.0%; Pred. No. 0.72; ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
```

```
The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence repersents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                         Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.5%; Score 37; DB 21; Length 18; 100.0%; Pred. No. 0.72; tive 0; Mismatches 0; Indels
                   Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                              Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM40747 standard; Protein; 196 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human pclypeptide SEQ ID NO 5678.
                                                                                                                                                                                                                                        99WO-FR02939.
                                                                                                                                                                                                                                                                              98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                              remsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                      (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RRF.FSVSV 9
                                                                                                                                                          WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1
                                                                                                                                                                                                                                                                              30-NOV-1.998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                    Jnident: fied.
                                                                                                                                                                                                                                          26-NOV-1.999;
                                                                                                                                                                                                  08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM40747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide antibiotics. Protegin antibiotics form part of the peptide antibiotics. Protegin antibiotics form part of the peptide by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and non-liver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                       Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide represents a linear derivative of the protegrin family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 20; Length 18;
; Pred. No. 0.72;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grassy G, Kaczorek M;
                                                                                                                                                                                                                                                                              Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.5%; Surevilence 100.0%; Previ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93616 standard; peptide; 18 AA.
                                                                                                                                                        AAW99403 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2000 (first entry)
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYNT-) SYNT: EM SA.
                                      18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RRRFSVSV 9
                RRRFSVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36-AUG-1998;
                                                                                                                                                                                                                                      08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1999.
```

Seguence

This

AAY93616;

AAY93616
ID AAY9
XX
AC AAY9
XX
DT 25-S

g

ð

Synthetic.

AAW99403;

AAW99403 RESULT

ö

ö

Gaps

٦, ٩٥ ٩, Tang YT,

Wang Zhao

```
990S-0128734
990S-0128714.
990S-0129845.
990S-0130077.
990S-0130449.
                                                                                                                                                                                                                                                990S-0130891.
990S-0131449.
990S-0132048.
990S-0132407.
                                                                                                                                                                                                                                                                                                                                               990S-0132863.
990S-0132863.
990S-0134256.
990S-0134218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0135124.
99US-0135353.
99US-0135629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0137222.
990S-0137528.
990S-0137502.
990S-0137724.
                                                                               990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0134221.
99US-0134370.
99US-0134768.
99US-0134941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0139452.
99US-0139453.
99US-0139492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139456.
99US-0139457.
99US-0139458.
99US-0139459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139763.
99US-0139817.
99US-0139899.
                                        2000EP-0301439
                                                                                                                                                     99US-0127462
                                                                                                                                                                                                                                                                                                                       99US-0132485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0136021.
99US-0136392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0136782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0138540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0139460,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139463.
99US-0139750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0138847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0140354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0140353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0140823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0141842
99US-0142154
                                        25-FEB-2000;
                                                                                                                                                                06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 - JUN - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7-JUN-
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system diseases, such as system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and c. N. S disorders.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                          Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries \boldsymbol{\cdot}
                                                                                                                                                                                                         Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 22; Length 196;
Pred. No. 35;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 74922.
                                                                                                                                                                                                       Qian XB,
Yang Y,
                                                                                                                                                                                                       Chen R, Ma Y, Xu C, Xue AJ, X, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 5678; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG58075 standard; Protein; 212 AA
                                                                                                                                                                                                    Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
                                               21-JAN-2000, 2000US-0488725.
25-APR-2000, 2000US-0552117.
09-UUL-2000; 2000US-059042.
19-JUL-2000, 2000US-0620312.
03-AUC-2000, 2000US-063450.
14-SEP-2000; 2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%;
illarity 66.7%;
Conservative
                                                                                                                                19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                        2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                           WPI; 2001-442253/47.
N-PSDB; AAI59903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRESVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::||||:||
72 fkrrfslsv
                     26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000
```

Sequence

δλ g AAG58075;

99US-0155139

```
990S - 0142055 . 990S - 0142055 . 990S - 0142390 . 990S - 0142390 . 990S - 01428390 . 990S - 0142920 . 990S - 0142920 . 990S - 0142920 . 990S - 0142927 . 990S - 0144332 . 990S - 0145919 . 990S - 0147302 . 990S - 0147303 . 990S - 0149319 . 990S - 0149338 . 990S - 0149328 . 990S - 0149328 . 990S - 0149323 . 990S - 0149328 . 990S - 0150S66 . 990S 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0151080.
99US-0151303.
99US-0151438.
99US-0151930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0153070
990S-0153758
990S-0154018.
990S-0154039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0152363
02-JUL-1999,
06-JUL-1999,
08-JUL-1999,
13-JUL-1999,
13-JUL-1999,
14-JUL-1999,
16-JUL-1999,
16-JUL-1999,
19-JUL-1999,
19-JUL-1999,
19-JUL-1999,
19-JUL-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02 - AUG - 1999;
03 - AUG - 1999;
04 - AUG - 1999;
05 - AUG - 1999;
06 - AUG - 1999;
06 - AUG - 1999;
09 - AUG - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999
27-AUG-1999
                                                                                                                                                                                                                                                                                                        21-JUL-1999
22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1999
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 74921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 2
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG58074 standard; Protein; 219 AA
             9905 - 0155486
9905 - 0155486
9905 - 0156596
9905 - 0156596
9905 - 0157753
9905 - 0157765
9905 - 0157865
9905 - 015823
9905 - 015823
9905 - 015929
9905 - 015929
9905 - 015929
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0160768.
990S-0160770.
990S-0160814.
99US-01609815.
99US-0160981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161404.
99US-0161405.
99US-0161406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0161359.
99US-0161360.
99US-0161361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.4%;
ilarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0121825
99US-0123180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 SEP - 1999
29 SEP - 1999
04 - 0CT - 1999
05 - 0CT - 1999
06 - 0CT - 1999
12 - 0CT - 1999
13 - 0CT - 1999
13 - 0CT - 1999
14 - 0CT - 1999
15 - 0CT - 1999
16 - 0CT - 1999
17 - 0CT - 1999
18 - 0CT - 1999
18 - 0CT - 1999
19 - 0CT - 1999
19 - 0CT - 1999
10 - 0CT - 1999
11 - 0CT - 1999
11 - 0CT - 1999
12 - 0CT - 1999
13 - 0CT - 1999
14 - 0CT - 1999
15 - 0CT - 1999
16 - 0CT - 1999
17 - 0CT - 1999
18 - 0CT - 1999
18 - 0CT - 1999
19 - 0CT - 1999
19 - 0CT - 1999
19 - 0CT - 1999
10 - 0CT - 1999
11 - 0CT - 1999
12 - 0CT - 1999
13 - 0CT - 1999
14 - 0CT - 1999
15 - 0CT - 1999
16 - 0CT - 1999
17 - 0CT - 1999
18 - 0CT - 1999
19 - 0CT - 1999
19 - 0CT - 1999
10 - 0CT - 1999
11 - 0CT - 1999
11
                                                                                                                                                                                                                                                                                                                                                                                                                       21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1.999;
05-MAR-1.999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG58074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
```

																								•																						
		2.4			0,0				-d+ 10°				 m m	.;		<u>.</u> .					~.	m 0			٠.		· ·				٠.		:		:			~: _:		<u>.</u> .	٠.	:_:			· · ·	
IS-0123548.	78	46	171	07	44	68	44	4.0	8 4	44	φ. 6 α	25	211	22	3/6	94	7 6	62	0 6	78.	22	525	72/	60	94.	11	4 5	49	457	45(	457	459	460	467	75(	763	68	354	69	991	287	154	390	803	977	542
123	126	127	128	130	130	130	131	132	132	132	132	134	134 134	134	134 134	134	135	135	136	136	137	137	137	138	138 138	139	139	139	139	139	139 139	139	139	139	139	98	139	140	140	140	141	142	142	142	142	143 143
0-0	0.5	0-0-	0-6	0.0	0-5	0-2	0-0	2-0	0-2	2-0	0-0	-0	0-0	0-0	0 0	0-8	0 0	0-9	0 0	-0	0	0 0	-0	0	0.0	-0	0	-0	00	0	00	9	90	0 0	0	0 0	0	9 9	0	99	0	9 9	99	9	500	9
060	90	D 10	100	2 5	90	90	90	90	90	90	90	56	D 0	06	9 5	90	90	90	0 0	90	90	90	90	90	35	90	בים	26	90	2		D	5 5	0 5	Ď.	0 0	0	2 5	0.5	2 2	0	Š	ÖÖ	0.5		9 6
000	עסע	σσ	0	ע ס	თი	עס ע	000	0	σσ	יסי	თ თ	, O	0 0	0,0	ע ע	0.0	א ס	0	ט ס	0	9	ס ס	9	თ ი	ע פע	000	עס עב	יסיי	ማ ଦ	0	ש פי	6	עס ע	σσ	Ó	ש פ	ó	עס עכ	6	20.00	0 0	ע ס	9 9	9.0	ט ס נ	ש מי
22.23		<u></u>					٠			٠,٠																										٠										
1999	200	566 6	666	900	966	999	666	666	666	900	666 666	999	6 6 6 6 6	666	9 6	666	9 0	666	200	999	666	7 7 7 7 7	966	666	999	999	200	99	000	666	999	660	90	666	66	200	66	200	999	200	660	99	99	99	900	99
								• • •								. , .					.,,		1 (-)		3	-		, — ,			7 (7				, ,								$\neg$		7 ~ ,	
9-MAR-	MAR	APF APF	APF	APF	APF	APF	APF	APF	MAY WAY	Ą	MAY VAY	ΑĀ	AA AA	WAY	ΨĀ	MAY	MAY WAY	MAY.	MAY V	Ψ¥	N I		Ĕ	N E				Į.		N		NO.			E N		N.		N	NO	N E	35	털털		35:	
23-	6	96-	8	၌ ရှ	-12	3 6	800	6	4.0	9	96-1	4	4 4	4		9.0	7	4	2 2	8-	Ξ,	5. 4 1. 1.	-	ر اع ق	56	4	وَا	-	6 6	6	ည်ထ	8	600	8	6	, i	2-	, w	4	9 9	0,	, ;; , ;;	9-1	800	י בי ל	. 4. 
○ (4 (	- 1.4		٠,٠	-	CA C	4 ( <b>4</b>	יאני	, (*)	<u> </u>	,	<u> </u>	, (-1 )			- <del></del>	Н.	v (V	CA (	40	4 (7)	J (	ے ر	0	- ب		Τ,			4 4		<del>-</del>	Н-				7 7	C) (	7 (7	<b>⊘</b> ·0	7 (7	m c	0	00	00	) H	
PR	X K	<u>بر</u> بر	8 0	¥ &	80.00	4 24	20.00	. K	8 c	<u>بر</u>	<u>د</u> د	2	<del>بر</del> بر	8 0	4 24	ĸ,	4 64	× 5	χg	i K	<del>بر</del> ز	×κ	ŭ	۳ ت	ĸκ	۳ i	Ŕĸ	ŭ,	ŭ ŭ	ă.	<b>κ κ</b>	ά ί	ξ <u>κ</u>	й й	ķί	ž ž	æ (	ŔŘ	άi	ĸά	œ ū	4 64	ŭ ŭ	ŭ,	4 24 4	ĸά
	4 14		<u>ш</u> г	- 14	щр	4 ()4	<u>ц</u>	1 111	ш п	, 124	<u>ы</u> р	141		14 D	4 14	14 [	4 14	ш, (	40	, 114	114 C	. 12.	124	ഥ	ı Dı	וא, ב	יים יי	D. (	ביים	щ	יי די	ביי ל	ц Д,	ու ո	ויםו	<u>ч</u> о	Ф.	יים יי	Д, С	<u>,</u>	ם ים	ц С.	д Д	<u>а</u>	יםי	υ. <b>С</b> .

15-JUL-1999; 99US-0144005.
16-JUL-1999; 99US-0144085.
16-JUL-1999; 99US-0144085.
19-JUL-1999; 99US-0144335.
19-JUL-1999; 99US-0144335.
19-JUL-1999; 99US-0144331.
19-JUL-1999; 99US-0144331.
19-JUL-1999; 99US-0144332.
20-JUL-1999; 99US-0144332.
22-JUL-1999; 99US-0144332.
23-JUL-1999; 99US-0144332.
23-JUL-1999; 99US-014591.
23-JUL-1999; 99US-014432.
23-JUL-1999; 99US-014591.
23-JUL-1999; 99US-0146386.
23-JUL-1999; 99US-0146386.
23-JUL-1999; 99US-01491.
23-JUL-1999; 99US-01591.
23-JUL-1999; 99

```
N-PSDB; AAZ46142.
                                                                                                                                                                                                                                     WO200006728-A2
       Modified-site
                         Modified-site
                                          Modified-site
                                                                            Modified-site
                                                                                              Modified-site
                                                                                                                Modified-site
                                                                                                                                  Modified-site
                                                                                                                                                    Modified-site
                                                                                                                                                                      Modified-site
                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                         Hillman JL,
Patterson C,
                                                                                                                                                                                                                                                                        28-JUL-1999;
                                                                                                                                                                                                                                                                                                                            19-NOV-1998;
22-DEC-1998;
12-JAN-1999;
12-JAN-1999;
                                                                                                                                                                                                                                                                                          28-JUL-1998
                                                                                                                                                                                                                                                                                                    14-SEP-1998
                                                                                                                                                                                                                                                                                                           14-OCT-1998
03-NOV-1998
                                                                                                                                                                                                                                                       10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                            Region
ö
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human phosphorylation effector PHSP-5.
                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; phosphorylation effector; PHSP; proliferative disorder;
Immune disorder; neuronal disorder.
                                                                                                                                                                                                                                                                                                  DB 21; Length 219; 40;
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note" "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note- "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note- "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note- "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note- "potential phosphorylation
                                                                                                                                                                                                                                                                                                  Score 34; DB 2
Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   AAY68773 standard; Protein; 474 AA.
                                                                                                                                                  99US-0160814.
99US-0160815.
99US-0160980.
99US-0160989.
99US-0161404.
                                                         990S-0159329.
990S-0159330.
990S-0159331.
990S-0159638.
990S-0159638.
                                                                                                              99US-0160741.
99US-0160767.
99US-0160768.
99US-0160770.
                                                                                                                                                                                                                                                                                                 Match 69.4%;
Local Similarity 87.5%;
les 7; Conservative
                                                                                                                                                                                                                                   99US-0161360.
                                                                                                                                                                                                                 99US-0161406
                                                                                                                                                                                                                            99US-0161359
                                                                                                                                                                                                                                                     99US-0161920
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                               2 RRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-2000
                                                                                                                                 1-OCT-1999;
1-OCT-1999;
                                                                                                                                                                     22-OCT-1999
                                                                                                                                                   -OCT-1999
                                                                                                                                                                                                                                   26-OCT-1999
26-OCT-1999
                                                                                                       18-OCT-1999
                                                                                                               -OCT-1999
                                                                                                                         -OCT-1999
                                                                                                                                                           -OCT-1999
                                                                                                                                                                                        22-OCT-1999
                                                                                                                                                                                                25-OCT-1999
                                                                                                                                                                                                         25-OCT-1999
                                                                                                                                                                                                                 25-OCT-1999
                                                                                                                                                                                                                           26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY68773;
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                         AAY 68773
```

g

õ

```
AMY68769-95 and AAY68797-99 represent human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing with increased PHSP expression/activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human phosphorylation effectors useful for the diagnosis, treatment and prevention of proliferative, immune and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;
Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                 note- "protein kinase family signature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 21; Length 474;
Pred. No. 90;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
'note= "potential phosphorylation site"
                                                        'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                            'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                       /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                'note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "potential phosphorylation site"
359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "potential phosphorylation site"
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "potential phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "potential phosphorylation site"
                                                                                                                                                                        note= "potential phosphorylation site"
                                                                                                                'note= "potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1: Page 83-84; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0152814.
98US-0173482.
98US-0106889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0113796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US17132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0109093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0123494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0229005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patterson C, Bandman O, A
Reddy R, Lu DAM, Shih LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.4
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-183125/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 AA;
```

1 YRRFFSVSV

QQ ò

10-AUG-2000

AAY94288;

Glycine max.

Soybean;

```
This sequence is an example of a cyclic peptides (I) of the invention, which has: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against E. coli, Pseudomonas aeruqinosa, methicilin-resistant Staphylococcus quireus (MRSA), vancomycin-resistant Enterococcus faecium and penicillin-resistant Streptococcus pneumoniae. More generally they are protozoa. Apart from clinical uses, (I) are also used as disinfectants protozoa. Apart from clinical uses, (I) are also used as disinfectants correstants for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protegrin type peptides), (I) and are more effective, (ii) better bioavailability and/or serum half-life (increased resistance to protecolysis). They are more sultable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                  Loop region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 19;
Pred. No. 4.9;
0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 155; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW52513 standard; peptide; 13 AA.
AAW52500 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclic peptide of the invention.
                                                                                                                         Cyclic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                 97WO-US12974.
                                                                                                                                                                                                                                                                                                                                                                                                         96US-0685589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1998 (first entry)
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J, . Gu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-120472/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 2 RRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 rrrfcvcvr
                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1997;
                                                                                                                                                                                                                                                                              WO9803192-A1
                                                                                                                                                                                                                                                                                                                                                                                                         24-JUL-1996;
                                                                                   01-JUL-1998
                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW52513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW52513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the soybean glutamyl-tRNA synthetase. This enzyme is an aminoacyl-tRNA synthetase (AARS). AARSs charge (acylate) specific tRNAS with amino acids for use in protein synthesis. Glutamyl-tRNA synthetase therefore charges an glutamyl-tRNA with glutamate. Since this enzyme has a crucial role in protein synthesis and therefore life, any agent that inhibits or disrupts protein synthesis is likely to be toxic. The present sequence could therefore be used as a basis for testing whether the encoded aminoacyl-tRNA synthetase is sensitive to known inhibitors or other chemicals and hence could be used in the discovery of potential herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                           glutamyl-tRNA synthetase; aminoacyl-tRNA synthetase;
rbicide; plant toxin; protein synthesis inhibition; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide encoding plant aminoacyl-tRNA synthase and the encoded polypeptide, useful e.g. for regulating gene expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 21; Length 94;
Pred. No. 25;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by TCCA"
                                                                                                                                                                                                                                                                                    Soybean glutamyl-tRNA synthetase # 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E I. (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Scor
100.0%; Prev
0; )
                                                                                                                                                      AAY94288 standard; Protein; 94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 42; Page 71; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US26478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107789
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.3
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                 AARS; herbicide; plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Famodu 00, Simmons C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-387421/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 83
                             ::||||:||
9 fkrrfslsv 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA27419.
      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RRRFSVS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||
2 rrrfsvs 8
```

WO200028057-A2

09-NOV-1999; 10-NOV-1998;

AAY94288

XXX
AAXA
AAXA
AAXA
AAXA
AAXA
AAXA
XXX
XX
XXX

18-MAY-2000

ö

Gaps

0;

Indels

Sequence

RESULT 11 AAW52500

q ŏ

٢

```
Synthetic
                                                                                                                                                                                                                                                                                                         analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY17324;
                                                                                                                                                                                                Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17324
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which has: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at thy sloop dral pti and (c) at least one basic aminon acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against E. coli, Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faccium and penicillin-resistant Streptococcus pneumoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and proservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachpolesin and protegrin type peptides), (I) and are more effective, with better bloavailability and/or serum half-life (increased resistance to protecolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
           cyclic peptide; antimicrobial; disinfectant; therapy; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loop region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is an example of a cyclic peptides (I) of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                  /note= "Cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No. 4
                                                                          Location/Qualifiers
13
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 155; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW52517 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclic peptide of the invention.
                                                                                                                                                                                                                                                                       (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%;
                                                                                                                                                                                                             97WO-US12974.
                                                                                                                                                                                                                                         96US-0685589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 77.0
Tr Conservative
                                                                                                                                                                                                                                                                                                    Chen J, Gu L;
                                                                                                                                                                                                                                                                                                                                  WPI; 1998-120472/11.
              cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
            Loop region; opreservative;
                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1998
                                                                                                                                                WO9803192-A1
                                                                                                                                                                                                             23-JUL-1997;
                                                                                                                                                                                                                                         24-JUL-1996;
                                                                                                                                                                              29-JAN-1998
                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                              analogues
                                                                                                                                                                                                                                                                                                     Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

ò g 

```
which has: (a) an amplipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological ph; and (c) at least one basic amino acid (aa) in LR or TR. (i) are broad spectrum antimicrobials, specifically for use against E. coli, Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faecium and penicillin-resistant Streptococcus penicillin-resistant Streptococcus penicillin-resistant Streptococcus penicillin-resistant streptococcus active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from Cilnical uses, (1) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (1.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tachyplesin and protegrin type peptides), (I) and are more effective, with better bloavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is an example of a cyclic peptides (I) of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           blocidal bacteria; yeast; Candida species; fungi; protozoa; Escherichia coli; Pseudomonas aeruqinosa; infection; preservative; vancomyclin-resistant Entercoccus faecium; disinfectant; food; methicillin-resistant Straphylococcus aureus; medical equipment; penicillin-resistant Straptococcus pneumoniae; cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial cyclic peptide SEQ ID NO:171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 155; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY17324 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                   (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
                                                                                                                                                                                                                               97WO-US12974.
                                                                                                                                                                                                                                                                                                       96US-0685589,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-120472/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 rrrfcvcvr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                       W09803192-A1.
                                                                                                                                                                                                                           23-JUL-1997;
                                                                                                                                                   29-JAN-1998
Synthetic.
```

INTR-) INTRABIOTICS PHARM INC

Gu L;

Chang C, Chen J,

97WO-US19557. 97WO-US19557

27-OCT-1997; 27-OCT-1997;

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vancomycin-resistant Entercocous faccium, methicillin-resistant staphylococus aureus and penicillin-resistant Straphylococus aureus and penicillin-resistant Straphylococcus aureus and penicillin-resistant Straphococcus aureus and penicillin-resistant Straphococcus pneumoniae. (A) are used to tract or prevent infections, in animals or plants, also as preservatives and disinfectants for medical equipment, foods, cosmetics, optionally as mixtures or in combination with other antimicrobials. Compensated with linear analogues, (I) are more effective with better bloavailability and/or serum half-life (better resistance to proteolysis, allowing lower doses and making them more suitable for oral delivery). Since (I) are structurally related to naturally occurring antimicrobial peptides, they are less likely to induce development of resistant strains.
                                                                                                                                                                                                                                                                                                                                   The present invention describes cyclic peptides (I): (i) comprising an amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C): (ii) having net positive charge at physiological pH; and (III) including at least one basic amino acid (aa) in (B) or (C). AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum antimicrobials (biostatic or biooidal), effective against bacteria, yeast (e.g. Candida species), fungi and protozoa. Particularly they are used to control Escherichia coli, pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biocidal; bacteria; yeast; Candida species; fungi; protozoa; biocidal; bacteria; yeast; Candida species; fungi; protozoa; Escherichia coli; Pseudomonas aeruginosa; infection; preservative; wancomyclin-resistant Entercoccus faecium; disinfectant; food; methicillin-resistant Staphylococcus aureus; medical equipment; penicillin-resistant Streptococcus pneumoniae; cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
                                                                                                                                                                                                                                                         Antimicrobial cyclic peptides with amphiphilic beta-sheet region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 20; Length 13;
Pred. No. 4.9;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial cyclic peptide SEQ ID NO:154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY17307 standard; Peptide; 13 AA
                                                                                                                                                                                                                                                                                                    Claim 11; Page 157; 167pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                 (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.3%;
77.8%;
                                                                       97WO-US19557.
                                                                                                              97WO-US19557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                        Chang C, Chen J, Gu L;
                                                                                                                                                                                                                             WPI; 1999-312941/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1999
                                                                         27-OCT-1997;
                                                                                                              27-OCT-1997;
W09921879-A1
                                    06-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY17307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

06-MAY-1999

Synthetic.

```
The present invention describes cyclic peptides (I): (i) comprising an camphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C); (ii) having net positive charge at physiological pH; cand (iii) including at least one basic amino acid (aa) in (B) or (C). (AAY09554 to AAY09683 and AAY1301 to AAY17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum artimicrobials (biostatic or biocidal), effective against bacteria, artimicrobials (biostatic or biocidal), effective against bacteria, cantimicrobials (biostatic or biocidal), effective against bacteria, are used to control Escherichia coli, Pseudomonas aeruginosa, are used to control Escherichia coli, Pseudomonas aeruginosa, are used to control acid terresistant Streptococcus (C) phants, also as preservatives and disinfectants for medical equipment, phants, also as preservatives and disinfectants for medical equipment, consmetter, or proteolysis, allowing lower doses and making them more suitable for coral delivery). Since (I) are structurally related to naturally coccurring antimicrobial peptides, they are less likely to induce corrections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                               Antimicrobial cyclic peptides with amphiphilic beta-sheet region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 20; Length 13; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 12, 2002, 12:30:32 Job time: 365 sec
                                                                                                                                                                                                                         Claim 11; Page 156; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 77.0.
77. Conservative
                                                                                                                                                    WPI; 1999-312941/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| | |||
4 rrrfcvcvr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dp
```

		and the second s		\$ 1 - 12		· · · · · · · · · · · · · · · · · · ·	7	
	₽.							
		· · · · · · · · · · · · · · · · · · ·			-			
		e de la companya de	•	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				
i kupa	· · · · · · · · · · · · · · · · · · ·						<b>&amp;</b>	,
Į.		•		4.				
	· ·							
	*						en e	
	in A. San Angelon An						•	
							**	
	,					and the second s	·	
					en e			
K.								
				1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1				
				S.				
				A year				
				\$		• • • • • • • • • • • • • • • • • • •		
			•	**************************************				
	the second of th							· •
	The second secon							
	*	, A		at ?				
			•					
C.								
3		•		**************************************			1.4. 4.	
		1					en e	À.
				. Y				
				•				.7
			•					
					•		A.	
24						* · · · · · · · · · · · · · · · · · · ·		
		*					Type of the second seco	
Ċ					e e e e e e e e e e e e e e e e e e e	* · · · · · · · · · · · · · · · · · · ·		
						· · · · · · · · · · · · · · · · · · ·		B .
	¥.	e a tradición de la companya de la c						
Ç.			- 142 - 142 - 142	*				· .
				w.				

```
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRRFSVSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRFFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLCGY:
US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-182-483A-28
6
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28, Appl
48, Appl
48, Appl
154, App
117, App
170, App
190, App
190, App
191, App
194, App
222, App
58, Appl
6, Appl
6, Appl
6, Appl
6, Appl
6, Appl
722, Appl
722, Appl
722, Appl
722, Appl
722, Appl
723, Appl
724, Appl
725, Appl
726, Appl
727, App
                                                                                                                                                                                  (without alignments)
2.121 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                         February 12, 2002, 12:32:23; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcatus_comB.pep:*
                                          Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-182-483A-28
US-08-243-879A-27
US-08-1499-523-48
US-08-165-589A-154
US-08-685-589A-171
US-08-685-589A-171
US-08-685-589A-191
US-08-685-589A-191
US-08-685-589A-191
US-08-685-589A-191
US-08-685-589A-191
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-685-589A-158
US-08-487-753-2
US-08-487-753-2
US-08-487-753-2
US-08-487-753-2
US-08-487-753-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-629-291A-33
US-08-658-335B-33
US-08-751-152A-2
US-08-752-852A-57
US-08-752-852A-59
US-08-752-852A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA:*
                                                                                                                                                                                                                                             US-09-485-571-22
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                   1 YRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                            protein
                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٠
9
```

```
ö
Sequence 230, Assequence 63, Assequence 65, Assequence 72, Assequence 72, Assequence 193, Asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                 Sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: USA
ZIP: 20006-1812
COMPUTER: USA
ZIP: 20006-1812
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29.959
REFERRINCE/DOCKET NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STORMS
TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & POERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                      US-08-752-852A-92
US-08-752-853-24
US-08-499-523-63
US-08-499-523-65
US-08-499-523-67
US-08-752-852A-86
US-09-128-345-63
US-09-128-345-63
US-09-128-345-67
US-09-128-344A-193
US-09-128-343-44
US-09-232-191-4
US-09-232-191-4
US-09-232-191-4
US-09-232-191-4
US-09-232-191-4
US-09-232-191-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARNIG, SYLVIA S.L.
ATTLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/08182483A patent No. 5693486 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.5%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
```

```
Score 37; DB 1; Length 18;
Pred. No. 0.59;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                          ACTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.24
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEEA: 90-4030
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONS LLP
STREET: 1155 AVENUE of the Americas
CITY:
    .... V
....ER: US/08/499,523
07-JUL-1995
NN: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-128-345-48; Sequence 48, Application US/09128345; Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                75.5%; Scc...
100.0%; Pre
0; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura, A.
REGISTRATION NUMBER: 30,70
REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.5
Best Local Similarity 100.
Matches 8; Conservative
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RRRFSVSV 9
                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-128-345-48
                                                                                                                                                                                                                                                                                                                                                                                      US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37; DB 1; Length 18; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                         CITI.
COUNTRY: USA
ZIP: 2006-1812
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
TING DATE: 17-MAY 1994
TILING DATE: 17-MAY 1994
TILING DATE: 17-MAY 1994
                                                                               Sequence 27. Application US/08243879A
Sequence 27. Application US/08243879A
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFREENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAS: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.5%; Sur-
100.0%; Pre
0; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08499523 Patent No. 5804558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.5
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Zuvo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 RRRFSVSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-08-243-879A-27
                                                                       US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
```

ó

Gaps

ó;

ô q

```
; OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"
US-08-685-589A-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08685589A
Setent No. 5916872
GENEMAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
Sequence 167, Application US/08685589A
Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIJU TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, version #1.30
CURREN? APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 2;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1.13
OTHER INFORMATION: /product= "Cyclic"
                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
TELER: 66141
INFORMATION FOR SEQ ID NO: 167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRAMDEDNESS: unk
                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-685-589A-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                 ;
                   Query Match 75.5%; Score 37; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 0.59; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 2; Length 13;
Pred. No. 3.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                        Sequence 154, Application US/08685589A

Sequence 154, Application US/08685589A

Batent No. 5916872

GENERAL INFORMATION:

APPLICANT: Chang, Conway

APPLICANT: Chan, Jie

TILLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TILLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE S: 222

CORRESPONDENCE Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING APPLICATION NUMBER:
FILING APPLICATION NUMBER:

ATONINEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-96-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: /product= "Cyclic" (US-08-685-589A-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1111 | 11
4 RRRECVCVR 12
                                                                                                                                2 RRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6.
US-08-685-589A-167
                                                                                                                                                                                                                                  US-08-685-589A-154
```

ö

Gaps

ö

õ a

```
; OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"
US-08-685-589A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-685-589A-190

Sequence 190, Application US/08685589A

Sequence 190, Application US/08685589A

Sequence 190, Application US/0868589A

PATENTY Chang, Conway

APPLICANT: Chang, Leo

APPLICANT: Chen, Jie

TITLE OF INVENTION: SPECTRUM ANIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GONDUTER: IBM PC compatible
OPERATING SYSTEM: PC C-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 2;
Pred. No. 3.8;
); Mismatches
                                                                                                                                                                                             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-999
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..14
OTHER INFORMATION: /product= "Cyclic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                     TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%;
77.8%;
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site LOCATION: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 14 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-JUL-CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
                                                                    FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RRRFCVCVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%; Score 32; DB 2; Length 13; 77.8%; Pred. No. 3.5; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AESON 170

Sequence 170, Application US/08685589A

Sequence 170, Application US/08685589A

Patent No. 5916872

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Conway

APPLICANT: Chang, Conway

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:
ADDRESSEE: Penniae & Edmonds LLP

STREET: 1155 Avenue of the Americas
                                                                                                                                                                          COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Date PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION: DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8067-026-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1.13
OTHER INFORMATION: /product= "Cyclic"
                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COCUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFRERNCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 171:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: unknown
TOPOLOGY: circular
MOLECULE TYPE: peptide
                                 CORRESPONDENCE ADDRESS:
           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 RRRECVCVR 12
                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-685-589A-171
                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

0; Gaps

0; Gaps

```
Score 32; DB 2; Length 14;
Pred. No. 3.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 14; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Loo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER FOLDAY

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,589A

FILING DATE: 24-JUL-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8067-026-999
                                                                   LOCATION: 1.14
COTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP STREEF: 1155 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-685-589A-194
; Sequence 194, Application US/08685589A
; Patent No. 5916872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUTA
REGISTRATION NUMBER: 30,742
REFERSANCE/DOCKET NUMBER: 8067-
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-790-9090
TELEFAX: 212-869-9741
INFORMATION FOR SEQ ID NO: 194:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                               65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
                                                                                                                                                            Query Match
Best Local Similarity 77.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 amino acids
 STRA.NDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: unknown
                    TOPCLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                        4 RRECVCVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNT RY:
                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 2; Length 14;
Pred. No. 3.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 191, Application US/0868589A

Patent No. 5916872

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gu, Leo
APPLICANT: Gu, Leo
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 1007
                                                    8067-026-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8067-026-999
                                                                                                                                                                                                                                                                                    .. NAME/KEY: Peptide
.. LOCATION: 1..14
... OTHER INFORMATION: /product= "Cyclic"
US-08-685-589A-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COCUZZI, LAUKA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141
INFORMATION FOR SEO ID NO: 191:
SEQUENCE CHARACTERISTICS:
ELENGTH: 14 annino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
77.8%;
                                                                                                 TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8.
                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-685-589A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
Query Match 63.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA ZIP: 07068 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                          CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RRRECVCIR 12
                                                                                                                                                                                                   usa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-599-171A-26
                                                                                                                                                                                                               10036
                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
ö
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 2; Length 14;
Pred. No. 3.8;
0; Mismatches 2; Indels
                                                                                                                                                      Sequence 222, Application US/08685589A

Sequence 222, Application US/0868589A

Patent No. 5916872

GENERAL INFORMATION:

APPLICANT: Chang, Conway

APPLICANT: Gu, Leo

TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: TBM PC COMPALIBLE
COMPUTER: TBM PC COMPALIBLE
COMPUTER: TBM PC COMPALIBLE
COMPUTER: TBM PC COMPALIBLE
COMPARE: PATCHIN PC POSYMS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
   2;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /product= "Cyclic" (US-08-685-589A-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8067-026-999
                                                                                                                                                                                                                                                                                                                                                      E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 158, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222:
   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.3
Best Local Similarity 77.8
Matches 7; Conservative
     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York COUNTRY: USA ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRRFSVSVR 10
                                         2 RRRFSVSVR 10
                                                                    4 RRRECVCVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-685-589A-158
                                                                                                                                                        US-08-685-589A-222
                                                                                                                                                                                                                                                                                                                                                                            STREET:
       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                g
                                               ò
```

```
APPLICANT: Chang, CONWAY
APPLICANT: Chang, CONWAY
APPLICANT: Cide, Ide
APPLICANT: Chan
APPLICANT: Chan
APPLICANT: Chan
APPLICANT: Chan
APPLICANT: Chan
APPLICANTON APPLICANTON APPLICANTON
APPLICANTON APPLICANTON
APPLICANTON APPLICANTON
APPLICANTON APPLICANTON
APPLICANTON APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
APPLICANTON
```

```
Search completed: February 12, 2002, 12:32:23 Job time: 451 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15

US-08-646-590B-26

Sequence 26, Application US/08646590B

Patent No. 596283

GENERAL INFORMATION:
APPLICANT: Warren, Patrick V.
APPLICANT: Warnson, Ronald V.
TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish-& Richardson, P.C.
STRRET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: OB-MAY-1996
CLASSIFICATION NUMBER: US/08/646,590B
FILING DATE: 08-MAY-1996
CLASSIFICATION NUMBER: PCT/US97/01094
FILING DATE: O9-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 109-FEB-1996
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 109-FEB-1996
APPLICATION NUMBER: PCT/US97/01094
FILING DATE: 109-FEB-1996
ATTORNEY/AGENT INFORMATION:
AMARE: Haile, Ph.D., Lisa A.
RESTERRENCE/DOCKET NUMBER: 09010/017001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.3%; Score 31; DB 2; Length 373; Best Local Similarity 55.6%; Pred. No. 1.6e+02; Matches 5; Conservative 3; Mismatches 1; Indels
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,171A
FILING DATE: CONCURRENTLY
APPLICATION NUMBER:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: HERRON, CHARLES J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 311400-38
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-599-171A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
Gaps
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                Length 373;
                                                                                                                                                                                                                              Score 31; DB 2; Length 373
Pred. No. 1.6e+02;
3; Mismatches 1; Indels
TELECOMMUNICATION INFORMATION:
TELESTONE: 619/678-5070
TELESTAX: 619/678-5099
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGHH: 373 antho acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-646-5908-26
                                                                                                                                                                                                                                63.3%;
                                                                                                                                                                                                                            Query Match 63.3'
Best Local Similarity 55.6'
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                        73 YRKKYSVEV 81
                                                                                                                                                                                                                                                                                                  1 YRRFSVSV 9
```

```
February 12, 2002, 12:34:38; Search time 126.85 Seconds (without alignments) 6.005 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                    219241
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                        US-09-485-571-22
49
1 YRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                    Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	etical p			probable toxin tra	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	transcription regu		hypothetical prote		hypothetical prote				hypothetical prote			aspartate aminotra	butyrophilin homol	hypothetical prote		hypothetical prote		glucose-6-phosphat	hypothetical prote		potassium channel
SUMMARIES	QI		Q2BPP4	A46458	A83127	T27376	T38430	T00547	D82876	F82380	S43540	S38191	B69343	T19552	T33956	T22726	QQBEB4	T46928	D65025	G85892	н83766	T09058	T24578	C84709	T33004	B83530	S54720	T15448	T17262	T13807
	80	7	-	7	7	7	7	~	~	7	~	7	~	7	7	~	П	7	ч	7	~	7	~	~	~	~	<del>, ,</del>	~	7	~
	Query Match Length DB		151	211	719	896	965	328	146	287	385	385	249	1188	146	167	325	344	353	353	385	391	395	415	419	450	511	558	633	1001
ď	Query Match	79.6	9.64	ω.	73.5	Э.	73.5	71.4	69.4	69.4	69.4	69.4	67.3	67.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3			65.3	
	Score	٣	39		36		36	35	34	34	34	34	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.		7	М		S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

30 32 65.3 1156 2 723308 31 32 65.3 1556 2 553933 32 65.3 1556 2 553933 33 31 63.3 107 2 H87729 34 31 63.3 107 2 H87729 35 31 63.3 107 2 H87729 36 31 63.3 107 2 H87729 37 31 63.3 10.2 166429 38 31 63.3 13.4 2 686890 41 31 63.3 345 2 686890 42 31 63.3 345 2 686890 43 13 63.3 345 2 686980 44 31 63.3 345 2 686980 44 31 63.3 345 2 666023 44 31 63.3 345 2 666023 44 31 63.3 345 2 666023 44 31 63.3 345 2 666023 44 31 63.3 345 2 666023 45 80 3 3 10.3 10.0 10.0 10.0 10.0 10.0 10.0	hypothetical prote probable membrane probable phosphati hypothetical prote monooxygenase homo lipoprotein-34 [im lipoprotein-34 pre probable aspartate probable aspartate probable peptide c hypothetical prote	ALIGNMENTS  hi-R73  sion 24-Jul-1992 #text_change 20-Sep-1999  ment with a P4-like cryptic prophage (retronphage 1286203  hypothetical 17.7K protein  Score 39; DB 2; Length 113;  Pred. No. 1;  Mismatches 1; Indels 0; Gaps 0;	phage P4 protein; ORF151 protein n 30-Jun-1989 #text_change 10-Sep-1999 4 ssential region of bacteriophage P4. 2840 , G.E.; Dale, E.C.; Deho, G.; Finkel, S.; Flen cteriophage P4. 1913
251 1111 11111 111111111111111111111111	723308 559393 740577 1405025 172602 772668 739699 785890 785890 785890 785890 785890 785890 785890 785890 785890 785890 785890	ALIG phi-R73 ision 2 lement w 9128620 hypoth hypoth Pred. 2; Miss	11te ph 7.7K pr 1sion 3 1984 he esse 8506284 8506284 6 pozte e bacte 90221911
251 1111 11111 111111111111111111111111		age _rev roel UID: 0%;	atel aal 1 cev of t uld: chrij uld: i NI
30 32 65.3 31 32 65.3 32 31 65.3 33 31 65.3 33 31 65.3 34 31 63.3 35 31 63.3 36 31 63.3 37 31 63.3 38 31 63.3 39 31 63.3 44 31 63.3 44 31 63.3 44 31 63.3 44 31 63.3 44 31 63.3 44 31 63.3 44 31 63.3 45 Accession: Ad1830 A; Residues: The mames: hypothetical protein of the prote	1156 2337 107 107 109 109 109 133 333 345 426 426 662	51 - ph 73 equence. Inouye 1-4181, f a ret 2465; M > M64113 te phag	
30 32 32 32 32 32 32 32 32 32 33 33 33 33		ein 1 1901 + 8 130	SVR 1
RESULT A41830 33 33 33 33 33 33 33 33 33 33 33 33 33	333333333333333333333333333333333333333	l tical prot es: phage 24-Jul-19 32-Jul-19 3-Jul-19 3-Jul-19 5-Jul-17 5-Jul-17 5-Jul-17 5-Jul-17 5-Jul-17 8-Jul-17 8-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul-17 9-Jul	1 YRRRFSV    :  :       :  :     2   2   2   2   2   2   2   3   3   3   3   3   3   3   3   3   3
	, , , , , , , , , , , , , , , , , , ,	RESULT A41830 hypothe (); Spothe (); Cate: (); Date: (); Access R; Sun, J; Bact, A; Refire A; Refire A; Refire A; Resid	Db D

QQ

ò

```
A Map position: 5
A; Introns: 21/3; 54/3; 115/3; 163/2; 189/3; 223/2; 273/1; 325/1; 642/2; 674/3; 783/1.
C; Superfamily: squid 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-ph
osphodiesterase domain Y homology
F;306-467/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain XI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein At2g39370 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F12L6.3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00547; E848H6
ER:Rounsley, S.D.; Lih, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T38430
R; Oliver, K; Harris, D; Barrell, B.G; Rajandream, M.A.; Wood, V.
Submitted to the RMEL Data Library, September 1997
A; Reference number: Z21748
A; Reference number: Z21748
A; Reference number: Z21748
A; Reference number: Z21748
A; Residues: T38430
A; Residues: T38430
A; Residues: L965 < OLI>A; Residues: L965 < OLI>A; Reperences: EMBL: Z39126; PIDN: CAB16196.1; GSPDB: GN00066; SPDB: SPAC26H5.11
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-896 <WIL>
A;Cross-references: EMBL:AL032663; PIDN:CAA21765.1; GSPDB:GN00023; CESP:Y75B12B.6
A;Experimental source: clone Y75B12B
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPAC26H5.11 - fission yeast (Schizosaccharomyces pombe)
                                                                                                  hypothetical protein Y75B12B.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T27376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 32;
5; Mismatches (
                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1998
A;Reference number: 220360
A;Accession: T27376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB
Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.5
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.5
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| |||:|
689 FRRRSSVSIR 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SPDB:SPAC26H5.11
A;Map position: 1
A;Introns: 938/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|:|:|:
847 YRKRYSISLK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: Y75B12B.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A46458

human CR1 homolog CRRP - guinea pig
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Date: 18-Unr.1993 #sequence_revision 18-Nov-1994 #text_change 07-Jul-1995
C; Accession: A46458
R; Moorer Jr., F. D.
J. Immunol. 147, 3615-3622, 1991
A; Title: CRRP: a guinea pig protein, identified by sequence homology to human CR1, which A; Reference number: A46458; MUID:92043737
A; Accession: A46458
A; Status: preliminary
A; Mocession: A46458
A; Status: preliminary
A; Mocession: A46458
A; Status: preliminary
A; Mocession: A66458
A; Status: preliminary
A; Mote: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:63906, NCBIP:63908)
C; Superfamily: complement factor H repeat homology <FH22>
F; 117-174/Domain: complement factor H repeat homology <FH22>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A83127
R.Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br andman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.D.; Warrener, P.; Hickey, M.J.; Br andman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.D.; Warrener, P.; Hickey, M.J.; Br andman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.D.; Warrener, P.; Hickey, M.J.; Br andman, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Ffitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon, A.Ffitle: Preliminary
A.Accession: A83127
A.A
                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain PAO1 C; Seperimental source: strain PAO1 C; Seperities: C; Seperities: A; Gene: PAA143 C; Superfamily: hemolysin secretion protein B; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%; Score 36; DB 2; Length 211; 75.0%; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%; Score 36; DB 2; Length 719; 77.8%; Pred. No. 24; Live 2; Mismatches 0; Indels
                                                                                                              Length 151;
                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
C; Superfamily: satellite phage P4 hypothetical 17.7K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                          Score 39; DB 1;
Pred. No. 1.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                          Query Match 79.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 77.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                     1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                |||:||: ||
45 YRRKFSILVR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRRFSVSLK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||||||:
91 YRRRFSIT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRRFESVS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

Dp

ò

ò qq

ö

Gaps

; 0

ö

Gaps ö

```
C;Species: Saccharomyces sp.
C;Date: 06:Sep-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Date: 06:Sep-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S43540
R;Adjiri, A ; Chanet, R.; Mezard, C.; Fabre, F.
Yeast 10, 309-317, 1994
A;Title: Sequence comparison of the ARG4 chromosomal regions from the two related y A;Reference number: S43538; MUID:94287708
A;Reference number: S43540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N'Alternate names: hypothetical protein YSC83
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Actesion: S38191, S46789; S30764
R;Rocco, V.; Daly, M.J.; Matre, V.; Lichten, M.; Nicolas, A.
Yeast, 9, 111-1120, 1193
A;Title: Identification of two divergently transcribed genes centromere-proximal to
                                                                                                                                                                                                                   A;Cross-references: GB:AE004433; GB:AE003853; NID:g9658519; PIDN:AAF96967.1; GSPDB:A;Experimental source: serogroup O1; strain N16961; biotype El Tor C;Genetics: A;Gene: VCA1074
A; Reference number: A82035; MUID:20406833
A; Reference number: A82035; MUID:20406833
A; Accession: F82380
A; Status: Freliminary
A; Molecute type: DNA
A; Residues: 1-287 < HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-385 <ROC>
A;Cross-references: EMBL:L06795; NID:g170952; PIDN:AAA56989.1; PID:g170953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2; Length 287;
Pred. No. 25;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YHR017w – yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-385 <AbJ>
A;Cross-references: EMBL:X73886; NID:g471338; PID:g471341
A;Note: the source is designated as Saccharomyces douglasii
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted to the EMBL Data Library, June 1994
A; Description: The sequence of S. cerevisiae cosmid L2825.
A; Reference number: $46774
A; Accession: $46789
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSD83 protein - yeast (Saccharomyces sp.)
                                                                                                                                                                                                                                                                                                                                                                                                               69.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 YRREFTVYI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:|||| |:
279 YKRRFSSSI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRREFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S38191
                                                                                                                                                                                                                                                                                                                                   A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: YSD83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Du, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S43540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
        A; Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.
A; Reference number: 214168
A; Accession: T00547
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-328 <ROU>
A; Residues: 1-328 <ROU>
A; Cloudie type: DNA
A; Residues: 1-328 <ROU>
A; Cloudies: 1-328 <ROU>
A; Cloudies: 1-328 <ROU>
A; Cloudies: 1-328 <ROU>
A; Cloudies: 1-328 <ROU>
A; Residues: 1-328 <ROU>
A; Roo, H; Moffat, K.S; Cronin, L.A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.;
A; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487
A; Residues: 1-328 <CSTO>
A; Coene: T12L6.3; At2939370
A; Coene: T12L6.3; At2939370
A; Map position: 2
C; Superfamily: Arabidopsis thaliana hypothetical protein At2939370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dypothetical protein UU563 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Accession: B8-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B8-2876
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, Pebruary 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Description: D8-2876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 cGLA>
A;Residues: 1-146 cGLA>
A;Cross-references: GB:AEC02154; GB:AF222894; NID:g6899557; PIDN:AAF30976.1; GSPDB:GN001
A;Coss-references: Serovar 3; biovar 1
C;Genetics:
A;Genetics:
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82380
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transcription regulator AraC/XylS family VCA1074 [imported] - Vibrio cholerae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Length 146;
Pred. No. 13;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2; Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.4
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 69.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| ||||:|
232 HRRSFSVSMR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||::| :|
70 YRREWAVKLR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F82380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

σ

1 YRRRFSVSV

Qγ

```
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Fesidues: 1-146 < SMI>
A.Gresidues: 1-146 < SMI>
A.Gross-references: EMBL: AF125954; PIDN: AAD14706.1; GSPDB:GN00023; CESP:Cl3B7.4
A.Experimental source: strain Bristol N2; clone Cl3B7
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F55C9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Deate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22726
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219605
A;Reference number: 22726
A;Accession: T22726
A;Accession
                                                                                                                                                                                                  hypothetical protein C13B7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33956
R;Smith, A; WamsLey, P; Hawkins, M.
R;Smith, A; WamsLey, P; Hawkins, M.
Submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid C13B7.
A;Reference number: 221445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 32/2; 75/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F55C9.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB : Pred. No. 37; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%; Score 32; DB 70.0%; Pred. No. 33; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 12, 2002, 12:34:39 Job time: 557 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 65.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::| :|
93 FRRYNVELR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRRRFSVSVR 10
                       :|||| :||
1110 FRRRFGLSV 1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 YRRRLMSSVR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: CESP:C13B7.4
A, Map position: 5
A, Introns: 64/2; 96/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP:F55C9.3
                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                      pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein AF0746 - Archaeoglobus fulgidus
c) species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: D5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C; Accession: B69343
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A; Reference number: A69250; MUID:98049343
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 12-49 <KLE>
A; Residues: 12-49 <KLE>
A; Residues: 12-49 <KLE>
A; Residues: 12-49 <KLE>
A; Cross-references: GB:AE001053; GB:AE000782; NID:92689376; PIDN:AAB90493.1; PID:9264986
C; Superfamily: conserved hypothetical protein MJ0144
A;Residues: 1-385 <DUZ>
A;Cross-references: EMBL:U10400; NID:9500701; PIDN:AAB68943.1; PID:9500708; MIPS:YHR017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C29E6.2 - 'Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1952
R;Dobson, R.
Submitted to the EMBL Data Library, May 1996
A;Reference number: Z19141
A;Accession: T1952
A;Actavis: preliminary; translated from GB/EMBL/DDBJ
A;Actavis: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1188 <WIL>
A;Cross-references: EMBL:Z72504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2
A;Experimental source: clone C29E6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.3%; Score 33; DB 2; Length 249;
66.7%; Pred. No. 35;
iive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                           Length 385;
                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                               Score 34; DB 2
Pred. No. 33;
2; Mismatches
                                                                                     A;Gene: SGD:YSC83
A;Gross-references: SGD:S0001059; MIPS:YHR017w
A;Map position: 8R
                                                                                                                                                                                                                                                                                                       69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 RRKFAVNVR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: C29E6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRRRESVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
T19552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

0;

Gaps

ö

Length 146; 3; Indels ö

Gaps

0;

;

ö

Gaps

ö

67.3%; Score 33; DB 2; Length 1188; larity 66.7%; Pred. No. 1.5e+02; Conservative 2; Mismatches 1; Indels

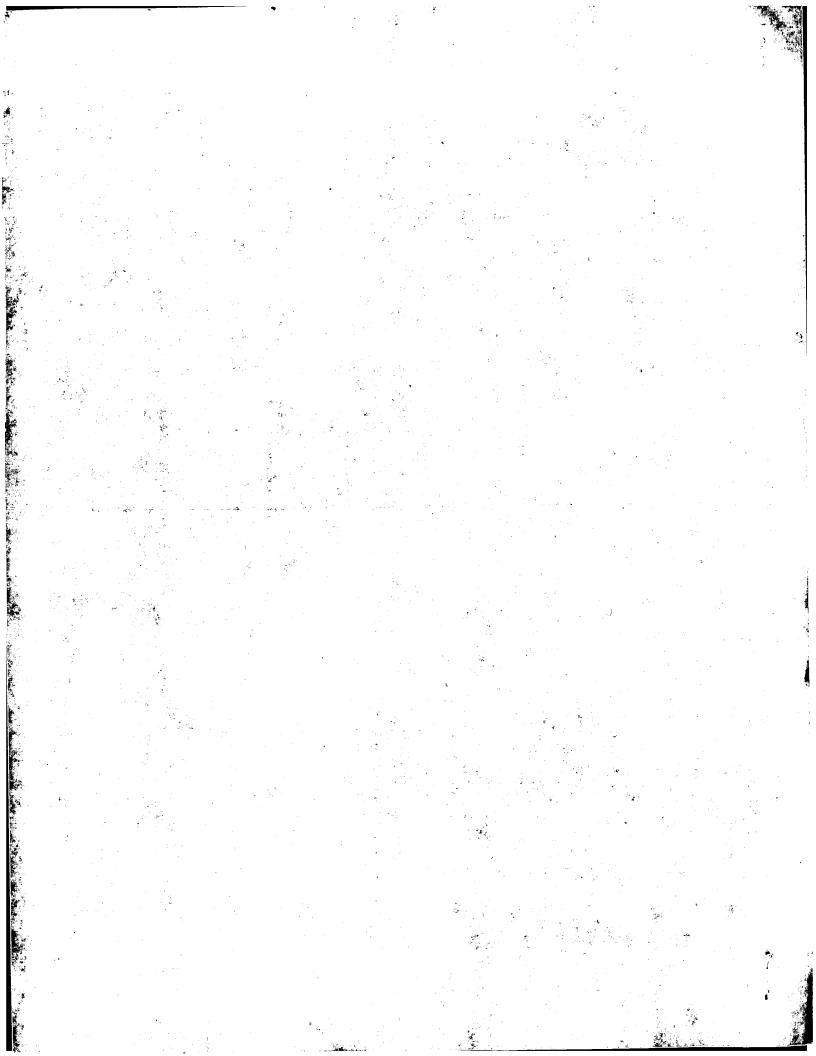
Best Local Similarity

Query Match

9

Matches

Length 167;



us-09-485-571-22.rsp

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P05464 bacteriopha P41907 saccharomyc P32792 saccharomyc P52069 methylobact 062725 mustela vis P16725 human cytom P77406 escherichia P48826 aspergillus P44764 emericella 094256 drosophila 01050 mycobacteri p39606 bacillus su P21167 escherichia 010443 mouse adeno 229450 pisum sativ P19317 escherichia P4794 haemophilus P4794 bacmorhabdi P39970 saccharomyc 014200 schizosacch P4733 mycoplasma P11071 escherichia p39370 satuus norv P53671 homo sapien P53671 avian adeno 04547 bacillus th P46018 oryctolagus P79990 phascolarct
SUMMARIES	Y17K_BPP4 YHH7_SACDO AAT_METEX PGH2_MUSVI U1/6_HCWVA PERK_ECOLI G6PD_ASPNG G6PD_ASPNG G6PD_ASPNG G6PD_ASPNG G6PD_ASPNG G6PD_ASPNG G7PD_ASPNG G7
DB	;
ngth	151 385 385 385 385 385 385 385 385
chy	600 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Score	0444mm8888811110000000000000000000000000
Result No.	1

049117 methylobact P50629 tomato bush P11691 tomato bush P50632 tomato bush P50634 tomato bush P50634 tomato bush P45643 solea seneg P5551 rhizobium s O82733 arabidopsis Q09112 caenorhabdi Q9pee6 xylella fas P56838 thermotoga				phages; Myoviridae.	.C., Debo G., Finkel S., ., Lin CS., ne M.G., Ziermann R.;		f bacteriophage P4.";	uced through a collaboration and the EMBL outstation -	its content is in no way sage by and for commercial p://www.isb-sib.ch/announce/	4 CRC64;	Length 151; 1; Indels 0; Gaps 0;		
153 1 YMEC_METEX 188 1 VP21_TBSV8 189 1 VP21_TBSVC 189 1 VP21_TBSVV 189 1 VP21_TBSVV 189 1 VP21_TBSVV 203 1 SOMA_SOLSE 292 1 Y4AD_RHISN 316 1 PP17_ARATH 311 SRA9_CAEEL 331 1 SRA9_CAEEL 339 1 LPXK_XYLPA 350 1 GALI_THEMA	ALIGNMENTS	STANDARD; PRT; 151 AA.	09, Created) 09, Last sequence update) 34, Last annotation update) KDA PROTEIN (ORF151).	ises, no RNA stage; Talled	SEQUENCE FROM N.A. MEDLINE=90221913; PubMed=2183201; Halling C., Calendar R., Christie G.E., Dale E.C. Flensburg J., Ghisotti D., Kahn M.L., Lane K.B., Lindqvist B.H., Pierson L.S., Six E.W., Sunshine "DNA sequence of satellite bacteriophage P4."; Nucleic Acids Res. 18:1649-1649(1990).	141 SEQUENCE FROM N.A. MEDLINE-85062840; Pubmed-6095206;	Nuclectide sequence of the essential region of bacterlophage P4 Nuclect Acids Res. 12:8667-8684(1984).	try is copyright. It is prodiced in the structure of Bioinformatics formatics in the structure of the structure in the struct	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; X51522; CAA35900.1; EMBL; X02534; CAA26380.1; EMBL; M11913; AAA92521.1; PIR; H20878; O2BPP4. PIR; JW0026; JW0026. Hypothetical protein; Early protein. SEQUENCE 151 AA; 17726 MW; A24874710C546844 CRC64	.6%; Score 39; DB 1; .0%; Pred. No. 0.31; e 2; Mismatches	. 0	STANDARD; PRT; 385 AA.
5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.		ST	(Rel. (Rel. (Rel. 17.7	NA viruse 0680;	M N.A. 11913; Calenc Ghis H., Pi e of S	M N.A	seduer Is Res	ROT er	this this	CAA CAA CABP O2BP JW00 Prote	h Similarity 70 7; Conservativ	SVR 10	STA
334 335 336 337 337 337 339 339 339 339 441 239 444 239 444 244 259		T 1 BPP4 Y17K_BPP4	AC (202464; DT 01-NOV-1988 (Rel. (DT 01-NOV-1988 (Rel. (DT 01-CTT-1996 (Rel. DE HYPOTHETICAL 17.7 P OS Bacteriophage P4.	Viruses; dsDNA v. NCBI_TaxID=10680	SEQUENCE FRC MEDLINE=9022 MEDLINE=9022 Halling C., Flensburg J. Lindqvist B. Lindqvist B. "DNA sequenc Nucleic Acid	SEQUENCE FRO MEDLINE-8506	"Nuclectide Nucleic Acid	This SWISS-P between the	use by non modified and entities required or send an e	EMBL; X51522 EMBL; X02534 EMBL; M11913 PIR; H23878; PIR; JW0026; Hypothetical	Query Match Best Local Simi Matches 7;	1 YRRESUSVR 10    :  :    45 YRRESILVR 54	RESULT 2 YHH7_SACDO ID YHH7_SACDO AC P41907;
ഡ ഡ ഡ ഡ ഡ <b>പ പ പ പ</b> ച് ച		RESUL Y17K_ ID	OS DE CO	008	R R R R R R R R R R R R R R R R R R R					S K R B B B B B B B B B B B B B B B B B B	Que Bes Mat	Qy Dp	RESULT YHH7_S ID Y

```
AAT_METEX
P52069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           AAT_METEX
                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                          q
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94378003; PubMed-8091229; Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Johnston M., Andrews S., Brinkman R., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Langston F., Latreille P., Louis E.J., Marci C., Mardis E., Menezes S., Mouser L., Nan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Materston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                  SEQUENCE FROM N.A.

MIDLINE-94287708; PubMed-8017101;
Adjiria A., Chanet R., Mezard C., Fabre F.;

"Sequence comparison of the ARG4 chromosomal regions from the two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                  Saccharomyces douglasii (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1995 (Rel. 21, Last annotation update)
01-FEB-1995 (Rel. 31, Last annotation update)
               Last sequence update)
Last annotation update)
PROTEIN IN SPO13-ARG4 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJUE-94078673; PubMed-8256520;
Rocco V., Daly M.J., Matre V., Lichten M., Nicolas A.;
Rocco V. Daly M.J., Matre V., Lichten M., Nicolas A.;
"Identification of two divergently transcribed genes
cartromere-proximal to the ARG4 locus on chromosome VIII of
Saccharomyces cerevisiae.";
Yeast 9:111-1120(1993).
                                                                                                                                                                                 related yeasts, Saccharomyces cerevisiae and Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                         69.4%; Score 34; DB 1; Length 385; 66.7%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 385 AA; 44409 MW; 189AA00F1A578A6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 9.6;
2; Mismatches
                                                                                                                                                                                                             Yeast 10:309-317(1994).
    Created)
                                                                                                                                                                                                                                                                                                                                                           EMBL; X73886; CAA52092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
 01-NOV-1995 (Rel. 32, C
01-NOV-1995 (Rel. 32, L.
20-AUG-2001 (Rel. 40, L.
HYPOTHETICAL 44.4 KDA PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||:| :
130 YRRRFTVYI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRRRFSVSV 9
                                                                                                          NCBI_TaxID=46617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHR017W OR YSC83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHH7_YEAST
P32792:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaudin M.;
                                                                                                                                                                                                     douglasii.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHH7_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyhydroxyalkanoic-acid-synthase structural gene.";
Appl. Microbiol. Biotechnol. 39:309-317(1993).
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE
'Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- COPACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
-i- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last semoctation update)
PUTATIVE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASPAI) (ORF2) (FRAGMENT).
Methylobacterium extorquens.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valentin H.E., Steinbuechel A.; "Cloning and characterization of the Methylobacterium extorquens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 385 AA; 44235 MW; FC054DFF4B75D904 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 AA; 10424 MW; 201376961C632611 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001511; Aminotran_1.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; PARTIAL.
Hypothetical protein; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=IBT 6;
MEDLINE=93305286; PubMed=7763712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.48;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L06795; AAA56989.1; -. EMBL; U10400; AAB68943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L07893; AAA72329.1; -.
                                                                       Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S38191; S38191.
PIR; S46789; S46789.
SGD; S0001059; YSC83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
'. Local 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRRFESVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=408;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
PROSTAGLANDIN G/H SYNTHASE 2 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE -2) (COX-2) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 2) (PROSTAGLANDIN H2
SYNTHASE 2) (PGH SYNTHASE 2) (PGHS-2) (PHS II).
PTGS2 OR COX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000501; EGF-like.
InterPro; IPR000501; EGF-like.
InterPro; IPR000501; EGF-like.
InterPro; IPR000536; Peroxdse_3.
PRINTS; PR000457; ANPEROXIDASE.
SMART; SM00181; EGF, I.
PROSITE; PS01086; EGF_l; FALSE_NEG.
PROSITE; PS01186; EGF_L; FALSE_NEG.
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THROMBOXANES.
-- SUBURIT: HOMODIMER (BY SIMILARITY).
--- SUBURIT: HOMODIMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOWAL MEMBRANE.
--- MISCELLANEOUS: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mustela vison (American mink).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H2+A+H(2)O. PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE.
DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- MISCELLANEOUS: THIS ENZYME IS THE TARGET OF NONSTEROIDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTAGLANDIN G/H SYNTHASE 2.
                           Score 33; DB 1; Length 93;
Pred. No. 3.2;
                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                      604 AA
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98344842; PubMed=9681517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF047841; AAC05637.1; -.
                        67.38;
66.78;
Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604
55
193
371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                    81 YORRFGVSL 89
                                                                                                                               1 YRRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASTICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Uterus
                                                                                                                                                                                                                                                                                                                   PGH2_MUSVI
062725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                  KESULT 5
PGH2_MUSVI
                                                                                                                                  ò
                                                                                                                                                                              g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 9026039; PubMed=2161319;
Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
Chee M.S., Bankier A.T., Towninson C.M., Mesting T., Martignetti J.A.,
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Forddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).

-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL24,
EHV-1 37, EBV BXRFI, HCNV UL76, ILTV ORF3, AND VZV 35.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
 PROXIMAL HEME LIGAND (BY SIMILARITY)
                                                                                                                                 . .) (POTENTIAL) . .) (POTENTIAL) . .)
                                                                                                                   . .) (POTENTIAL)
                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                       Score 33; DB 1; Length 604;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.3%; Score 32; DB 1; Length 325; 60.0%; Pred. No. 21;
            BY SIMILARITY.
N-LINKED (GIGNAC...) (POTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                            N-LINKED (GLCNAC. . .) (POR E28D19F47CD926F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01646; Herpes_UL24; 1.
SEQUENCE 325 AA; 36069 MW; 5BCD72EC8E8F9BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
PROTEIN UL76.
                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X17403, CAA35391.1;
PIR; S09839, QOBEB4.
InterPro, IPR002580; Herpes_UL24.
                                                                                                                                                                             Ψ.
                                                                                                                                                                                                                       67.3%;
85.7%;
                                                                                                                                                                             68950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
374
32
42
42
54
145
561
                                                                                                                                                                                                                                  Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| : ||
63 YRRRLFIEVR 72
                                                                                                                                                                                                                                                                                               1 YRRRFSV 7
                                                                                                                                                                                                                                                                                                                                                                                 UL76_HCMVA
P16725;
                                                                                                                                  CARBCHYD
CARBCHYD
CARBCHYD
SEQUENCE
             DISULFID
DISULFID
                                                        DISULFID
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                   CARBOHYD
                                            DISULFID
                                                                                       MOD_RES
BINDING
                                                                                                                                                                                                                                                                                                                                                       RESULT 6
UL76_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                        QΩ
                                                                                                                                                                                                                                                                                                                                                                                     FFFFFFFFFF
S
                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

```
SEQUENCE
                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P48826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G6PD_ASPNG
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrews S.C., McClay J., Ambler A., Quail M., Berks B.C., Guest J.R.; Subdrews S.C., McClay J. the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTEWIAL).
-!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY. STRONG, TO H.INFLUENZAE H10237/38.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97349980; PubMed-9205837;
WEDLINE-97349980; PubMed-9205837;
Yamamoto Y., Aiba H., Baba T., Baba T., Makino K.,
Yamamoto Y., Aiba H., Baba T., Makino K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makamura Y., Nashimoto H.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Salto N., Sampei G., Satoh Y., Sivasundaram S.,
Oshima T., Oyama S., Salto N., Sampei G., Satoh Y., Sivasundaram S.,
Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Construction of a contiguous 874-kb sequence of the Escherichia coli
"Alz genome corresponding to 50.0 68.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-10.10.7.

MEDLINE-1074935; PubMed-11206551;
MEDLINE-1074935; PubMed-11206551;
Merna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Burlan S., Boutin A., Shao Y., Miller L.,
Grofaleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Mach C. R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; science 277:1453-1474(1997).
                                                                                     35, Last sequence update)
                                         353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                        PUTATIVE PERMEASE PERM.
PERM OR B2493 OR Z3755 OR ECS3355.
                                    M_ECULL SIGNIES
PTAT06; P71230;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque
01-NOV-1997 (Rel. 40, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 279-353 FROM N.A.
                                                                                                                                                      Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                  NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                          Escherichia
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CBS 120.49 / N400;
STRAIN=CBS 120.49 / N400;
MEDLINE=95272533; PubMed=7753033;
MEDLINE=95272533; PubMed=7753033;
MEDLINE=95272533; PubMed=7753033;
Wan den Broek P., Goosen T., Wennekes B., van den Broek H.;

"Isolation and characterization of the glucose-6-phosphate dehydrogenase encoding gene (gsdA) from Aspergillus niger.";
Mel. Gen. Genet. 247:229-239(1995).
--- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) = D-GLUCONO-1-CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE PATHWAY.
--- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
--- SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.3%; Score 32; DB 1; Length 353; 100.0%; Pred. No. 23; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ElCB8EB1E242FC3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 AA
                                                                                                                                                                                                                                                                                                                                                                     Complete prot
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                        EMBL, AB005479, AAGS7603.1; --
EMBL, AP002561; BAB36778.1; --
EMBL, M63654; AAB8875.1; ALT_SEQ.
ECGENE; EG14221; PERM.
Interpro; IPR002549; UPF0118.
Pfan; PF01594; UPF0118; 1.
Transmembrane; Transport; Complete P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM;
                                                                                                                                                          EMBL; AE000335; AAC75546.1; -.
EMBL; D90878; BAA16382.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330
39194 ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
217
240
281
310
353 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5061;
                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NRRL 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||||
|9 YRRRFS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSDA OR G6PDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRRFS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G6PD_ASPNG
                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
```

```
SEQUENCE
    CONFLICT
                                                                                                                                                                                                                                                                                                   ORK1_DROME
                                                                                                                                                                                                                                                                                                                           FJ
                                                                                                                                                                         ò
                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X778JV,

( HSSP) P1441; 2DPG.

R InterPro: IPR001282; G6PD.
)R PF00479; G6PD; DR PF00479; G6PD; DR PRINTS; PR00079; G6PD; DR PRINTS; PR00079; G6PD; 1.

DR PRODOM; P0001129; G6PD; 1.

DR PROSITE; PS00069; G6P_DEHYDROGENASE; 1.

DR PROSITE; PS00069; G6P_DEHYDROGENASE; 1.

NAT_SITE 198 198 BY SIMILARITY.

AAT_SITE 198 198 MISSING (IN REF. 1).

RSYIKTPTKE -> DTLRPRORK (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van den Broek P., Goosen T., Wennekes B., van den Broek H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE + NADP(+) = D-GLUCONO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELTA-LACTONE 6-PHOSPHATE + NADPH.
PATHWAY: FIRST STEP IN PENTOSE PHOSPHATE PATHWAY.
SIMILARITY: BELONGS TO THE GLUCOSE-6-PHOSPHATE DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                    DB 1; Length 510; 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G6PD_EMENI STANDARD; PRT; 511 AA.
P41764: Q92408;
D1NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD).
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FGSC 4;
Schaap P.J., Muller Y., Visser J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Glucose metabolism.

Glucose metabolism.

BY SIMILARITY.

L -> F (IN REF. 2).

NRL -> TVCK (IN REF. 2).

9950 MW; FDDF3F5025483AF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                    Score 32; DB 1; Pred. No. 34; 0; Mismatches
                                                                                                 PRIMES: PR00079; G6PDHDRCNASE.
PRODOM; P0001129; G6PD.
PROSITE; P800009; G6P_DEHYDROGENASE; 1.
OX.4Goredctase; NADP; G1ucose metabolism.
ACT_SITE 198 198 BY SIMILARITY
CONFLICT 135 135 L. -> F (IN RE
CONFLICT 508 510 NRL -> TVCK (
SEQUENCE 510 AA; 58950 MW; FDDF3F50254
                                                                                                                                                                                                                                                                                                     65.3%; Sc._
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X84001; CAA58825.1; -. EMBL; X77830; CAA54841.1; -. HSSP; P11411; 2DPG.
EMBL; X87942; CAA61194.1; -. EMBL; X77829; CAA54840.1; -. HSSP; P11411; 1DPG.
                                                             InterPro; IPR001282; G6PD.
Pfam; PF00479; G6PD; 1.
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                              413 YRRRFS 418
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSDA OR G6PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WG096
                                                                                                                                                                                                                                                                                                                                                                                                      1 YRRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G6PD_EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
  DR DR DR DR DR NO BR NO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
```

```
REDEINE-20196006; Pubmed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe O., Chen L.X.,
RA Baradon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfelffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Becson X.Y., Bernos P.V., Bernam B.P., Bhandari D., Bolshakov S.,
RA Berson X.Y., Bernos P.V., Bernam B.P., Bhandari D., Bolshakov S.,
RA Berson X.Y., Bernos P.A., Deng Z., Mays A.D., Dew T., Distar S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ray R., Dunkov B.C.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,
RA Good K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Admenl E.E., Kadpred C.H., Ke Z., Kenniscon J.A., Rettmen R.A., Howiton K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M. P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M. P., McPherson D.,
RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Pacler F., Shen H.,
RA Reinert K., Remington K., Saunders R., Volleeler F., Shen H.,
RA Palazzolo M., Pittman G.S., Pan S., Polladra J., Wang A., H., Wang A.,
Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shier B.C., Siden-Kiamos I., Sungson M., Skupski M., Ray R., Respector C., Turner R., Venter E., Wang A.H., Wang X.-Y., Wang R., Wang Z.-Y., Wang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (TWO PORE DOMAIN POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goldstein S.A.N., Price L.A., Rosenthal D.N., Pausch M.H.; "ORKI, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster by expression in Saccharomyces cerevisiae.":
                                                                                                                                                                                                                            ö
                                                                                                                                                 Length 511;
                                                                                                                                                                                                                            Indels
L -> LP (IN REF. 1).
66BC15B72878A475 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996)
                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1001 AA.
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                            Pred. No.
                                                                                                                                                 65.3%; Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE*Larva;
MEDLIND=97075152; PubMed=8917578;
                                                                                                                                                                                                                            ..
                               58977 MW;
                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
352
511 AA;
                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHANNEL ORK1).
ORK1 OR CG1615.
                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                      1 YRRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORK1_CROME
Q94526;
```

<u>.</u>

s:

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mattow J., Jungblut P.R., Mueller E.-C., Kaufmann S.H.E.; "Identification of acidic, low molecular mass proteins of Mycobacterium tuberculosis strain H37Rv by matrix-assisted laser desorption/ionization and electrospray ionization mass spectrometry."; Proteomics 1:494-507(2001).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland Son R., Gwinn M.L., Haft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Salzberg S.L.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome comparison of Mycobacterium tuberculosis clinical and
   Mediania, Navi, Mediania, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 36.6 KDA PROTEIN IN QOXD-VPR INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%; Score 31; DB 1; Length 124; 75.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
PROTEIN RV1269C.
1BCECB3EFAE4FCOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YWCH OR IPA-44D.
Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: TO M. TUBERCULOSIS RV1813C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE007005; AAK45567.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION BY MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31, Created)
31, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 124 AA; 12550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z77137; CAB00910.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT1307; -.
Tuberculist; Rv1269c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 RRRFAVAV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RRRFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YWCH_BACSU
P39606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
YWCH_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@laboration.ch).
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong F.N., Zhong F.N., Stong F.N., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000).

-- FRUCTION: BACKGROUND POTASSIUM CHANNEL. RECTIFICATION IS DEPENDENT ON EXTERNAL POTASSIUM CONCENTRATION. ACTS AS AN OUTWARDLY RECTIFITED CHANNEL BACKGROUND FOR STREAM POTASSIUM LEVELS INCREASE, THIS
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGEST
EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                               IN LARVA AND EWBRYO.
MISCELLANEOUS: INHIBITED BY BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel; Transmembrane; Ion transport; Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W, 09AE1A3669072E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 1; Length 1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PORE-FORMING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PORE-FORMING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-00T-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTEIN VIL269C PRECURSOR.
VIL269C OR MI1307 OR MICK50.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 72;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U55321; AAC69250.1; -.
EMBL, AE003484; AAF47972.1; -.
FlyBase; FB9n0017561; OrKl.
InterPro; IPR003280; ZporeK_channel.
InterPro; IPR001622; Channel_pore_K.
InterPro; IPR000099; TWIK_channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
27
111
140
170
191
224
264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         875 FRRRFSV 881
                                                                                                                                                                                                                                                                                       IS REVERSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRRRFSV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YC69_MYCTU
```

TRANSMEM DOMAIN TRANSMEM TRANSMEM TRANSMEM

DOMAIN

SEQUENCE

Matches

g δy

YC69_MYCTU
IID YC69_M
AC 011050
DT 01-0CT
DT 01-0CT
DT 20-AUG
DE RV1269
GN RV1269
GN RV1269
GN ACTINC
OX NCBL_II

011050

DOMAIN

ö

Gaps

ö

Indels

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L2MU_AD3M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALICHOR
                                                                                                                                                                                                                                         STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         010443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L2MU_ADEM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
    RRARRAR RRARR RRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OS OS OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tiedemann A.A., Demarini D.J., Parker J., Smith J.M.;
"DNA sequence of the purc gene encoding 5'-phosphoribosyl-5-
aminoimidazole-4-N-succinocarboxamide synthetase and organization of
the dapA-purc region of Escherichia coli K-12.";
J. Bacteriol. 172:6035-6041(1990).
                                                                                                                                                                                                 97
                                                                          MEDLINE-95020537; PubMed-7934828;
Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.;
"Bacillus subtlils genome project: cloning and sequencing of the 9
kb region from 325 degrees to 333 degrees.";
MOI. Microbiol. 10:371-384 (1993).
-1- SIMILARITY: TO BACTERIAL ALKANAL MONOOXYGENASE ALPHA AND BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouvier J., Pugsiey A.P., Stragier P.; "A gene for a new lipoprotein in the dapA-purC interval of the Escherichia coli chromosome."; J. Bacteriol. 173:5523-5531(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1; Length 333;
Pred. No. 34;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein; Complete proteome.
333 AA; 36557 MW; B593613BB8FD8BC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P21167: P76564;
01-MAY-1991 (Rel. 18, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIPOPROTEIN-34 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subtilist; BG10590; ywcH.
InterPro; IPR002103; Bac_luciferase.
Pfam: PF00296; bac_luciferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12;
MEDLINE-91008982; PubMed-2120198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K12;
MEDLINE-91358331; Pubmed-1885529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X73124; CAA51600.1; -. EMBL; Z99123; CAB15836.1; -. PIR; S39699; S39699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLPB OR DAPX OR B2477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1:||| ||
205 YKRRFKPSV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRRFFSVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
  NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 33
                                                                                                                                                                                                                                                                               CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLPB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamagata S., Horiuchi T.; "Construction of a contiguous 874 kb sequence of the Escherichia coli - KI2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features."; DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE-97426617; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse adenovirus type 1 (MAV-1).
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: NON-ESSENTIAL LIPOPROTEIN.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 1; Length 344;
Pred. No. 36;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coll K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M33928; -: NOT_ANNOTATED_CDS.
EMBL; AE000335; AAC75530.1; ALT_INIT.
EMBL; D90876; BAA16354.1; -.
EMBL; D90877; BAA16364.1; -.
PIR; B36146; B36146.
PIR; B35426; S25426.
ECGGENE; EG10658; nlpB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 N-ACYL DIGLYCERIDE.
36842 MW, 49991F277D9D923C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LATE L2 MU CORE PROTEIN PRECURSOR (PMU) (PROTEIN X).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97349980; PubMed-9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X57402; CAA40661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || || |: :||:
| 157 YRGRYQISVK 166
```

```
Search completed: February 12, 2002, 12:39:51 Job time: 804 sec
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRFFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 RRSISVSVR 62
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Intro position as an evolutionary marker of thioredoxins and thioredoxin domains.";
J. Mol. Evol. 42:422-431(1996).
J. Mol. Evol. 42:422-431(1996).
FUNCTION: PARTICIPATES IN VARIOUS REDOX REACTIONS THROUGH THE REVERSIBLE OXIDATION OF THE ACTIVE CENTER DITHIOL, TO A DISULFIDE. THE F FORM IS KNOWN TO ACTIVATE A NUMBER OF ENZYMES OF THE PHOTOSYMTHETIC CARBON CYCLE.
FUNCTION OF CHLOROPLAST.
SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lear,
MEDIINE-92256804; PubMed=1581563;
MEDIINE-92256804; Gadal P., Cretin C.;
Lepiniec L., Hodges M., Gadal P., Cretin C.;
Lepiniec L., Characterization and nucleotide sequence of a full-length
"Isolation, characterization and nucleotide sequence of a full-length
"Isolation, characterization and nucleotide sequence of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                             Meissner J.D., Hirsch G.N., Larue E.A., Fulcher R.A., Spindler K.R.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE ROLE OF THE PRECURSOR MIGHT BE TO CONDENSE THE VIRAL PROCHROMATIN FOR ENCAPSIDATION BY VIRTUE OF THE TWO BASIC DOMAINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pisum sativum (darden pea).

Bukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Bokaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Bopmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;

Bornatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;

Bornatophyta; Rabales; Fabaceae; Papilionoideae; Vicieae; Pisum.

NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
MEDLINE-96215867; PubMed-8642611;
Sahrawy M., Hecht V., Lopez Jaramillo J., Chueca A., Chartier Y.,
Meyer Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                       CLEAVAGE (BY ADENOVIRUS PROTEASE)
                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY ADENOVIRUS PROTEASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 1; Length 74;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                          POTENTIAL.
LATE L2 MU CORE PROTEIN.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                       647AC6A52D9670AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                 EMBL; U95843; AAB53758.1; -. Core protein; DNA-binding; Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pea cDNA encoding thioredoxin-f."; Plant Mol. Biol. 18:1023-1025(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              8316 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.2
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                                                                               44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || || || |::|
8 YRFRFPVALR 17
                                                                                                                                                                                                                                                                                                                                                                                                                               74 AA;
             NCBI_TaxID=10530;
                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                       Core protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=reaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THIF_PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                    CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIE_PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Redox-active center; Electron transport; Chloroplast; Transit peptide.
TRANSIT 1 69 CHLOROPLAST (POTENTIAL).
CHAIN 70 182 THIOREDOXIN F-TYPE.
DISULEID 106 109 REDOX-ACTIVE (BY SIMILARITY).
SEQUENCE 182 AA; 19775 MW; 158FC352CB9E0FFI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 1; Length 182; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                         EMBL; X63537; CAA45098.1; --
EMBL; U35830; AAC49357.1; --
PIR; S20929; S20929.
HSSP; P10599; JAIU.
InterPro; IPR000063; Thiored.
Pfam; PP00085; thiored; 1.
PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.2%;
```

us-09-485-571-22.rsp

<b>y</b> (1) (2) (3)					
					·
			e de la companya de		o4
					er Vision San Comment of the Comment
e de la companya de La companya de la co		eries de la companya		orthography (1997) State of the state of th	
		- 6. - 10.			
					e e e e e e e e e e e e e e e e e e e
		ar en	<b>3</b>		
					\ <b>\</b>
		<b>4</b>		in the second of	
					<u>.</u>
			***		
	en de la companya de La companya de la co				
		<i>*</i>			
			- 1. 1		
		e de la companya de l			tan a sa s

```
us-09-485-571-22.rspt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          February 12, 2002, 12:38:39; Search time 232.64 Seconds (without alignments) 6.287 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $P.plant:*
sp_rodent:*
sp_rodent:*
sp_vortue:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                      Wed Feb 13 07:52:05 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-485-571-22
49
1 YRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
The state of the s
```

			porce	monas	habdi	sacch	dopsis	dopsis	dopsis	asma	chol	rella	bacte	ella	dol lob	sativ	turkey herp	turkey herp	brachydanio	acter	actin
		Description	Q60400 cavia porce	O9hwn8 pseudomonas	09xwb7 caenorhabdi	013992 schizosacch	09sr02 arabidopsis	O9fyd4 arabidopsis	080624 arabidopsis	09pps7 ureaplasma	Q9kkm9 vibrio chol	Q9cix3 pasteu	09x6y5 bifidobacte	Q916q1 salmonella	029512 archaeoglob	09xqp7 oryza sativ	O9ibw2 turke	O9e6q4 turke	012989 brack	Q9a718 caulobacter	Q9kwr2 thermoactin
SOUTHINGS		Q	060400	SHWN8	9XWB7	13992	Q9SR02	Q9FYD4	080624	9PPS7	ОЭККМЭ	9CJX3	9X6Y5	91601	29512	Q9XGP7	Q9IBW2	Q9E6Q4	012989	29A718	29KWR2
		1 80	11	2	2	3	10	10	10	2	2	2	7	2	1	10	12	12	13	2	2
		Match Length DB	180	719	968	965	1703	284	328	146	287	437	1023	125	249	252	513	513	532	589	651
đ	Query	Match	73.5	73.5	73.5	73.5	73.5	71.4	71.4	69.4	69.4	69.4	69.4	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3
		Score	36	36	36	36	36	35	35	34	34	34	34	33	33	33	33	33	33	33	33
	Result	No.	-	7	٣	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19

4	Oyxuyy caenornabdı O4514O caenornabdı O9gm27 macaca fasc Q9n4y6 caenornabdi		02251 caenorhabol Q15044 homo sapien O04344 arabidopsis O61519 caenorhabdi	ω.	Q9uis/ nomo sapien Q9vxq6 drosophila Q9h9i2 homo sapien Q9bwh6 homo sapien	
5 Q18297 13 P79754 5 Q9UAU6 2 Q91266	5 Q9XUY9 5 O45140 6 Q9GM27 5 Q9N4Y6	4 Q9NSQ5 2 Q9KEB7 11 Q35441	5 022251 4 Q15044 10 004344 5 061519	2 Q91525 4 Q9UKLO 5 Q17797 10 Q9M6N8	4 Q9UFS/ 5 Q9VXQ6 4 Q9H9I2 4 Q9BWH6	5 Q21214 4 Q9P2E4 3 Q06554
1188 1328 146 153	167 294 301 323	344 385 391	396 415 419	482 558 593	633 762 772	1156 1337 1556
67.3 67.3 65.3	65.3 65.3 65.3	65.3 65.3	വവവവ	655.3 65.3 65.3 65.3	65.3 65.3 65.3	65.3 65.3 65.3
m m m m n	33533	355	3522	2222	3555	35 35 35 35
20 22 23 23	25 25 26 27	28 29 30	33 33 34	35 37 38	4 4 4 4 2 4 4 2 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 5 5 4 5

## ALIGNMENTS

NCBI_TaxID=287; Pseudomonas

```
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RI Head and a sequence from chromosome iii of C.

RI Nature 368:32-38(1994).

BR HSSP; 1910688: 10AS.

RI HEAP 1910688: 10AS.

RI INTERPO: IPR001192; PI_PLC.

RI INTERPO: IPR001192; PI_PLC_X.

RI INTERPO: IPR00111: PI_PLC_X.

RI PFONS PRO01301: PI_PLC_X:

READ BRINES PRO0380; PI_PLC_X:

READ BRINES PRO0380; PI_PLC_X:

READ BRINES PRO0380; PI_PLC_X:

READ BRINES PRO0380; PI_PLC_X:

READ BRINES PRO01202; PI_PLC_X:

READ BRINES SM00148; PLCX: 1.

READ BRINES SM00148; PLCX: 1.

READ BRINES SM00148; PLCX: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YD8557.13C.
EMBL; 299166; CAB16196.1; -.
InterPro; IPR001489; PH.
Pfam; PF00169; PH; 2.
SWART; SMO0233; PH; 2.
SWART; SM50023; PH; 2.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , DB 3; Length 965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                        Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 110.9 KDA PROTEIN C26H5.11 IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                965 AA; 110904 MW; 921BA5E3D16639F7 CRC64;
                                                                                                                                                                                                                                                                                  property, psycology, ppp.C. DOMAIN; 1.
PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SEQUENCE 896 AA; 103803 MW; BD6D50916DF0C2EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaces; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1703 AA.
                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          965 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 5
Pred. No. 62;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Q9SR02;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                               73.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 YRKRYSISLK 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRRFFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |||:|
689 FRRRSSVSIR 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRRFESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPAC26H5.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SR02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                013992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
Q9SR02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     013992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pp
                              RA
RT
RT
RL
DR
DR
DR
DR
DR
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE FARM N. B. PubMed=7906398; WEDLINES-94150718; PubMed=7906398; Wardines-94150718; Pubmed=7906398; Manderson R., Ainscough R., Anderson K., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Craxton M., Dear S., Du Z., Puthins T., Jier M., Johnston L., Gardner A., Green P., Hawkins T., Hallier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Jones M., Rershaw J., Kirsten J., Roopra A., Saunders D., Shownkeen R., Falchtning J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                            ö
                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004831; AAG07530.1; -.

EMBL; AE004831; AAA.

InterPro; IPR001349; AAA.

InterPro; IPR001349; ABC_transporter_tmem.

InterPro; IPR001687; ATP_GTP_A.

InterPro; IPR001687; ATP_GTP_A.

InterPro; IPR001687; ATP_GTP_A.

InterPro; IPR00182; ABC_transportr.

InterPro; IPR00182; ABC_transportr.

INTERPROSIDE; ABC_transportr.

RART; SM00382; AAA: 1.

RART; SM00382; AAA: 1.

RARP-binding; Complete proteome; Transport.

RARP-binding; Complete proteome; Transport.

REQUENCE 719 AA; 79569 MW; B7ABEF72D66883F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                        01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROBABLE TOXIN TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 36; DB 2
; Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      896 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, C: 01-NOV-1999 (TrEMBLrel. 12, Li 01-NOV-1999 (TrEMBLrel. 17, Li 75B12B.6 FROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity //...
Triconservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
```

09XWB7; Q9XWB7

RESULT 3

Q9XWB7

48

g οχ

White

Trans.

ö

Gaps

;

ö

Gaps

; 0

```
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Rounsiev S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,
Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,
Somerville C.R., Venter J.C.;
Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004218; AAC27828.1; -.
SEQUENCE 328 AA; 37138 MW; E258DA27FA7F0F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20500219; Pubmed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmioutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 10; Length 328;
Pred. No. 36;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE002154; AAF30976.1; -.
Hypothétical protein: Complete proteome.
SEQUENCE 146 AA; 17597 MW; 01678E52CBCBF55E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) .
01-MAR-2001 (TrEMBLrel. 16, Last annotation update) .
HYPOTHETICAL PROTEIN UU563.
                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287
                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KKM9 PRELIMINARY; PRT; Q9KKM9; 01-0CT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                   71.48;
70.08;
               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, F12L6.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 407:757-762(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                              :|| ||||:|
232 HRRSFSVSMR 241
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||::| :|
70 YRRRWAVKLR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SEROVAR 3;
                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urealyticum.";
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PPS?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9PPS?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9KKM9
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Suromids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                            STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Arabidopsis thaliana chromosome III BAC F7018 genomic sequence.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC011437; AARO4900.1; -.
SEQUENCE 1703 AA; 185507 WW; 5C68D7E02FB66A39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bevan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J., Volckaert G., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                   73.5%; Score 36; DB 10; Length 1703; 60.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 284;
                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL391716; CAC05509.1; -.
InterPro; IRR001594; Znf-DHHC.
Pfam; PF01529; zf-DHHC; 1.
ProDom; PD003041; Znf-DHHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32202 MW; 60F8A52CD8F171A4 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 10;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 AA.
                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.48;
60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.4
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
5, Conserve
                                                                                                                                                                                                                                                                                                                                                                                             ||:||:| :|
1234 YRKRFAVDMR 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 AA;
                                                                                                                                                                                                                                                                                                                                                                             1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                  SEQUENCE FROM N.A.
                             F7018.23 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEM
01-JUN-2001 (TrEM
REC-LIKE PROTEIN.
                                                                                                                     NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09FYD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             080624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FYD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
080624
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FYD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩI
                                                                                                                                                                                                                                                                                                                                                                                                         g
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

Gaps

. ..

ö

Gaps

ó

Gaps

ö

Length 437; Indels

```
Rossi M., Altomare L., Brigidi P., Gonzalez-Vara A., Matteuzzi D.;
Rossi M., Altomare L., Expression and transcriptional analysis of the
"Nucleotide sequence, expression and transcriptional analysis of the
bifidobaterium longum MB219 lacZ gene.";
Submitted (MAY-1999) to the EMBL/GenBank/PDBJ databases.

BMBL; AJZ42596; CAB44428.1;
INTERPO DO722; HBGL.
INTERPO IPRO01649; Glyco_hydro_2.
PRGM: PR00703; Glyco_hydro_2:
PRINTS: PR00132; GLYCOSYL_HYDROL_F2_1;
SEQUENCE 1023 AA; 114497 MW; 9B8BEB478641B60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium LT2.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.4%; Score 34; DB 2; Length 1023; 75.0%; Pred. No. 1.8e+02; .ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Salmonella typhimurium Genome Sequencing Project."; submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SGSC1412;
Waterston R.;
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF23324; AAF33451.1; -.
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-00T-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMBLrel. 15, Last annotation update)
STMD1.49 PROTEIN.
                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
Score 34; DB 2;
Pred. No. 77;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AA
                                                                                                                                                                                                          PRT; 1023 AA.
                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17)
        69.4%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.4
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                            Conservative
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=SGSC1412;
                                                                                                                                                                                                                                                                                                              BETA-GALACTOSIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=99287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:|:||
| 128 YRRKFTVS 135
                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                  1 YRRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRRRFSVS 8
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
Q9L6Q1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9L6Q1
                                                                                                                                                                                                                    09X6Y5
                                                                                                                                                                                                                                        09X6Y5;
                                                                                                                                                                                11
                                                                                                                                                                                RESULT
Q9X6Y5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οg
                                                                                                                                                                                                                                      δλ
                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                        SEQUENCE FROW N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-LOR 06833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Heidelberg J.F., Eisen J.A., Nelson W.C., Umayam L.A.,

Gill S.R., Haft D.H., Hardey E.K., Peterson J.D., Umayam L.A.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzaberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PW U;

MEDLINE=21145866; PubMed=11248100;

MAY B. J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. NaLl. Acad. Sci. US.A. 98:3460-3465(2001).

EMBL; AE006224; AAK03950.1;

InterPro; IPR000551; SAM_bind.

InterPro; IPR001566; TRMA_l.

PROSITE; PS01230, TRNA_l.

PROSITE; PS01230, TRNA_L.

Hypothetical protein; Complete proteome.

SEQUENCE 437 AA; 50021 MW; 03D4876D3533BECI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                        Nature 406:477-483(2000).
                                                            Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; PF00165; HTH_ARAC.
PRINTS: PR001032; HTHRARAC.
SMART; SM00342; HTH_ARAC.
PROSTTE: PS00041; HTH_ARAC_FAMILY_1; 1.
PROSTTE: PS01124; HTH_ARAC_FAMILY_2; 1.
COMplete proteome; DNA-binding; Transcription regulation.
SEQUENCE 287 AA; 31460 MW; 7FDSFB18E68C08B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN PM1866.
      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSCRIPTIONAL REGULATOR, ARAC/XXLS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB Pred. No. 50; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; VCA1074; -.
InterPro; IPR000005; HTHAraC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.4%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004433; AAF96967.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||| |:
279 YKRRFSSSI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRRRESVSV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORS.
```

RESULT 10

q

δ

ö

S

ö

Gaps

ö

;

2;

10; Length 252; Indels

Score 33; DB Pred. No. 70; Mismatches

```
Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.; "Marek disease virus encodes a basic-leucine zipper gene resembli the fos/jun oncogenes that is highly expressed in lymphoblastoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JEASTER, Wu P., Sui D., Ren D., Kung H.J.;
Lee L.F., Wu P., Sui D., Ren D., Kung H.J.;
The Complete UL Sequence of Serotype I Marek's Disease Virus.";
Proc. Natl. Acad Sci. U.S.A. 0:0-0(2000).
EMBL, AF17806; AAF6749.1;
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR001990; Ser_khr_kinactsite.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
                         Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
clone:P0026F07.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%; Score 33; DB 12; Length 513; 60.0%; Pred. No. 1.4e+02; live 3; Mismatches 1; Indels
                                                                                           Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AP000364; BAA81774.1; -.
InterPro; IPR000051; SAM_bind.
InterPro; IPR002935; Methyltransf_3.
Pfam; PF01596; Methyltransf_3; 1.
SEQUENCE 252 AA; 27771 MW; E4FC076B47483926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
NCBI_TaxID=10390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 12, 2002, 12:38:39
Job time: 752 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92237304; PubMed-1315048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Kinase; Transferase
SEQUENCE 513 AA; 58905 MW; D7
                                                                                                                                                                                                                                                                                              67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-JUN-2001 (TrEMBLrel, 17,
                                                                                                                                                                                                                                                                                              Query Match 67.3
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
     STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turkey herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRRRESVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||| ::|
77 HRRRESDNIR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||::|
215 RRFSVAIR 222
                                                                                                                                                                                                                                                                                                                                                                                               3 RRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q91BW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9IBW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9IBW2
     RR RA RA DOR DOR DOR SO
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; Pubmed-9389475.

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Klohadson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,

KIKNess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ESTS A0030740(E60171).
07yza sativa (Rice).
07yza sativa (Rice).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1937).
EMBL; AE001053; AAB90493.1; -.
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.3%; Score 33; DB 1; Length 249; 66.7%; Pred. No. 69;
                                                                         Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                         1; Indels
125 AA; 14296 MW; F2871B309FAA0180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 protein; Complete proteome.
249 AA; 27620 MW; 36D4DCCFF0501C9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-AUG-1998 (TrEMBLrel. 07, Last annotation update) CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                         5,
                                                                                                                                                                                                                                                                                                                                              249 AA.
                                                                       Score 33; DB Pred. No. 34; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                         67.38;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-AUG-1998 (TrEMBLrel. 07.
                                                                    Query Match 67.3
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RRRFSVSVR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11:|:|:|1
71 RRKFAVNVR 79
                                                                                                                                                                                                3 YRREFEVA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                    1 YRRRESVS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
SEQUENCE 2
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                         RESULT 13
029512
AC 029512
AC 029512
DT 01-JAN
                                                                                                                                                                                                                                                                                                                                            029512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XGP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                       õ
                                                                                                                                                                                                                  용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

resembling

Last sequence update) Last annotation update)

Created)

513 AA.

ö

Gaps

ö

D73D04608C32DC07 CRC64;

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                OM protein - protein search, using sw model
```

February 12, 2002, 12:30:32 ; Search time 242.57 Seconds
 (without alignments)
 3.054 Million cell updates/sec Run on:

US-09-485-571-23 50

1 RRLSYSRRFF 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

522463 seqs, 74073290 residues Searched:

Total number of hits satisfying chosen parameters:

522463

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDSB/gggdata/geneseq/genesegp/AA1980.DAT:*
/SIDSB/gggdata/geneseq/genesegp/AA1981.DAT:*
/SIDSB/gggdata/geneseq/genesegp/AA1981.DAT:*
/SIDSB/gggdata/geneseq/genesegp/AA1983.DAT:*
/SIDSB/gggdata/geneseq/genesegp/AA1983.DAT:*
/SIDSB/gcgdata/geneseq/genesegp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/genesegp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/genesegp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/genesegp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/genesegp/AA1986.DAT:* A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Protegrin derivati	Protegrin-like pep	Peptide which may	Protegrin derivati	Protegrin derivati	Protegrin derivati	Protegrin-like pep	Protegrin-like pep	Peptide which may	Peptide which may	Antimicrobial prot
	ID	AAW99410	AAY93189	AAY93618	AAW99411	AAW99412	AAW99403	AAY93177	AAY93179	AAY93615	AAY93616	AAW36264
	DB	20	21	21	20	50	20	21	21	21	21	18
	Query Match Length DB	10	10	10	15	18	18	18	18	18	18	14
æ	Query Match	100.0	100.0	100.0	100.0	90.0	90.0	90.0	90.0	90.0	90.0	80.0
	Score	50	20	20	20	45	45	45	45	45	45	40
	Result No.	1	7	m	4	2	9	7	80	6	10	11

16 18 AAW36279 17 18 AAW36440 18 18 AAW3647876 18 18 AAW18153 10 18 AAW36285 18 18 AAW36285 18 18 AAW36285 18 18 AAW36285 10 10 AAR78766 045 20 AAY077482 045 21 AAW36265 11 18 AAW36262 11 18 AAW36263	Antimicrobial prot Protegrin peptide Cationic, antimicr C glutamicum prote Protegrin peptide Antimicrobial prot Antimicrobial prot Cationic, antimicr Antimicrobial prot	
	10 P m m 44 10 m m m m m 10 10 10 m m m 44 44 10 10	
88877777777777777777777777777777777777	4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	

## ALIGNMENTS

AA. AAW994.0 standard; peptide; 10 (first entry) 08-JUN-1999 AAW99410; AAW99410 RESULT 

Protegrin derivative peptide SM2195.

Linear; protegrin; peptide antiblotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.

Synthetic.

WO9907728-A2

18-FEB-1999.

98WO-FR01757. 06-AUG-1998;

97FR-0010297. 12-AUG-:1997;

(SYNT-) SYNT:EM SA.

Kaczorek M; Grassy G, Chavanieu A, Calas B,

WPI; 1999-190034/16.

- nsed Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells

```
AAY93618
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) XI- XI6; WXBXXXXBBXXXXXXBSX, or (c) BXXXXXXXXXXXXXXXBSX, where: each of XI-XI6
                     This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the against to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, fragments), anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nseful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "linked to doxorubicin via a succinate
  (-Co-(CH2)2-CO- linker"
                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                   100.0%; Score 50; DB 20;
100.0%; Pred. No. 0.002;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Protegrin-like peptide antibiotic Doxo-SynB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example III; Page 22; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                            AAY93189 standard; peptide; 10 AA.
        Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98FR-0015074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                          1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                       AAY93189
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                    AAY.93189
```

δ Q

```
cc are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is aa containing a side chain that includes a basic group; can deach X is an aliphatic or aromatic aa. The linear peptide may be cretro forms of (a)-(c) containing D and/Or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive aa from (a)-(c) containing at least 5, preferably at least 7 consecutive aa from (a)-(c) containing at least 6, preferably at least 7 consecutive aa from (a)-(c) techyplesins, transportan, etc. of these several families have cytolytic techyplesins, transportan, etc. of these several families have cytolytic categories based on their structure: (j) peptides with alpha-helices, c. ceropins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides of the invention protesidues, e.g. protegrin, tachyplesins, defensins; (iii) peptides con protegrical and pads). The peptides of the invention categories defined above: (a)-peptides con the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides. (b)-peptides are based on tachyplesins. This sequence con the presents a synthetic linear peptide designed on peptide able to cross the BBB and is conjugated to a doxorubicin molecule by a succinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzhelmer's or parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least on peptide that can transport it into cancer cells and which inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 50; DB 21;
100.0%; Pred. No. 0.002;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93618 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaczorek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       remsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
```

```
AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Calas B,
     Query Match
Best Local
                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                       qq
                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear; protegrin; peptide antiblotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                     100.0%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grassy G, Kaczorek M;
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protegrin derivative peptide SM2193.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW99411 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97FR-0010297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                          1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                  10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAW99411
```

g

δ

88888888888888

```
ö
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonacledides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Derivatives of antibiotic peptides lacking disulfide bridges – used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                           ö
            Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 20; Length 18;
Pred. No. 0.032;
0; Mismatches 0; Indels
                                                             Indels
100.0%; Score 50; DB 20; 100.0%; Pred. No. 0.003; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                               Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                                                                                                  AAW99412 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.0°,
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99403 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97FR-0010297.
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-190034/16.
                                   Similarity
                                                                                                           1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEE-1999.
                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW99403
ID AAW9
XX
```

us-09-485-571-23.rag

08-JUN-1999

AAW99403;

06-AUG-1998; 12-AUG-1997;

18-FEB-1999.

W09907728-A2.

Synthetic.

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier of diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous constant. The linear peptide preferably has the formula: (a) XI-XI6 (b): BXXXXXXXBBXXXXXXXXXXBBXB, where: each of XI-XI6 (c): BXXXXXXXBBXB, where: each of XI-XI6 (c): BYXXXXXXBBXB, where: each of XI-XI6 (c): BYYB, each B: da containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive as from (a)-(c). The containing D- and/or L-form as, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Eachyplesins, transportan, etc. of these several families have cytolytic tachyplesins, transportan, etc. of these several families have cytolytic etgeories based on their structure: (i) peptides with alpha helices, categories based on their structure: (i) peptides with alpha helices, categories based on their structure: (i) peptides with alpha helices, categories, e.g. bactericins and PR19. The peptides of the presence of with no major structure but containing bends due to the presence of the number of are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the BBB and (c)-peptide are based on tachyplesins. This sequence proteptins; and (c)-peptide are based on tachyplesins and propertide designed on peptides are based on the BBB and is conjugated to a doxorubicin molecule by a succinate the BBB and is conjugated to a doxorubicin molecule by a succinate the BBB and also on the branch of the peptide are based on tachyper of the peptide are based on tachyper by a perception of the branch of the base are based on the base are based on the base and also be linked to a benzylpenicillin molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                          _note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.0%; Score 45; DB 21; Length 18; 100.0%; Pred. No. 0.032; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93179 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Temsamani J;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example I; Page 13; 54pp; French
                                                                                                                                                                                                                                                                    99WO-FR02938
                                                                                                                                                                                                                                                                                                                         98FR-0015074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.0
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 rlsysrrrf 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 AA;
                                                                                                                                                                  WO200032236-A1.
                Key
Modified-site
                                                                                                                                                                                                                                                                          26-NOV-1999;
                                                                                                                                                                                                                                                                                                                            30-NOV-1998;
                                                                                                                                                                                                                    08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KX B
              Пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the adsulphide bridge. The nevel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, fragments and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                          Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.0%; Score 45; DB 20; Length 18; Best Local Similarity 100.0%; Pred. No. 0.032; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grassy G, Kaczorek M;
                                                                                                                                Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93177 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                    nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
```

ö

Gaps

0;

06-DEC-2000

AAY93177;

AAY93177 RESULT

qq δλ

Sequence

Synthetic.

S

```
The invertion trained by the constitution able the cross the blood-brain barrier of diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formular (a) X1-X16; (b): BXXBXXXXXBBS or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formular (a) X1-X16; are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp; each B is an containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be containing at least 7 consecutive aa from (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 7 consecutive aa from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia.

C retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive aa from (a)-(c). Peptides and are termed peptide antibiotics. They fall into 3 main categories per expense of the structure but containing bedies with disulphide bond-linked contained by a cercopins and maganins; (ii) peptides with disulphide bond-linked contained antibiotic attegories defined above: (a) peptides with no major structure but containing bends due to the presence of protegrins; and (c)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the RBB and is conjunated to a dalarrin molecule by a signibility of a dalarrin m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                 Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood'brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                               /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                                               Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example II; Page 20; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98FR-0015074
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                     Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000
                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells

Colin De Verdiere A;

Kaczorek M,

Temsanani J,

(SYNT-) SYNT:EM SA.

30-NOV-1998;

WPI; ::000-412166/35.

99WO-FR02939. 98FR-0015073

WO200032237-A1

08-JUN-2000

Unidentified

cancer.

Anticancer agent; cancer cell; resistance; P-glycoprotein pump;

Peptide which may be linked to anticancer agents.

(first entry)

25-SEP-2000

AAY93615;

AAY93615 standard; peptide; 18 AA

g

```
The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the P-31ycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.0%; Score 45; DB 21; Length 18; 100.0%; Pred. No. 0.032; 1. O. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93615 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-3000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 rlsysrrrf 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93616
Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XEXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 45; DB 21; Length 18
100.0%; Pred. No. 0.032;
.ive 0; Mismatches 0; Indels
```

Query Match 90.0 Best Local Similarity 100. Matches 9; Conservative

2 RLSYSRRFF 10

õ

ô

Gaps

```
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| | | ||||
| rrlcycrif 10
                                                                                                                                                                                                                                                    WPI; 1997-297871/27.
                                                                                                                                                                                                                          Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998
                                                                                                  21-NOV-1996;
22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
           WO9718826-A1
                                                                     22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36279;
                                         29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                 The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, produced by chemical synthesis, can be coupled easily to the agent, proceptors mammalian cell membranes rapidly by a passive mechanism (no cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; gram-negative; hIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porchne; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                          New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
    Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 45; DB 21;
100.0%; Pred. No. 0.032;
Live 0; Mismatches 0.
                                                                                                                                                                                                                                      Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial protegrin peptide PC34 (64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36264 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 34pp; French.
                                                                                                                                                     99WO-FR02939.
                                                                                                                                                                               98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                          WPI; 2000-412166/35.
                                                                                                                                                                                                               (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA;
                                                                                          WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                            Unidentified.
                                                                                                                                                       26-NOV-1999;
                                                                                                                         08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW36264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
```

δŏ g

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, containing pram-positive and gram-negative bacteria, yeast, fungl, including gram-positive and gram-negative bacteria, yeast, fungl, contour be used to preserve or disinfect a variety of materials, contact lens including medical equipment, foodstuffs, cosmetics, contact lens including medical equipment, foodstuffs, cosmetics, contact lens contains, medicaments or other nutrient containing materials. It solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial contained by containing materials. It keratitis, corneal ulcers, stomed, ulcers associated with keratitis, corneal ulcers, stomed, ulcers associated with the lifections, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, sepsis, endocarditis, pneumonia and other respiratory infections, critis biostatic or biocidal against clinically relevant pathogens this biostatic or biocidal against clinically relevant pathogens chibiting multi-drug resistance, e.g. vancomycin resistant exhibiting multi-drug resistance, e.g. vancomycin resistant staphylococcus streptococcus pneumoniae and methicillin resistant staphylococcus cure work (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 ct 1 mg/Kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 18; Length 14;
Pred. No. 0.22;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin peptide PC34a (79).
                                                                                                                                                                                                                                                                                                                                                                                     Gu CL, Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW36279 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                        (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                     95US-0562346.
96US-0649811.
                                                                                                                                                                                                     96US-0690921
96WO-US18544
                                                                                   96US-0752852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
```

Antimicrobial protegrin peptide (240).

Page

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, can be used for an estatuse bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal uleres, stomach uleres associated with telicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens extincting multi-drug resistance, e.g. vancomycin resistant certains and methicillin resistant Staphylococcus cureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 creptoroccus methods and methicillin resistant Staphylococcus con microbial management and methicillin resistant staphylococcus contains and methicillin resistant staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                               respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; pentoillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial protegrin peptide(s) - having activity against
bacteria, yeast, fungi, protozoa and certain strains of viruses
(e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 40; DB 18; Length 16; 80.0%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lehrer RI, Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36440 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-297871/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| | ||||
| rrlcycrrrf 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA;
                                                                                                                                                                                                                                                                                                                                                                              WO9718826-A1.
                                                                                                                                                                                                                                                 Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW36440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
AAW36440
```

8

ð

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

Including medical equipment, foodstuffs, cosmetics, contact lens controlling medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomench ulcers associated with telicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus facculus, peniciallin resistant Staphylococcus aurens (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                 disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; pram negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Straphylococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                              Antinicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. 3IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 18; Length 17; Pred. No. 0.27; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steinberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 23; Page 111; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                    96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0752852
                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0562346.
96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0690921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-297871/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| | ||||
2 rrlcycrrf 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                                          WO9713826-A1
                                                                                                                                                                                                                                                                                                                                                                                    22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1996;
                                                                                                                                                                                                                                                      Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

```
Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
Cationic, antimicrobial, virus-neutralising protegrin PC-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 12, 2002, 12:30:32
                                                                                                                                                                                                                                                      Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 64; 106pp; English
                                                                                                                                                                                               95US-0499523.
                                                                                                                                                                         96WO-US07594
                                                                                                                                                                                                            95US-0451832
                                                                                                                                                                                                                                                                                   WPI; 1997-033984/03.
                                                                                                                                                                          24-MAY-1996;
                                                                                                                                                                                                                                                             Harwig SSL,
                                                                                                                              WO9637508-A1
                                                                                                                                                                                                   07-JUL-1995;
                                                                                                                                                                                                              26-MAY-1995;
                                                                                                                                                     28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                       Synthetic.
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in peptides are local B amino acids in length both animals and plants. The peptides are 16-18 amino acids in length, and are characterised by four invariant cys residues at positions 6, 8, and 15 and either (1) by a characteristic pattern of basic and 13 and 15 and either (1) by a characteristic pattern of basic and prophobic amino acids and/or (2) being isolatable from animal (e.g. hydrophobic aminos of these peptides in which 1-4 of the portions) leukocytes; or analogues of these peptides in which 1-4 of the cys residues is/are replaced by hydrophobic or small amino acids. The peptides can be produced synthetically and some can be produced for the peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino cid residues can be present.

The present sequence is a specific example of the protegrin The present sequence is a specific example of the protegrin produced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                       Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                        protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 16
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                 Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW18153 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 19; 80pp; English.
                                 AAR78776 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.0%;
                                                                                                                                                                                                                                                             93US-0093926.
93US-0095769.
94US-0182483.
94US-0243879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1997 (first entry)
                                                                                                                                                                                                                                       94WO-US08305.
                                                                                                                                                                                                                                                                                                                                                  Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                        Protegrin peptide sequence
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:|||||
|4 risfsrrrf 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                            26-JUL-1993;
13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                           20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                      Harwig SSL,
                                                                                   08-OCT-1995
                                                                                                                                                                                           WO9503325-A.
                                                                                                                                                                                                                   02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW18153
                                                                                                                                                antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                    Synthetic.
                                                           AAR78776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW18153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SX Z
                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

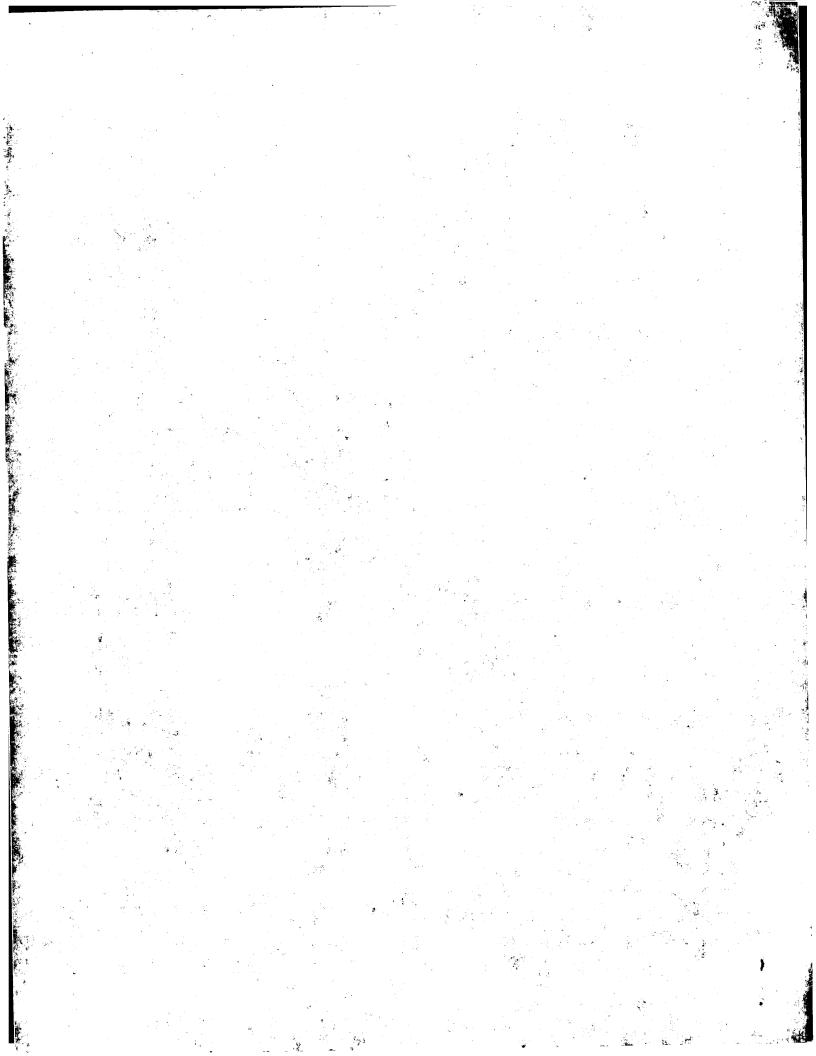
```
The present sequence is a specifically claimed example of a peptide, crecombinantly produced, corresponding to the generic formula: recombinantly produced, corresponding to the generic formula: Al-A2-A4-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A2-A4-A4-A5-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16 (A17-A18)

CC As, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A4 a a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, acid or proline: A17 may be absent or a basic, neutral/polar, or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid. This has a charge of neutral/polar, hydrophobic or small amino acid. This has a charge of contral/polar, hydrophobic or small amino acid. This has a charge of esterified forms, hydrophobic or small amino acid. This poptide or small amino acid. This poptide is in snake form where all the cysteine bridge. This poptide is in snake form where all the cysteine bridge. This poptide is in snake form where all the cysteine bridge. This poptide is in snake form where all the cysteine bridge or alanine in this case). Peptides of this formula are cysteine bridge and are useful as anti-bacterial, anti-viral and anti-tungal agents in plants and animals. The protegrins confer cresistance to microbia or viral infection in plants by preventing the resistance to microbia or viral infection in plants by micropanisms e.g. creatment of sexually transmitted disease caused by micropanisms e.g. candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Naisseria gonorrhoeae. They can also be used in eye care solutions and physiological conditions (e.g. in the presence of serum) than certain province of physiological conditions (e.g. in the presence of serum) than certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 18;
Pred. No. 0.45;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:|:||||
4 rlayarrrf 12
```

Job time: 365 sec

us-09-485-571-23.rag



```
GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 12:30:32; Search time 242.57 Seconds

(without alignments)
4.581 Million cell updates/sec

Title: US-09-485-571-24

Perfect score: 71

Russysrkrsysyr 15

Sequence: 1 RRLSYSRRRFSySYR 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum Maxch 100%

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database: A_Geneseq_1101:*
```

e : A_Geneseq_1101:*

1. \S1DS8\gcgdata\geneseq\geneseqp\AA1980.DAT:*
2. \S1DS8\gcgdata\geneseq\geneseqp\AA1981.DAT:*
3: \S1DS8\gcgdata\geneseq\geneseqp\AA1981.DAT:*
4: \S1DS8\gcgdata\geneseq\geneseqp\AA1982.DAT:*
4: \S1DS8\gcgdata\geneseq\geneseqp\AA1982.DAT:*
5: \S1DS8\gcgdata\geneseq\geneseqp\AA1981.DAT:*
5: \S1DS8\gcgdata\geneseq\geneseqp\AA1986.DAT:*
7: \S1DS8\gcgdata\geneseq\geneseqp\AA1986.DAT:*
8: \S1DS8\gcgdata\geneseq\geneseqp\AA1986.DAT:*
7: \S1DS8\gcgdata\geneseq\geneseqp\AA1980.DAT:*
9: \S1DS8\gcgdata\geneseq\geneseqp\AA1980.DAT:*
10: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
11: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
13: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
14: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
15: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
16: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
16: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
16: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
16: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
17: \S1DS8\gcgdata\geneseq\geneseqp\AA1990.DAT:*
18: \S1DS8\gcgdata\geneseq\geneseqq\geneseqp\AA1990.DAT:*
18: \S1DS8\gcgdata\geneseq\geneseqq\geneseqp\AA1990.DAT:*
18: \S1DS8\gcgdata\geneseq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq\geneseqq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Antimicrobial prot Antimicrobial prot	anti anti pept	Streptococcus pneu Striptococcus pneu Antimicrobial prot Human chondrocyte- Human cytoskeleton	6187444	Antimicrobial prot Antimicrobial prot Antimicrobial prot Protegrin peptide Protegrin peptide Protegrin peptide Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial prot
AAW36264 AAW36279 AAW36440 AAW36285 AAW36429	AAW18153 AAW09084 AAW09085 AAR78768	AAM16152 AAB12717 AAW36318 AAY07482 AAY91947	AAG92371 AAW99409 AAW36265 AAW36628 AAW36602 AAW35602	AAW36263 AAW36261 AAW36262 AAR78755 AAR78756 AAR78766 AAR78766 AAR36278 AAW36270 AAW36270
18 18 18 18	118	77 77 77 77 77 77 77	75 75 75 75 75 75 75 75 75 75 75 75 75 7	188 188 188 188 188 188 188 188 188 188
14 16 17 17 18	18 118 118 118	526 14 1045 1045	104 108 138 13 14	14 115 115 116 116 117
888844		000000		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
200000	000000	00000		M M M M M M M M M M M
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4444	2.4 422 442 1144 1144	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
12 13 14 15 16	18 220 221 221	2 2 2 2 2 4 2 4 2 4 2 4 2 4 2 4 2 4 2 4	2 3 3 3 3 5 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## ALIGNMENTS

AA;

```
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                AAY93616;
          Sequence
                                                                                                                                                                                                                                                                                                                             cancer.
                                                                              Matches
                                                                                                                                                                                       AAY93616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δà
XX
So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide represents a linear derivative of the protegrin family of peptide antiblotics. Frotegrin antiblotics form part of the peptide antiblotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibudura agents, fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                             ö
                     This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibumur agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                    Length 15;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                    100.0%; Score 71; DB 20; 100.0%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
Kaczorek M;
                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                          AAW99403 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 28; 37pp; French
        Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                             1 rrlsysrrrfsvsvr 15
                                                                                                                                                                                                                                                                                              1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW99403;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                              AAW99403
                                                                                                                                                                                                                                                                                                                                                                    RESULT
```

δλ q

```
ö
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the speptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, marticularly produced by chemical synthesis, can be coupled easily to the agent, produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.9%; Score 61; DB 21; Length 18; 100.0%; Pred. No. 0.00015; Live 0; Mismatches 0; Indels
  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide which may be linked to anticancer agents.
Score 61; DB 20; L
Pred. No. 0.00015;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colin De Verdiere A;
                                                                                                                                                                                                                                                                                 AAY93616 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 8; 34pp; French.
       ch 85.9%; Sci
1 Similarity 100.0%; P:
13; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 rlsysrrrfsvsv 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLSYSRRFFSVSV 14
                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 AA;
               Query Match
Best Local Similarity
                                                                                                                2 RLSYSRRFFSVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jnidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000.
```

```
peptide antibiotics. Protegina antibiotics form part of the peptide antibiotics. Protegina antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivities and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver acitive agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                        Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide represents a linear derivative of the protegrin family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 20; Length 18; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
    Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93177 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                         Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.68;
91.78;
                                                                                                                                                                                                                                                                   98WO-FR01757
                                                                                                                                                                                                                                                                                                         97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 91.7 nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RESYSRRFSVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                     W09907728-A2
                                                                                                                                                                                                                                                                 06-AUG-1998;
                                                                                                                                                                                                                                                                                                         12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000
                                                                                                                                                                                                                             18-FEB-1999.
                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93177
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in beth animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. pyrchobic amino acids and/or (2) being isolatable from animal (e.g. portine) leukocytes; or analogues of these peptides in which 1-4 of the Cys residues is/are replaced by hydrophobic or small amino acids. The cys residues can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or c-terminal amidation or resterification, and can be in linear or cystine-bridged form. D-Amino can be present sequence is a specific example of the protegrin analogues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections
                                                                                                                                                                             protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.5%; Score 55; DB 16; Length 18; 84.6%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                  -AAR78776 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW99412 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0095769.
94US-0182483.
94US-0243879.
                                                                                                                                                                                                                                                                                                                                                                94WO-US08305
                                                                                                                                                                                                                                                                                                                                                                                                      93US-0093926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kokryakov VN,
                                                                                                                                           Protegrin peptide sequence
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                20-JUL-1994;
                                                                                                   08-OCT-1995
                                                                                                                                                                                                                                                                                  WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1993:
                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1993;
13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999
                                                                                                                                                                                                                                                                                                                          02-FEB-1995
                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                        AAR78776:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAW99412
AAR78776
```

NAMES OF COLOR OF STREET O

ò a SXEX SEE

ö

Gaps

ö

1; Indels

- used

Ξ

Kaczorek

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous cc for diagnosis or treatment of disorders localised in the central nervous cc system. The linear peptide preferably has the formula: (a) X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must care amino acids (aa), of which 6-10 of them are hydrophobic and X1-X16 and each X is an aliphatic or aromatic aa. The linear peptide may be containing a least 5, preferably at least 7 consecutive as from (a)-(c) containing D- and/or L-form aa, or a fragment retro forms of (a)-(c) containing D- and/or L-form aa, or a fragment corresponds and each x is an aliphatic or aromatic active and are termed peptide antibiotics. They fall into 3 main effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, categories based on their structure: (i) peptides with alpha-helices, with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of all into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides and co-peptide are based on tendention peptide estimated by a succlinate the BBB and is conjugated to a doxornbicin molecule by a succlinate the based on the antennapedia family peptide and a benzylpenicillin molecule by a a uncommidential and any or a procession or a peptide estimate and benzylpenic may also be linked to a benzylpenicillin molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by a glycoamide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                          useful for
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                         diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53; DB 21; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                              Use of linear peptides as vectors for active ingredients, diagnosis and treatment of central nervous system diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protegrin-like peptide antibiotic Dal-SynB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                     Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                  Example I; Page 13; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93179 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                               99WO-FR02938.
                                                                                                                                                                     98FR-0015074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLSYSRRFSVS 13
                                                                                                                                                                                                                                                         Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                              WPI; 2000-422871/36.
                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-2000
                                                       WO200032236-A1
                                                                                                                                                                          30-NOV-1998;
                                                                                                                                   26-NOV-1999;
                                                                                            08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPXEX
```

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous for diagnosis or treatment of disorders localised in the central nervous composition are formed by the composition of the containing a side chain that includes a basic group; and each X is an aliphatic or aromatic as. The linear peptide may be containing of and/or Liform as, or a fragment retro forms of (a)-(c) containing D- and/or Liform as, or a fragment containing at least 7 consecutive as from (a)-(c). Containing D- and/or Liform as, or a fragment retro forms of (a)-(c) containing D- and/or Liform as, or a fragment containing at least 7 consecutive as from (a)-(c). Containing D- and/or Liform as, or a fragment cert of these several families have cytolytic tachyplesins, transportan, etc. Of these several families have cytolytic categories based on their structure: (i) peptides with alpha-helices, categories based on their structure: (i) peptides with alpha-helices, categories based on their structure: (i) peptides with alpha-helices, categories and magnins; (ii) peptides with disulphide bond-linked e.g. occropins and magnins; (ii) peptides with alpha-helices, categories e.g. bactericins and PR39. The peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on tare based on the Antennapedia family peptides; (b)-peptides are based on tare based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides of the linear peptides and alpha conjugated to a dalargin molecule by a disulphide linker. The BBB and is conjugated to a dalargin molecule by a disulphide articularly cused to treat, prevent or diagnose brain 
analgesic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrob blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                           /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 2
Pred. No. 0.004
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Temsamani J;
                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example II; Page 20; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.6%;
                                                                                                                                                                                                                                                                                                                                                           99WO-FR02938.
                                                                                                                                                                                                                                                                                                                                                                                                    98FR-0015074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 rlsysrrrfsts 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLSYSRRFSVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-422871/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                             WO200032236-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                             26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Si
Matches 11;
                                                                                                                                                                                                                                                                                                                    08-JUN-2000
                                                                                                                                                                                         Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                             Synthetic.
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

ŀ

```
99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-NOV-1999;
                                  W09907728-A2
                                                                             06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0002-NUC-80
                                                       18-FEB-1999
             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93189;
                                                                                                                                             Calas B,
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Mat.ch
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93189
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                    comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                       New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                              The specification describes a pharmaceutical composition, which
                                                                                                            Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to treat cancer. The present sequence represents a probe linked to the anticancer agents of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 74.6%; Score 53; DB 21; Length 18;
Local Similarity 91.7%; Pred. No. 0.004;
hes 11; Conservative 0; Mismatches 1. דיארור
                                                                                       Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                               Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protegrin derivative peptide SM2195.
                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99410 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 34pp; French.
                     AAY93615 standard; peptide; 18
                                                                                                                                                                                                             99WO-FR02939
                                                                                                                                                                                                                                   98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                               Temsamani J, Kaczorek M,
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLSYSRRFFSVS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 rlsysrrrfsts 15
                                                                                                                                                                                                                                                                                                  WPI; 2000-412166/35
                                                                                                                                                                                                                                                       (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AA;
                                                                                                                                                                 WO200032237-A1
                                                                                                                                            Unidentified
                                                                                                                                                                                                             26-NOV-1999;
                                                                                                                                                                                                                                  30-NOV-1998;
                                                                 25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                       08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Si
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                           AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW99410;
œ
         AAY93615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW99410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The nevel derivatives are used to deliver active agentis to an organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                      - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blood-brain barrier, diagnostic, central nervous system; protegrin;
Antennapedia; tachyplesin; peptide antiblotic; Alzhelmer's disease;
cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO- linker"
                                                                                                                                                                                                                                                                                   Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 20; Length 10;
Pred, No. 0.0074;
                                                                                                                                                                      Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protegnin-like peptide antibiotic Doxo-SynB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.4%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93139 standard; peptide; 10 AA.
                                                                                                                                                                      Grassy G,
                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 28; 37pp; French
98WO-FR01757.
                                                     97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                   Chavanieu A,
                                                                                                                                                                                                                              WPI; 1999-190034/16.
                                                                                                             (SYNT'-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
```

30-NOV-1998;

Clair P,

```
The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits. development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, produced by chemical synthesis, can be coupled easily to the agent, receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; dislanfection; prophylaxis; treatment; infection; disease; connectivitis; keratitis; corneal ulcer; stomach ulcer; STD; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidasis.
                                                                                                                                                                                                                                                                                        New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.0074; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin peptide PC34 (64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36264
ID AAW36264 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-1998 (first entry)
                                                                                                98FR-0015073.
                                           99WO-FR02939.
                                                                                                                                                                                                     Femsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                       WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa.
                                                 26-NOV-1999;
                                                                                                     30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous (c for diagnosis or treatment of disorders localised in the central nervous cc for diagnosis or treatment of disorders localised in the central nervous (b); BXXBXXXBBXXXXBBXB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X must cc and each X is an allaphatic or aromatic aa. The linear peptide may be cc and each X is an allaphatic or aromatic aa. The linear peptide may be cretro forms of (a)-(c) containing a least 7 consecutive aa from (a)-(c). peptides able to cross the BBB include protegrins, Antennapedia, containing at least 7 consecutive aa from (a)-(c) containing at least 7 consecutive aa from (a)-(c) containing at least 7 consecutive and are termed peptide antibiotics. They fall into 3 main effects and are termed peptide antibiotics. They fall into 3 main effects and are termed peptide antibiotics. They fall into 3 main creased on their structure: (i) peptides with alpha-helices, e.g. cecrophins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. bactericins and pR39. The peptides of the invention creased on the Antennapedia family peptides; (b)-peptides are based on creased on the Antennapedia family peptides; (b)-peptides are based on creased on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Mtennapedia family peptides are based on the BBB and is conjugated to a doxorubicin molecule by a succinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                            use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 50; DB 21; Length 10; 100.0%; Pred. No. 0.0074; 2.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93618 standard; peptide; 10 AA.
                                                                                                                                                       Temsamani J;
                                                                                                                                                                                                                                                                                                                                                            Example III; Page 22; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2000 (first entry)
                                                 98FR-0015074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                         Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RRLSYSRRRF 10
                                                                                                                                                                                                           WPI; 2000-422871/36.
                                                                                                        (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AA;
```

WO200032237-A1 Unidentified.

AAY93618;

RESULT 11 AAY93618

ò g

Sequence

ö

Gaps

;; 0

```
13-FEB-1998
                                                                                                                22-NOV-1996;
                                                                                                                                                                     22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                          01-AUG-1996;
                                                                                                                                                   21-NOV-1996;
                                                                           29-MAY-1997
     Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW36440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                               The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medicament, foodstuffs, cosmetics, contact lens solutions, medicament, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulores, stomach ulorers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Staphylococcus cureus (MRSA). It is a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; hrv; human immunodeficiency virus; preservation; dishifection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Hellcobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepais; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogon; multi-drug resistance; penicillin resistant Stephylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                        New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 18; Length 14; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                   Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial protegrin peptide PC34a (79).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                  Lehrer RI,
                                                                                                                                                                                                                                                                                                    Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36279 standard; peptide; 16 AA.
                                                                                           (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.8%;
71.4%;
                                                                                                                                                  Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| | |||| | |
| rrlcycrrfcvcv 14
                                                                                                                                                                                     WPI; 1997-297871/27
                                                                                                                                                Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
                                    17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1998
21-NOV-1996;
22-NOV-1995;
                                                                                                                                                  ပ္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                  Chang
```

ò g 

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungl, rolling gram-positive and gram-negative bacteria, yeast, fungl, protocoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or orber nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens thereococcus faecium or faecalis, penicillin resistant Staphylococcus surens, MRSA, it is given at a dosage of 0.1 to 5, preferably 0.5 areas a brook of the contains of the contains and acted to 5, preferably 0.5 areas surens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; errovirus; HIV; human immundeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%; Score 46; DB 18; Length 16; 71.4%; Pred. No. 0.064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu CL, Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protegrin peptide (240).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Page 106; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36440 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     (INTE-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                        96US-0752852.
95US-0562346.
96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to 1 mg/kg/day, by injection.
                                                                                                                                                     96WO-US18544.
                                                                                                                                                                                                                                                                                                                                          96US-0690921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-297871/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
W097.18826-A1.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, has a broad spectrum of activity against microbial targets, concluding gram-positive and gram-negative bacteria, yeast, fungi, including gram-positive and gram-negative bacteria, grass, e.g. HIV.

Deprotozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medicaments or other nutrient containing materials. It can also be used for the prophlaxis or treatment of microbial can also be used for the prophlaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, infections or diseases in plants and orients associated with the choosecter pylori, sexually transmitted diseases, gram-negative Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, systemic candidiasis and oral mucositis. It is blostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant

Enterococcus faccium or faccilis, penicillin resistant staphylococcus currents (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection. MRSA; protozoan; warocomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 18; Length 17;
Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW09078 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 111; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                   (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.88;
                                                                                                                                                                                                                                                                                                                95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                             96WO-US18544.
                                                                                                                                                                                                                                                                                               96US-0752852.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang CC, Chen J, Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| | |||| | ||
2 rrlcycrrfcvcv 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-297871/27.
                                                                                                                                                                                                                                                                                                                22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                            WO9718826-A1
                                                                                                                                                                                                                                                               22-NOV-1996;
                                                                                                                                                                                                                             29-MAY-1997.
                                                                                                                                                        Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW09078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW09078
                 DXXXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δý
```

```
The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

a recombinantly produced, corresponding to the generic formula:

c recombinantly produced, corresponding to the generic formula:

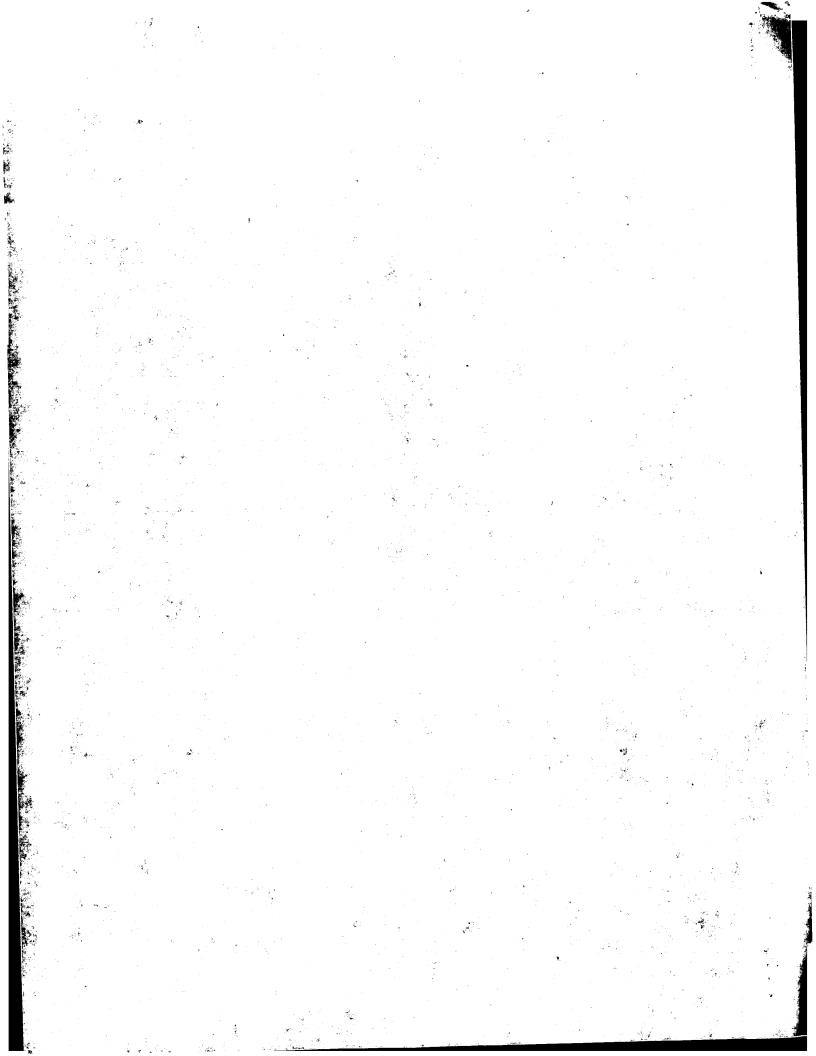
c Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

c Ab. A12 and A1 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; main acide forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cysteine bridge, Peptides of this formula are designated protegrins and area of an animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe or are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly useful for the sexually are form who are all the man all sexually are form also the area and an also and are accounted by microorganisms e.g. Candida albicans. Here they are also content and also an area content and a preservation and also area content and also and a preservation and also area content and also area conten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 18; Length 17;
Pred. No. 0.068;
); Mismatches 4; Indels
                                              Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
  Cationic, antimicrobial, virus-neutralising protegrin PC-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 63; 106pp; English.
                                                                                                                                                                                                                                                                                   'note= "Acylated"
                                                                                                                                                                                                                                                                                                                                                                             /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the presence of serum) tha cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                             6..15
8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                     Synthetic.
```

2 RLSYSRRFFSVSVR 15

ŏ

Search completed: February 12, 2002, 12:30:32 Job time: 365 sec



```
Gaps
       Sequence Seq
                                                                                                                                                                                                                                                                                                           Sequence Sequence (Sequence Sequence Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washinglow.
STATE: DC
COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
TITING DATE: 13-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 1; Ler
Pred. No. 0.0024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
US-09-128-345-59
US-08-752-852A-66
US-08-752-852A-240
US-08-752-852A-64
US-08-752-852A-63
US-08-752-852A-63
US-08-182-483A-5
US-08-182-483A-6
US-08-182-483A-18
US-08-243-879A-17
US-08-243-879A-17
US-08-243-879A-17
US-08-243-879A-17
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
US-08-499-523-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-0540.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTOREX/AGENT INPORMATION:
NAME: MURASHIGE, FE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.5%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.5
Best Local Similarity 84.6
Matches 11; Conservative
       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLSYSRRRFSVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-08-182-483A-28
           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48, Appl
48, Appl
80, Appl
242, Appl
67, Appl
86, Appl
230, Appl
67, Appl
67, Appl
119, Appl
40, Appl
40, Appl
41, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appl
Appl
                                                                                                                                                                                                                                                                                                               (without alignments)
3.181 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                February 12, 2002, 12:32:23 ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-182-483A-28
US-08-243-879A-27
US-09-128-345-48
US-08-752-852A-65
US-08-752-852A-80
US-08-752-852A-80
US-08-752-852A-80
US-08-499-523-67
US-08-128-345-67
US-09-128-345-67
US-09-128-345-67
US-09-128-345-67
US-08-499-523-40
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-128-345-53
US-09-128-345-58
US-08-499-523-54
US-08-499-523-59
US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                      US-09-485-571-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
```

. .. ..

Š.

Result

Database :

sed

Minimum DB Maximum DB

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

ö

```
Score 55; DB 1; Length 18;
Pred. No. 0.0024;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITI:
STATE: New You.
COUNTRY: USA
COMPUTER: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
TIING DATE: 03-AUG-1998
TILING DATE: 03-AUG-1998
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRE...
APPLICATIO..
FILING DATE: 03...
FILING DATE: 03...
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET UNBER: 8657-0054-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                  FILING DATE: ... 514
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REBERENCE/DOCKET NUMBER: 2000-0540.24
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRAX: (202) 887-0763
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                              07-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROFEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09128345
Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.5%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-128-345-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 1; Length 18;
Pred. No. 0.0024;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-499-523-48

US-08-499-523-48

Sequence 48, Application US/08499523

GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                               APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIP: 20006-1812
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATABLE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-NAY-1994
CLASSIFICATION: APPLICATION: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
RELEPAN: (202) 887-1500
TELEPAN: (202) 887-1500
TELEPAN: (202) 887-0763
TELERAN: 99-4030
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           ; Sequence 27, Application US/08243879A
; Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.5%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2000 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                             US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð. a
```

0

Length 18;

```
64.8%; Score 46; DB 2; 71.4%; Pred. No. 0.068; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                 APPLICANT: Chen, Jie APPLICANT: Steinberg, Deborah APPLICANT: Lehrer, Robert APPLICANT: Harwig, Sylvia TITLE OF INVENTION: FIRE-TUNED PROTEGRINS NUMBER OF SEQUENCES: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8067-034-999
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 242, Application US/08752852A
; Patent No. 5994306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COTUZZI, LEUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECCHMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEEX: 212-869-9741
TELEX: 6141
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                     Chang, Conway
Gu, Chee-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESSE: PENNIE & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-752-852A-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-752-852A-80
                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                     Gaps
                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
             Score 55; DB 4; Length 18;
Pred. No. 0.0024;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.8%; Score 46; DB 2; Length 14; 71.4%; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                 APPLICANT: Chang, Conway
APPLICANT: Chee.Liang
APPLICANT: Gu, Chee.Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                           US-08-752-852A-65
Sequence 65, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 80, Application US/08752852A Patent No. 5994306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LGUERA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMHUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPHONE: 212-869-9741
             77.5%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-869-9741
TELEX: 6641
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 64.8
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLCYCRRFCVCV 14
                                                                                                          2 RLSYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-752-852A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                       ò
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Gaps

ö

Length 16;

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: group(6, 8, 13, 15)
CTHER INFORMATION: /note= "X is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                        NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid"

US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGN.

STATE: DOCUMENTY: USA

STATE: 20006-1812

COUNTRY: USA

SIGNATION THE: FLORPY disk
MEDIUM TYPE: FLORPY disk
COMBUTER: LIBM PC COMPATIBLE
COMBUTER: PATENTIN PELEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-UUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: WIRRARIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELEPHONE: (202) 887-1500

TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1;
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                63.4%;
TELEFAX: (202) 897-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 69.2°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLSYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                        TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAIL.
COUPRY: USA
ZIP: 20006-1812
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: MARCHAILOR
SOFTWARR: PAPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
TIING DATE: 07-01L-1995
TIING DATE: 7.**TION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MORRISON & FOERSTER STREFT: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pred. No. 0.073;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                              ALIONALE, TALENTA A. REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 8067-034-999
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                  CCUNTRY: USA
2IP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DAPR:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/08499523;
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHERE, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORREWOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.8%;
71.4%;
                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RRICYCRRFFCVCV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-752-852A-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-499-523-63
```

g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 2; Length 18; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                    APPLICANT: Chen, Jie APPLICANT: Chen, Jie APPLICANT: Steinberg, Deborah APPLICANT: Lehrer, Robert APPLICANT: Harwig, Sylvia TITLE OF INVENTION: FINE-TUNED PROFECRINS NUMBER OF SEQUENCES: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KORRYAKOV, VLADIMIR N.
TITLE CF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORFORMANE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
                                                                                                                                                                                                                                                ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
     Chang, Conway
Gu, Chee-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 69.27
المحمد 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPCLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RICYARREFAVCV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RESYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                    ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                             ó
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.4%; Score 45; DB 2; Length 18; 69.2%; Pred. No. 0.11; 2; Indels ive 2; Mismatches 2; Indels
  DB 1; Length 18;
                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: New York
  Score 45; DB 1;
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 230, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              US-08-752-852A-86

Sequence 86, Application US/08752852A

Patent No. 5994306

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 86:
Ouery Match 63.4%;
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 21-NOV-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.4
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                               4 RLAYCRRFCVAV 16
                                                                                                               2 RLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-752-852A-86
                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                  ö
```

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                           Score 45; DB 4; Length 18;
Pred. No. 0.11;
0; Mismatches 4; Indels
                                                                                                          NAME/KEY: Modified-site 15, LOCATION: group(6, 8, 13, 15); LOCATION: group(6, 8, 13, 15); orter invormation: // // // // // OTHER INFORMATION: small, or a large polar amino acid"; US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08182483A

Sequence 20, Application US/08182483A

Patent No. 56593486

GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYRE Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-708/182,483A
FILING DATE: 13-708-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REPERENCE/DOCKET UNMBER: 29,959
REPERENCE/DOCKET UNMBER: 2000-0540.21
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino Actal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1.
Pred. No. 0.15;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%;
69.2%;
                                                                                                                                                                                                                                                                    Query Match 63.4%;
Best Local Similarity 69.2%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                    18 amino acids
                      LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RLGYGRRRFGVCV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLSYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                           2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                               4 RLXYXRRFXVXV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRIS
STREET: 2000 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
| LOCATION: group(6, %, 13, 15) | COTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" (US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 4; Length 18;
pred. No. 0.11;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTE: New IOLA
COMPUTER: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FLING DATE: 03-MG-1998
CLASSIFCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COPUTEX, Laura, A.
NAME: COPUTEX, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Peterlin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-199
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, Laulra, A.
REGISTRATION NUMBER: 8067-0054-999
REPERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-9090
TELEPAN: (212) 790-9090
TELEPAN: (212) 869-9741
INFORMATION FOR EGO ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 minto acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 67, Application US/09128345
Sequence 67, Application US/09128345
Patent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVERTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.4%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.4
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRECT: 1155 ...
STREET: 1155 ...
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-128-345-67
```

pp δλ

ö

```
RESULT 15
US-08-243-879A-19
Sequence 10. Application US/08243879A
Fatent No. 5708145
Factor No. 5708145
Factor No. 5708145
FAPLICANT: LERRER, ROBERT I.
APPLICANT: LERRER, ROBERT I.
APPLICANT: LERRER, ROBERT I.
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READ FOEMS:
MEDIUM TYPE: Floppy disk
COMPUTER: LERRER COMPUTER: 18M PC
COMPUTER: LERRER: DC-DSS/MS-DOS
SOCTMAKE: Patentin Release #1.0, Version #1.25
COMPUTER: IN THE NOW 194
CLASSIFICATION NUMBER: US/08/243,879A
FILIN DATE: II-MAY-194
CLASSIFICATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
RECISTRATION OF SEQ ID NO: 19:
SEQUENCE CHARACTION: 1NOW 19:
SEQUENCE CHARACTION: SEQ ID NO: 19:
SEQUENCE CHARACTION: SIGNIE HELERAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 10-4030
INFORMATION POR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS
TYPE: anino acid
TYPE: anino acid
TYPE: Anino acid
STRANDENESS: single
```

Oy 2 RLSYSRRFSVSV 14

| | | | | | | | |

Db 4 RLGYGRRRFGVCV 16

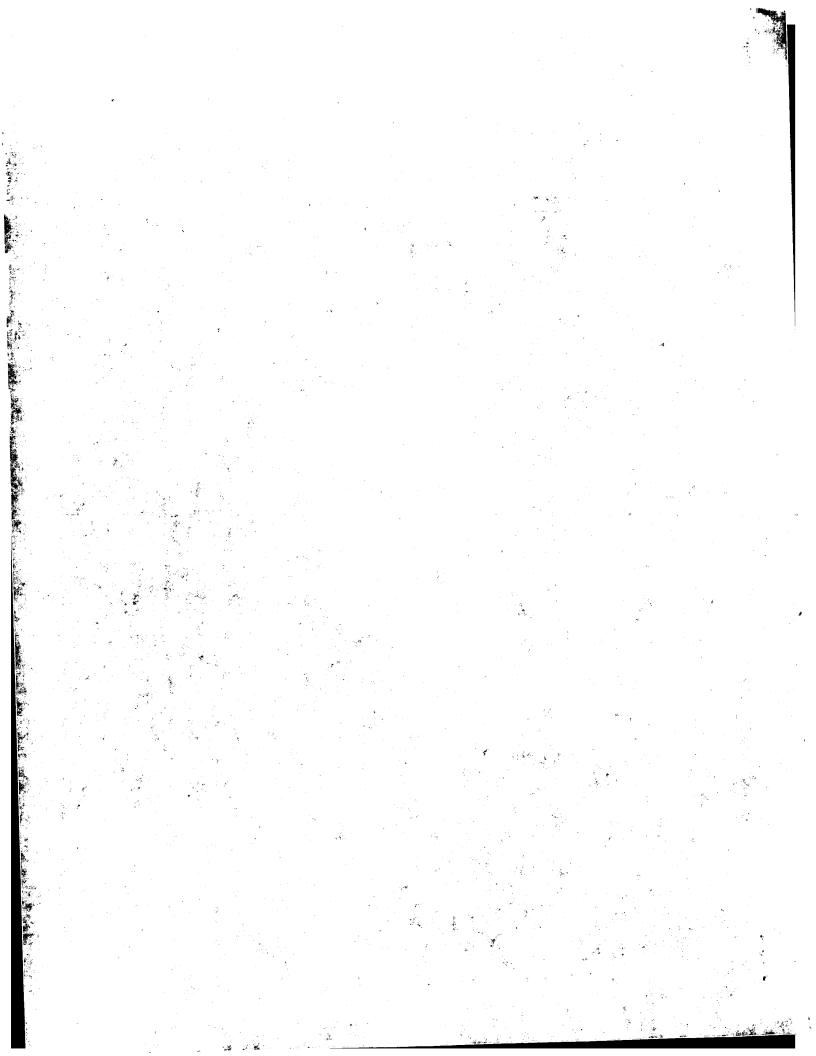
Search completed: February 12, 2002, 12:32:23
Job time: 451 sec

ö

0; Gaps

62.0%; Score 44; DB 1; Length 16; 69.2%; Pred. No. 0.15; tive 0; Mismatches 4; Indels

Query Match 62.0 Best Local Similarity 69.2 Matches 9; Conservative



ľ

```
February 12, 2002, 12:34:39; Search time 126.85 Seconds (without alignments) 9.008 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  219241 segs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                            US-09-485-571-24
71
                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                            Scoring table:
                                                                       OM protein
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Database :

CDEP protein - hum hypothetical prote spermatid-specific spermatid-specific spermatid-specific protegrin 1 precur IgA For receptor prings of protection protec spermatid-specific H-transporting AT 35K GPP-binding pr Ras-like protein K hypochetical prote hypothetical prote uridylyltransferas probable tetraacyl probable proline-r ribosomal protein protegrin 3 precur human CR1 homolog hypothetical prote H+transporting AT hypothetical prote hypothetical prote Description SUMMARIES JC5795 PN0641 PN0641 A40973 A40973 A60234 A60234 FCCSOAG JN0900 JN0900 B86273 F47575 S56117 S56117 F47575 F T41618 D96798 S01147 T36109 S76106 G84693 S77123 A53895 A46458 Query Match Length DB rununununununununununun Score Result 

ö

Gaps ö

Score 42; DB 2; Length 79; Pred. No. 1.9; 2; Mismatches 2; Indels

59.2%; 69.2%;

Query Match Best Local Similarity 69.2 Matches 9; Conservative

1 RRLSYSRRFFSVS 13

ò

18284 192554 192554 193556 183556 183556 183556 183556 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18356 18	6 50.7 368 2 H8284 6 50.7 495 2 S7190 6 50.7 614 2 JS5508 6 50.7 614 2 JS5508 6 50.7 624 2 JS5108 6 50.7 624 2 JS5108 6 50.7 624 2 JS5108 6 50.7 698 1 IRECS 6 50.7 719 2 A8112 6 50.7 746 2 S7189 7 80.7 2 S7462 5 50.0 74 2 T4230 5 49.3 132 2 S7189 7 80.2 29 2 T3576 5 49.3 132 2 S8008 7 80.2 29 2 T3576 7 80.0 74 2 T4230 8 8 8 8 9 1 INCAC 8 8 7 8 7 8 7 8 8 7 8 8 8 8 8 8 8 8 8 8	conserved hypothet RNA-directed DNA p probable membrane regulatory protein colicin V secretio probable toxin tra RNA-directed DNA p RND1 protein - yea hypothetical prote hypothetical prote conserved hypothet RN1 protein - toma ovulation hormone probable methionin	ALIGNMENTS	evision 13-Mar-1998 #text_change 16-Jul-1999  n, M.; Yan, W.; Noshiro, M.; Fujii, K.; Kato, Y. 241, 369-375, 1997  characterization of CDEP, a novel human protein cont. D:98086358  30  lived in the adhesion, proliferation, and differentia the homology; protein 4.1 membrane-binding domain homombrane-binding domain homombrane-binding domain homomprane-binding domain homomprane-bind	re 43; DB 2; Length 1045; d. No. 14; Mismatches 3; Indels 0; Gaps 0;		pyrrocinia (fragment) 103-May-1994 #text_change 09-Jun-1994 R.; van Pee, K.H. e from Pseudomonas pyrrocinia: sequence, expr
36 50.7 368 2 36 50.7 495 2 36 50.7 612 2 36 50.7 612 2 36 50.7 625 2 36 50.7 625 2 36 50.7 628 1 36 50.7 746 2 36 50.7 746 2 36 50.7 746 2 36 50.7 746 2 36 50.7 746 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 50.0 74 2 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 35 49.3 257 1 36 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	30 36 50.7 368 2 31 36 50.7 495 2 32 36 50.7 612 2 33 36 50.7 612 2 33 36 50.7 625 2 34 36 50.7 625 2 35 36 50.7 628 1 36 50.7 628 1 38 5 50.7 746 2 39 36 50.7 746 2 39 36 50.7 746 2 39 36 50.7 746 2 39 36 50.7 746 2 39 40.3 35 50.0 74 2 41 35.5 50.0 299 2 42 35.5 50.0 74 2 43 35 49.3 359 1 44 35.5 50.0 774 2 44 35.5 50.0 774 2 45 35 49.3 359 1 45 35 49.3 359 1 45 35 49.3 359 1 45 35 50.0 774 2 47 35.5 50.0 774 2 48 35 49.3 359 1 48 56 60.8 \$ 49 3 135 49.3 359 1 48 50 60 68 \$ 49 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40 60 68 \$ 40	HB2843 S71900 S71900 S55084 S55084 S16420 IKEC5B A31327 S54624 E96683 T42300 T42300 ONGAOL	ALI	vision vision 41, 369 Haracte 1980863 Ved in homolow bear hoped brane-b peat hoped	Sco Pre 5;		monas p a vision tzel, R ng gene :933458
36 50.7 368 36 50.7 495 36 50.7 495 36 50.7 625 36 50.7 625 36 50.7 625 36 50.7 628 36 50.7 746 36 50.7 746 36 50.7 746 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 35 50.0 74 36 50.7 70 37 49.3 257 38 49.3 257 38 49.3 257 39 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.3 257 30 49.	30 36 50.7 368 32 36 50.7 495 32 36 50.7 612 33 36 50.7 612 33 36 50.7 612 33 36 50.7 612 35 36 50.7 612 35 36 50.7 612 35 36 50.7 612 35 36 50.7 719 37 36 50.7 719 37 36 50.7 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 41 35.5 50.0 710 64 61 61 61 61 61 61 61 61 61 61 61 61 61	011000000000000000000000000000000000000		Shen Shen 1. 2 id c dulb 2. 2 id c dulb 2. 3 id c dulb 3. 3 id c d	7. 7.	_	eudo cini e_re Mu codi AUID
36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 36 50.7 35 50.0 35 50.0 35 50.0 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 49.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.3 35 40.	30 36 50.7 31 36 50.7 32 36 50.7 33 36 50.7 34 36 50.7 36 50.7 36 50.7 37 36 50.7 38 50.7 39 36 50.7 39 36 50.7 39 36 50.7 39 36 50.7 39 36 50.7 39 36 50.7 40 35.5 50.0 42 35.5 50.0 42 35.5 50.0 42 35.5 50.0 42 35.5 50.0 43 35 49.3 44 35 49.3 44 35 49.3 45 49.3 45 49.3 46 49.3 47 35.5 50.0 48 49.3 48 49.3 49.3 49.3 49.3 49.3 49.3 49.3 49.3	368 495 612 625 628 716 716 716 717 717 718 719 72 73 74 74 74 74 74 74 74 74 74 74 74 74 74		sequence sequence . Commun oning an UST95; b DDJ:AB00 In is in in is in in is in extrin rep	at		79 - Pse s pyrroo sequence ens, F 93 dase-enc NO828; b
36 36 36 36 36 36 37 38 38 38 38 38 38 38 38 38 38	30 31 31 32 33 34 35 36 36 37 38 39 30 31 31 31 32 33 33 34 31 32 33 34 35 35 42 35 35 44 35 35 44 35 35 44 35 35 45 35 45 35 45 35 45 35 45 35 45 35 45 35 45 35 45 35 45 35 45 45 35 45 45 35 45 45 35 45 45 35 45 45 35 45 45 35 45 45 35 45 45 45 45 45 45 45 45 45 4	7.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		human o sapie 55798 # 55799 # (75. Res 11ar cl 11ar cl 11ar cl 1045 cK (1045 cK (1045 cK plecks: plecks: ezinesi	lmilari Cons	SRRRES: 1:11	rotein adomona -1994 # N0641 : Ling 135, 19 operoxi nber: J n0641 n0641 n0641 re: DNA
	330 331 331 332 332 3333 3333 334 337 337 337 337 337 337 3	സ ന ന ന ന ന ന ന ന ന ന ന ന ന ന ന ന ന ന ന		rotein - ies: Homc s: 24 - Ju s: 24 - Ju s: 25 - Ju s: 26 - Ju m. Bioph e: Molecu ctors: crence nu ssion: Ju dues: 1-J dues: 1-J dues: 1-J fu / Domain: 10/Domain:	Matc Local Les		etical pi ies: Fset : 03-May : 03-May : 330, 131, framm, C. framm, C. framm, C. framm, C. ssion: Py ssion:

65 RRRSYSRRRY 74

g

g

```
A; Molecule type: mRNA
A; Residues: 1-149 <22H2>
A; Residues: 1-149 <22H2>
A; Residues: 1-149 <22H2>
A; Cross-references: GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
A; Cross-references: GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036
B; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; E.
R; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; E.
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequ
A; Reference number: S36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Protegins: leukocyte antimicrobial peptides that combine features of cort. A;Reference number: S34585; MUID:93327946 A;Recession: S34585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S36820
A; Molecule type: protein
A; Residues: 131-148 <MIR>
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS. Lett. 327, 231-236, 1993
                                                                                                                                           Special specific protein T1 - longfin squid
C; Species: Loligo pealeii (Longfin squid)
C; Species: Loligo pealeii (Longfin squid)
C; Species: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C; Species: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C; Accession: S56116
B; Mouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, P. Blochem, J. 309, 529-534, 1995
A; Title: Squid spermiogenesis: molecular characterization of testis-specific pro-pro
A; Reference number: S56116; MuID:95351983
A; Accession: S56116
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1.79 < WOUS
C; Superfamily: sperm histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA Caross : 1-149 < Card Shabo; C: Liu, L: Lehrer, R.I. R; Zhao, C: Liu, L: Lehrer, R.I. FEBS Lett. 346, 285-288, 1994 A; Title: Identification of a new member of the protegrin family by cDNA cloning. A; Reference number: $45712; MUID: 94283613 A; Reference number: $45712; MUID: 94283613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.Alternate names: neutrophil peptide 1
N.Alternate names: neutrophil peptide 1
C.Species: Sus screfa domestica (domestic pig)
C.Species: Sus screfa domestica (domestic pig)
C.Species: 19-oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C.Saccession: S66284; S45712; S36820; S34585; S57607
C.Saccession: S66284; S45712; S36820; S34585; S57607
R.Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202, 197-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Introns: 66/3; 102/3; 126/3
C.Superfamily: cathelin; cystatin homology
C.Superfamily: amidated carboxyl end; antibacterial; neutrophil
C.Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: saguence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CXS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 2;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 131-148 < KOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŏ
                                                                                                                                                                                                         B40973

B40973

Spermatid-specific protein T2 precursor - common cuttlefish

Spermatid-specific protein T2 precursor - common cuttlefish

N.Alternate names: arginine-rich proteanine; testis-specific protein T2

N.Alternate names: arginine-rich proteanine; testis-specific protein T2

C.Species: Sepia officinalis (common cuttlefish)

C.Species: Sepia officinalis (common cuttlefish)

C.Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998

C.Accession: B40973; S14086

R.Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van Dors

A.Recession: B40973

A.Recession: B40973

A.Molecule type: protein

A.Residues: 1-77 < KWOUD

R.Wartin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van R. Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van R. Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van R. Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, A.; Reference number: S14085; MUID:91153298

A.; Accession: S14085; MUID:91153298

A.; Accession: S14085; MUID:91153298

A.; Accession: S14086

C.; Reywords: DNA binding; nucleus; phosphoprotein; spermatogenesis

C; Reywords: DNA binding; nucleus; phosphoprotein experimental <AMED <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van Bur. J. Biochem. 195, 611-619, 1991

Eur. J. Biochem. 195, 611-619, 1991

A; Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants. A; Reference number: S14085; MUID:91153298

A; Accession: S14085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Van Dors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    var
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    two.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Specific protein T1 precursor - common cuttlefish Natternate names: arginine-rich protamine; testis-specific protein T1 Natternate names: arginine-rich protamine; testis-specific protein T1 C; Species: Sepia officinalis (common cuttlefish) C; Accession: A40973; S14085 C; Accession: A40973; S14085 C; Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998 C; Accession: A40973; S14085 C; Apr-1992 C; Martin-Ponthieu, A; Boutillon, C; J; Biol. Chem. 266, 17388-17395, 1991 J; Martin-Ponthieu, A; Boutillon, C; A; Reference number: A40973; MuID:91373359 C; Ascession: A40973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: sperm histone C;Reywords: DNA binding; nucleus; phosphoprotein; spermatogenesis C;Reywords: DNA binding; nucleus; phosphoprotein; signal sequence #status predicted <51G>F;1-21/Domain: signal sequence #status predicted <AMT>F;22-78/Product: protamine variant Spl #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2; Length 77;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2;
Pred. No. 2.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 57.7%;
Local Similarity 80.0%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 22-78 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-78 <WOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RRLSYSRRRF 10
50 RRGAYSRRSFTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
```

g ŏ

Óχ

ö

Gaps

0;

1

```
C;Species: Streptococcus agalactiae
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C;Accession: S1330; S20240; S17031
R;Jarlstroem, P.G.; Chhatval, G.S.; Timmis, K.N.
Mol. Microbiol. 5, 843-849, 1991
A;Title: "The 1gA-binding Deta antigen of the c protein complex of Group B streptoco A;Reference number: S15330; MUID:91312121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-914, E', 916-1164 <JE3>
A; Cross-references: EMBL:X59771; NID:q46522; PIDN:CAA42442.1; PID:q46523
A; Cross-references: EMBL:X59771; NID:q46522; PIDN:CAA42442.1; PID:q46523
C; Superfamily: 1gA Fc receptor
C; Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane proteif F; 1-377Domain: signal sequence #status predicted <SIG>
F; 38-1164/?roduct: 1gA Fc receptor #status experimental <MAT>
F; 199-438 /Domain: 1gA binding #status predicted <IGAl>
F; 439-826/Domain: 1gA binding #status predicted <IGAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pypothetical protein NMB1317 [imported] - Neisseria meningitidis (strain MC58 serog C;Species: Neisseria meningitidis (C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: D81096 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. A;Tuthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58 A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002480; GB:AE002098; NID:g7226555; PIDN:AAF41692.1; PID:g7
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 1164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CWS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:827-945/Region: proline-rich repeats
F:946-1131/Domain: cell wall-spanning #status predicted </
F:1132-1159/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2;
Pred. No. 6.9;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Jerlstreem, P.G.
submitted to the EMBL Data Library, August 1991
A;Reference number: S17038
A;Accession: S17038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.78;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.3%;
                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1164 <JER1>
A;Cross-references: EMBL:X59771
A;Accession: S20240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1.
احد 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |||: || :||
34 KTLSYNLSRFKISIR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:: || |:||| |
8 RKMRYSIRKFSVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 38-48 <JE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: D81096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: NMB1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
A60234
IGA For receptor precursor - Streptococcus agalactiae (strain SB35)
Nicontains: beta antigen
Nicontains: beta antigen
C: Species: Streptococcus agalactiae
R: Heden, L.O.; Frithz, E.; Lindahl, G.
A: Residues: 1-1134 < HED>
A: Residues: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: $14595
A; Accession: $14595
A; Reference number: $14595
A; Reference number: $14595
A; Residues: 1-134 <-HE2>
A; Residues: 1-134 <-HE2>
A; Cross-references: EMBL: X58470; NID:g46520; PIDN:CAA41384.1; PID:g46521
A; Cross-references: EMBL: X58470; NID:g46520; PIDN:CAA41384.1; PID:g46521
A; Note: the source is designated as Streptococcus agalactiae
R; Lindahl, G.; Akerstroem, B.; Vaerman, J.P.; Stenberg, L.
Eur. J. Immunol. 20, 2241-2247, 1990
A; Tilliachl, G.; Akerstroem, B.; Vaerman, J.P.; Stenberg, L.
A; Reference number: A60230; MUID:91055597
A; Accession: A60230
A; MUID:91055597
A; Accession: A60230
A; MUID:91055597
A; Residues: 'X', 39-48, X', 50-52, 'X', 54-56 <LIN>
C; Superfamily: IgA Fc receptor
C; Keywords: cell wall: immunoglobulin receptor; tandem repeat; transmembrane protein
F; 137-Domain: signal sequence #status predicted <IGA1>
F; 139-812/Domain: IgA binding #status predicted <IGA2>
F; 38-1134/TPC promain: IgA binding #status predicted <IGA2>
F; 39-812/Negion: proline-rich repeats
F; 102-1101/Domain: cell wall-spanning #status predicted <TWM>
F; 102-1129/Domain: transmembrane #status predicted <TWM>
                                                                                          g
F;30-130/Domain: propeptide #status predicted <PRO>F;131-148/Product: protegrin 1 #status experimental <MAT>F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%; Score 41; DB 2; Length 1134; 57.1%; Pred. No. 33;
                                                                                                                                                                                            2; Length 149;
                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IgA Fc receptor precursor - Streptococcus agalactiae N;Alternate names: beta antigen
                                                                                                                                                                                                                           ed. No. 5.1;
Mismatches
                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                Score 41;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ښ</u>
                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                        57.7%;
69.2%;
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                         134 RLCYCRRFCVCV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:: || |:||| |
8 RKMRYSIRKFSVGV 21
                                                                                                                                                                                                                                                                                                                                             2 RLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Las 8; Conserve
                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

ö

ö

Gaps

; 0

; 0

```
ATP-binding protein PhnP (phnP) homolog - Archaeoglobus fulgidus

ATP-binding protein PhnP (phnP) homolog - Archaeoglobus fulgidus

C; Species: Archaeoglobus fulgidus

C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C; Accession: F63309

C; Accession: F63309

E; Rish, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do

E; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Alathors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef

A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykef

A; Accession: F69309

A; Accession: F69309

A; Accession: F69309

A; Residus: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-254 <KLE>

A; Residues: 1-254 <KLE>

A; Cross references: GB: AEO01071; GB: AEO00782; NID: g2689394; PIDN: AAB90764.1; PID: g26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F24B22.120 - Arabidopsis thaliana hypothetical protein F24B22.120 - Arabidopsis thaliana (mouse-ear cress) (speciess: Arabidopsis thaliana (mouse-ear cress) (species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000 (spacession: T47575 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000 RiBlocker, H.; Mowes, H.W.; Lemcke, K.F.X.; Quetier, F.; Salanoubat, submitted to the Protein Sequence Database, January 2000 A; Reference number: 223016 A; Accession: T47575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 284/3; 331/3
A;Note: F24B22.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
                                        ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Length 249,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-434 <BLO>
A,Cross-references: EMBL:AL132957
A,Experimental source: cultivar Columbia; BAC clone F24B22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spermatid-specific protein T2 precursor - longfin squid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
    .;
;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
    DB
12;
                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No. 2
    Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%;
53.3%;
        56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.3
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRLSYSRRFFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : |:||| | :
28 RRKGWERKRFSVMVQ 42
                                                   Conservative
                                                                                         1 RRLSYSRRRFSVSVR 15
                                                                                                                    ||:| |||| ||:
49 RRISISRRHFVSCK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S56117
                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                    δλ
                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bubols hypothetical protein AAD39285.1 [imported] - Arabidopsis thaliana hypothetical protein AAD39285.1 [imported] - Arabidopsis thaliana (c. Species: Arabidopsis thaliana (mouse-ear cress) c. Species: Arabidopsis thaliana (mouse-ear cress) c. Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C. Accession: B86273 R. Prheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huidas, B.; Kim, C.A.; Liu, Z.A.; Lucs, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucs, J.S.; Maiti, R.; Marziali, R.; Rochey, T.; Rowley, D.; Sakano, H. Southwick, A.W.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, A; Reference and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-249 <STO>
A; Cross-references: GB: AECO5172; NID: 95080775; PIDN: AAD39285.1; GSPDB: GN00141
A; Cross-references: GB: AECO5172; A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2;
pred. No. 7.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.3%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | | |||| : |
| 134 RLCYCRRRFCICV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLSYSRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οy
```

Σ

ö

ö

```
RESULT 15
Solida
H+-transporting ATP synthase (EC 3.6.1.34) protein 6 - Allomyces macrogynus mitochondric
C; Species: mitochondrion Allomyces macrogynus
C; Date: 19-War-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C; Accession: S63648
R; Paquin, B.; Lang, B.F.
J. Mol. 1810. 1255, 688-701, 1996
A; Title: The mitochondrial DNA of Allomyces macrogynus: the complete genomic sequence fr
A; Reference number: S63638
A; Reference number: S63635, MUID:96226032
A; Molecule type: DNA
A; Residues: 1-262 < PAQ>
A; Residues: 1-262 < PAQ>
A; Residues: 1-262 < PAQ>
A; Rossidues: 1-262 < PAQ
A; Rossidues: 1-262
N;Alternate names: sperm protamin SP
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; S
Bucchem. J. 309, S29-334, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami
A;Reference.number: S56117
A;Accession: S56117
A;Accession: S56117
A;Accession: preliminary
A;Acteule type: protein
A;Residues: 1-118 <a href="Moute: Moute: Novembed">Moute: Novembed = Nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.5%; Score 38; DB 2; Length 118; 88.9%; Pred. No. 14; 1.1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2; Length 262;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.5
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 111111
65 RRRSYSRRR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

Search completed: February 12, 2002, 12:34:40 Job time: 558 sec

ò 셤

ö

Gaps

ö

2; Indels

Mismatches

	•					
ing the state of t				₩ ₩ 1		end.
				**		
•	***					
		and the second second				4. ************************************
		*** **********************************				
					10 (10 m)	
No de la companya del companya de la companya del companya de la c		7. W.				
		±		and the second		
9 <b>%</b>			X			
		en e				
				\$ 1 m		
		**************************************				
			and the second s			
				100 mg		
				and the second s		
			<b>x</b>			
		* #				10

nicotiana t rhizobium m salmonella caemorhabdi autographa bacteriopha

lymnaea sta aquifex aeo tomato mott

homo sapien

lycopersico

099216 | 006661 | 006661 | 006661 | 0066514 | 0066514 | 007262 | 007262 | 007262 | 007362 | 007433 | 001687 | 001687 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 00067 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 000667 | 00

```
ALIGNMENTS
                       VBR1_TMOV
OVUH_LYMST
GLNA_AOUAE
1A12_LYCES
1A1C_TOBAC
NIFA_RHIME
PGTB_SALTY
PTP1_CAEEL
Y140_NPVAC
VREP_BPPHH
1062
257
259
469
485
491
541
593
1026
60
89
7.00.4

4.00.4

4.00.4

4.00.4

4.00.4

4.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4

6.00.4
  P42142 macropus ru
P42131 caenolestes
P42135 dasyurus vi
P42137 macropus ag
P42130 macropus gi
O18745 antechinus
P42130 antechinus
P42131 macropus ru
O18768 parantechinus
P42151 sarcopulus
P42151 sarcopulus
P42151 antechinus
P42152 artichosurus
P42152 artichosurus
P42152 artichosurus
P42120 antechinus
P42120 antechinus
P42120 astechinus
P42120 astechinus
P42120 astechinus
P42120 astechinus
P42130 antechinus
P63013 septa offic
P6303 allomyces m
P55041 mus musculu
O59819 schizosacch
P15012 rhodospiril
P95012 rhodospiril
                                                                                                                                                                                                    (without alignments)
8.184 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                          February 12, 2002, 12:39:52; Search time 67.2 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100059
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP1_MACRU
HSP1_CAEFU
HSP1_DACSVI
HSP1_MACGI
HSP1_MACGI
HSP1_MACGI
HSP1_MACGI
HSP1_MACGI
HSP1_MACRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                          1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                 US-09-485-571-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559
660
661
661
661
677
77
77
77
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                           OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                  Sedneuce:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
```

HSPT ID	HSP1_MACRU ID HSP1_MACRU	STANDARD;	PRT;	59 AA.			
255	01-NOV-1995 (Rel.	32,	Created)	anda to			
2523	01-NOV-1997 (Rel. 3 SPERM PROTAMINE P1.	, as	Last annotation update)	update)			
2 0	Magronie ruf	park bod, on	[epoM) (oone	oia rufa)			
38	Eukaryota; M	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,	data; Crania	ta; Vertek	rata; Eutele	Euteleostom1;	
88	Mammalia; Me	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.	protodontia;	Macropodi	dae; Macropu	18.	
N N	NCB1_10X1D=9321; [1]	341;					
RP	SEQUENCE FROM N.A	M N.A.					
RC :	TISSUE-Sperm;	1					
RX G	MEDLINE-9521	MEDLINE=95215351; PubMed=7700877;	-7700877; Hoottoman	744,52	F 0 4 5 6	2	
Z Z	Relie. J.D., Aldjewski C., Westerman M., Winklein K.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes.";	hylogeny and	., westerman	f marsuple	l protamine	Pl gene	
RL	Proc. R. Soc	Lond., B,	Biol. Sci. 2	59:7-14(19	95).		
ပ္ပ	-! - FUNCTION	PROTAMINES	SUBSTITUTES	FOR HISTO	NES IN THE C	HROMAT	IN OF
ຍູເ	SPERM DU	SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED. STABLE AND INACTIVE COMPLEX	LOID PHASE O	F SPERMATO	GENESIS. THE AND INACTIVE	SY COMP	i ci
ខ្ល	-i- SUBCELLU	SUBCELLULAR LOCATION: NUCLEAR.	: NUCLEAR.	77000	und timestati		;
ပ္ပ	-i- TISSUE S	TISSUE SPECIFICITY: TESTIS.	TESTIS.				
ပ္ပင္ပ	TO CHEST OF THE						
38	This swiss-P between the	SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -	copyrignt. tute of Bioi	it is proc nformatics	uced through	MBL ou	stat
ပ္ပ	the European	Ħ	ics Institut	e. There	are no rest	riction	no st
ပ္ပ	use by non	non-profit ins	institutions as long	long as	its content	is in	00 (
ນູ	modified and	modified and this statement is not removed.	ent 1s not 1 nse agreemer	emoved.	is not removed. Usage by and for commercial	od tor	Somme:
ខ	or send an e	or send an email to license@isb-sib.ch).	nse@isb-sib.	ch).	761	10.010	
ပ္ပ							
DR	EMBL; L35447	EMBL; L35447; AAA74616.1; -					
DR G	InterPro; IP	InterPro; IPR000221; Protamine_Pl.	tamine_Pl.				
DR	PROSITE: PS0	PROSITE: PS00048: PROTAMINE P1: 1.	INE P1: 1.				
KW	Chromosomal	Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;	leosome core	; Spermato	genesis; DNA	1-bindi	; bt
ΚW	Testis; DNA	Testis; DNA condensation; Nuclear protein.	; Nuclear pr	otein.			,
SO	INIT_MET SECUENCE 5	0 0 59 AA; 8230 MW;		BY SIMILARITY. 78F1AE592B4B2FA2 CRC64;	CRC64;		
Que	atch cal Simi		78; Scc 78; Pre	11; DB 1; 40. 0.4;	5		
Wa	Matches 8;	Conservative	1;	Mismatches	2; Indels	ö	Gaps
ΟŊ	1 RELSYSRRES	YSRRFS 11					
qq	43 RFRGYSRRYS	RRYS 53					
1							
HSP1_C	KESULT Z HSP1_CAEFU TD HSP1_CAEFU	CHANDARD	. E40	4			
ì	112 T T CUEE C	יחייםחווים	FNT	5			

azospirillu azospirillu escherichia saccharomyc

Q03153 P54929 P30667 P22520 Q02805

YMY8_YEAST NIFA_AZOLI NIFA_AZOBR CVAB_ECOLI ROD1_YEAST

149 147 147 262 262 295 241 339 1113 1113 612 624 628 638

saccharomyc

```
RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95215351; PubMed=7700877; MEDLINE-95215351; PubMed=7700877; MEDLINE-95215351; PubMed=7700877; Medline-919161; Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsuplal protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
                                                                                                                                                                                  Retief JD., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SIBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasyurus viverrinus (Southeastern quoll), and
Dasyurus hallucatus (Satanellus/Northern quoll).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1; Length 60; Pred. No. 0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clear protein.
BY SIMILARITY.
7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AA
                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP1_DASVI STANDARD; PRT P42135; P42133; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequen 15-JUL-1999 (Rel. 38, Last annota SPERM PROTAMINE P1.
                                                                                                                                                                     TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AA; 8514 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L35332; AAA74598.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                      Caenolestes fuliginosus.
                    01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 RRRGYSRRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                            SPERM PROTAMINE P1.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=37696;
                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_DASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retief J.C., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular Judgeny and evolution of marsupial protamine P1 genes."; "Molecular phylogeny and evolution of marsupial protamine P1 genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

-i. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DIXING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-i. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR00221; Protamine_Pl.
PROSTIE; PS00260; protamine_Pl: 1.
PROSTIE; PS00048; DNA-binding: 1.
PROSTIE; DNA condensation; Nuclear Protein.
INIT_MET O BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

INIT_MST 0 BY SIMILARITY.

SEQUENCE 60 AA; 8246 MW; 615b3D85E7123025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macropus agilis (Agile wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
STABLE AND INACTIVE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32, Last sequence update)
35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
       SPERM DNA INTO A HIGHLY CONDENSED, -:- SUBCELLULAR LOCATION: NUCLEAR. -:- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl; 1.
PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L35451; AAA74615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L35340; AAA74599.1; -. EMBL; L35341; AAA56795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 RRRGYSRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP1_MACAG
P42137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
```

٠.

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
           Antechinomys laniger.
                                          NCBI_TaxID=60701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_ANTSW S
P42130; P42146;
01-NOV-1995 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                     Chromosoma1
                                                                                                                                                                                                                                                                                                                                                        INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
HSP1_ANTSW
 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                     ö
                                                                                                                                                                                                                                                                                                                       Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
--- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIATO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 60;
                                60;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.

SEQUENCE 60 AA; 8415 MW; 1DC25C80C490BC90 CRC64;
96255C818921EB85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                ;
                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                     60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA.
                               Score 41; DB Pred. No. 0.4;
                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                  Macropus giganteus (Eastern gray kangaroo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                            MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.78;
72.78;
                              57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L35333; AAA74604.1; -
8338 MW;
                   Query Match
Best Local Similarity 72.,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                          01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32, 01-NOV-1997 (Rel. 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRRFS 11
                                                                                              53
                                                                          1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRRGYSRRYS 54
                                                                                                                                                                                                           SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
AA;
                                                                                      43 RRGYSRRYS
                                                                                                                                                                                                                                                                  NCBI_TaxID=9317;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998
15-JUL-1998
15-JUL-1998
                                                                                                                                                     HSP1_MACGI
P42139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSP1_ANTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              018745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
HSP1_ANTLA
                                                                                                                                RESULT 5
HSP1_MACGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825558
                                                                          ò
                                                                                             qq
                                                                                                                                                      ò
```

```
the European Bioinformatics Institute.

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm;
SPECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm;
MEDLINE-95215351; Pubmed-7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                      Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                    SEQUENCE FROM N.A. SPECIES=N.lorentzii, D.albopunctatus, D.geoffroii, and D.spartacus; Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID-9284, 9295, 32551, 32545, 63143, 32546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.7%; Score 41; DB 1; Length 61; 72.7%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neophascogale lorentzii (Long-clawed marsupial mouse),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
E021567627E562B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dasyurus albopunctatus (Native cat),
Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antechinus swainsonii, Phascolosorex dorsalis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF001587, AAB91377.1; -.
InterPro; IPR000221; Protemine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
SEQUENCE FROM N.A. MEDLINE-97446280; Pubmed-9299228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Native cat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AA; 8409 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FRLSYSRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM PROTAMINE PI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dasyurus spartacus
```

ö

```
email to license@isb-sib.ch).
     or send an
                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
HSP1_MACRG
                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                              g
       CCC
CCC
DR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way undified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retief J.D., Krijewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
"Molecular phylogeny and evolution of marsupial protamine P1 genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DIXING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                        cytochrome b, 12S frna, and protamine P1 gene trees.";

J. Mammal. Evol. 4:217-236(1997).

J. Mammal. Evol. 4:217-236(1997).

J. Mammal. Evol. 4:217-236(1997).

SPERM DIVING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIVING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPLEX.

SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

-1. SUBCELLULAR LOCATION: NUCLEAR.

-1. TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
           "Reconstructing the taxonomic radiation of dasyurine marsupials with cytochrome b, 12S rRNA, and protamine Pl qene trees.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PF00260; protamine_Pl; 1. PROSITE: PS00048; PROTAMINE_Pl; 1. Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus. NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 61;
Pred. No. 0.41;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 0 BY SIMILARITY.
61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macropus eugenii (Tammar wallaby).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                               EMBL; L35339; AAA74601.1; -.
EMBL; AF010267; AAB69297.1; -.
EMBL; AF010272; AAB69302.1; -.
EMBL; AF010274; AAB69304.1; -.
EMBL; AF010275; AAB69305.1; -.
InterPro; IPR000221; Protaming_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.78;
                                                                                                                                                                                                                                                                                                                          EMBL; L35338; AAB95429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                             L35339; AAA74601.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 RRRGYSRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSP1_MACEU
P42138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP1_MACEU
```

g ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macropus rufogriseus (Red-necked wallaby), and Macropus bicolor (Swamp wallaby). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus. NCBI_TaxID=9320, 9330;
                                                                                                                                       Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                     Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                              Culculosomat processing the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1;
Pred. No. 0.41;
!; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP1_MACRG STANDARD; PRT; 61 AA. P42141; P42153; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PRM1.
                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
EMBL; L35450; AAA74614.1; ...
InterPro; IPR000221; Protamine_Pl.
Pfam; PF00200; protamine_Pl.
PROSITE; PS000048; PROTAMINE_L1; 1.
Chromosomal protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L35329; AAA74610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         57.78;
72.78;
                                                                                                                                                                                                                                                                              61 AA; 8495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                 1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 RRRGYSRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Sperm;
```

S

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                         SPECIES-D. maculatus;
Krajawaki C., Young J., Buckley L., Woolley P.A., Westerman M.;
Rrajawaki C., Young J., Buckley L., Woolley P.A., Westerman M.;
Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S rRNa, and protamine P1 gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBSCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsuptal protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259;7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UNCLEAR.
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testis; DNA condensation; Nuclear protein.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 61 AA; 8410 MW; 4A215D3D85E71230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl. 1.
PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L35324; AAA74608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF010276; AAB69306.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FRLSYSRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9337
                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=:Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosoma1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_TRIVU
P42152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                            Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S rRNA, and protamine P1 gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIATO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-I- SUBCELLULAR LOCATION: HUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dasyurus maculatus (Tiger quoll).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                         Parantechinus bilarni (Broad-footed marsupial mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clear protein.
BY SIMILARITY.
C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE Pl.
                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AA.
                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sarcophilus harrisii (Tasmanian devil), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.harrisii; TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF010277; AAB69307.1; -.
                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00260; protamine_P1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AA; 8421 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                           STANDARD;
                                                                                                                                                  (Rel. 36, C
(Rel. 36, I
(Rel. 37, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9305, 9281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || |||||||||||| 45 RRGYSRRRYS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRLSYSRRFFS 11
54
                                                                                                                                                                                                                       SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=32555;
44 RRRGYSRRYS
                                                                                                                                                15-JUL-1998 (
15-JUL-1998 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP1_SARHA
P42151;
                                                                                                         PARBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                           HSP1_PAF
018768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSP1_SARHA
                                                                                    HSP1_PARBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
```

ò g

ö

Gaps

Gaps

;

Indels

5

Matches

g

δ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; US/139; ABB91327.1; -
EMBL; U87139; ABB91327.1; -
EMBL; U87140; ABB91328.1.
InterPro; IPRO00201; Protamine_Pl.
PROSTIE: PS00048; PROTAMINE_Pl. 1.
PROSTIE: PS00048; PROTAMINE_Pl. 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                               Murexia longicaudata,
Murexia longicaudata,
Murexia longicaudata (Common wambenger),
Sminthopsis crassicaudata (Fat-tailed dunnart),
Myrmecobius fasciatus (Numbat), and
Thylacinus cynocephalus (Tasmanian wolf).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Murexia.
NCBI_TAXID=37736, 9293, 9301, 55782, 9275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomar process, acceptant protein.
Testis; DNA condensation; Nuclear protein.

0 BY SIMILARITY.
CEOTRACE 62 AA: 8566 MW; 99C02857CBB73429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1;
Pred. No. 0.42;
!; Mismatches
                                                                                                                                                          HSP1_MURLO STANDARD; PRT; 62 AA. P42140; P42150; P42154; P42150; P42154; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) SPERM PROTAMINE P1.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissue=sperm;
MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L35336; AAA74600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AA; 8566 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L35327; AAA74606.1; -. L32743; AAA99478.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                     1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                       45 RRRGYSRRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET
SEQUENCE
     8
                                                                                                                                    RESULT 14
HSP1_MURLO
         Matches
                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                               δλ
                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                0;
         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                              Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

INIT_MET O BY SIMILARITY.

SEQUENCE 61 AA; 8571 MW; 802287E627EE816C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse). Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasykaluta. NCBI_TaxID=33560, 9291, 9299;
                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 1; Length 62; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                             Score 41; DB 1; Length 61; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mail protein, National Collins

DNA condensation; Nuclear protein.

DNA condensation; Nuclear protein.

DNA condensation; Nuclear protein.

DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP1_DASRO STANDARD; PRT; 62 AA. p42134; P42144; P42149; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NUV-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                    Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                    IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L35325; AAA74605.1; -. EMBL; L35326; AAA74607.1; -. EMBL; L35337; AAA74603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8585 MW;
                                                                                                                                                                                                                                                                                                      57.78;
72.78;
                                                                                                                    EMBL; L32744; AAA99479.1; -.
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restis;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
HSP1_DASRO
```

ö

Gaps

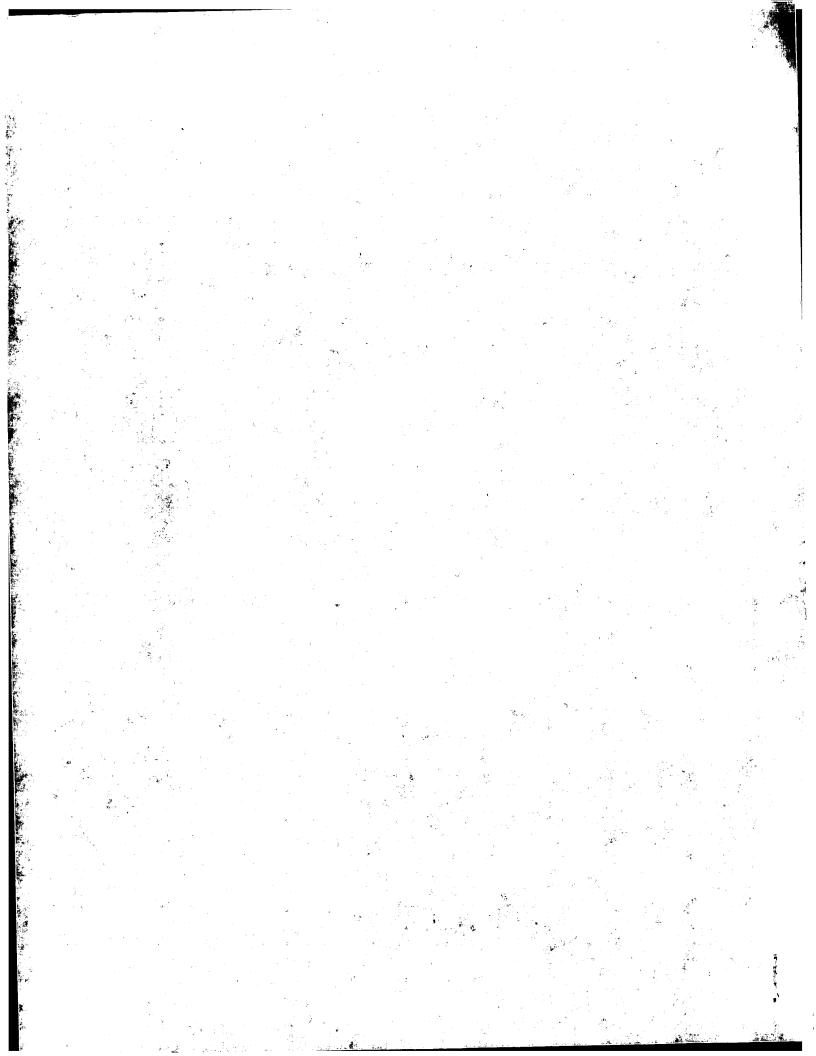
0;

Length 62; Indels

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl. 1.
PROSITE; PS00048; PROTAMINE_Ll; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT_MET 0

BY SIMILARITY.
                                                                                                              Antechinus stuartii (Brown marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 57.7%; Score 41; DB 1; Length 63; Best Local Similarity 72.7%; Pred. No. 0.43; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AA; 8722 MW; D4FF992DAAB56D61 CRC64;
                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SPERM PROTAMINE Pl.
                63 AA
                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L35335; AAB95428.1; -. InterPro; IPR000221; Protami
                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
              HSP1_ANTST
P42129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
HSP1_ANTST
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

Search completed: February 12, 2002, 12:39:52 Job time: 805 sec



Perfect score:

Run on:

Scoring table: Sequence:

Searched:

```
Ogratia streptococc
Ogkkio streptococc
Ogkkio streptococc
Ogkki streptococc
Ografi streptococc
Ografi streptococc
Ografi streptococc
Ografi streptococc
Ogkki streptococc
Ogkki streptococc
Ogkki streptococc
0991q2 lagorcheste
09heb6 neurospora
099051 streptococc
091x33 netsseria m
09x188 arabidopsis
09Jmf9 arabidopsis
09Jmf9 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strept.ococcus pneumoniae.
sateria: Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus.
NCBL_THXID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Iannelii F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF154042; AAF73815.1;
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002865; P_rich_extensn.
Pfam; FR00746; Gram_pos_anchor; I.
PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 465 AA; 51584 MW; F2C2572BF5FF06CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2;
Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
  099GL02
09HEB6
099051
09JZ33
09JZ33
09JZ38
09JZ38
09JZ38
09JZ38
09KZ15
09KK15
09KK15
09KK41
09KK41
09KK41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FDQ1
Q9KK37
Q9LQX6
Q67615
Q9RQT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                       09KK40
09KK24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09RQT6
09KK34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, SURFACE PROTEIN PSPC.
                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9K2I5
Q9K2I5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
        244444
244444
244444
244444
24444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2446
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2444
2446
2444
2444
2444
2444
2444
2446
2446
2446
2446
2446
2446
2446
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29K215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09kk09 streptococc
09kk12 streptococc
09kk45 streptococc
09kk25 streptococc
09y4f1 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               macropus pa
onychogalea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potorous lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     onychogalea
sminthopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          petrogale x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9k2i5 streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aepyprymnus
                                                                                                                                                                                                                         (without alignments)
9.431 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peradorcas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                          February 12, 2002, 12:38:40; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09cu47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          099195
099193
099193
099198
099191
099197
099197
099197
099197
099190
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM protein – protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09K215
09KK09
09KK12
09KK12
09KK45
09CU47
09CL03
09CL03
09CL03
09CL03
09CL03
09CL04
09
                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4: sp_human:*
5: sp_invertebrate:*
6: Sp_mammal:*
77: sp_mho.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                        RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
                                                                                                                                                                                                                                                                                          US-09-485-571-24
71
1 RRLSYSRRFFSVSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622.0
662.0
662.0
552.0
557.7
557.7
557.7
557.7
557.7
557.7
```

580 AA

PRT;

PRELIMINARY;

Q9KK09 Q9KK09;

RESULT Q9KK09 ID Q9 AC Q9

bettongia p sminthopsis sminthopsis

dorcopsulus

Score

Result ٠ چ 7

```
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tannelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
Tannelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
Iannelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein Pspc (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; Length 763;
Pred. No. 13;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%; Score 44; DB 2; Length 587; 64.3%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                              Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS4014; AFR77322.1;
InterPro; IFR01899; Gram_Pos_anchor.
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL. AF154033; AAF73803.1: -
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002965; P_Iich_extensn.
pfam; PR001217; PRCHEXTENSN.
PRINTS; PR01217; PRCHEXTENSN.
PROSTTE; P800343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 763 AA; 85198 MW; 0FE48A286F6EB197 CRC64;
                                                                                                                                                                                                                                                                                                                                                pfam; PF00746; Gram_pos_anchor; 1.
PRINTS; PR01217; PRTCHEXTENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 587 AA; 65798 MW; 1F7FB5ACD988299E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      763 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches-
587 AA.
                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
SURFACE PROTEIN PSPC.
                                 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                         pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||: || |:||| |
REMRYSIRKFSVGV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRLSYSRRFFSVSV 14
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SURFACE PROTEIN PSPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1313;
                                                                                                                                                             Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                               Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9KK25
Q9KK25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
     Q9KK45
Q9KK45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KK25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
       Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                        Streptococcus pneumoniae.
Bactilus/Clostridium group; Streptococcaceae; Streptococcus.
Streptococcus.
NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lannelli F., Oggioni M.R., Spinosa M.R., Pozzi G.;
"Allelic variants of surface protein PspC (SpsA, CbpA, PbcA) of
                                                                                                                                                                                                  SEQUENCE FROM M.A., Spinosa M.R., POZZI G.;

"Allelic variants of surface protein Pspc (SpsA, CbpA, PbcA) of
"Allelic variants of surface protein Pspc (SpsA, CbpA, PbcA) of
Streptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF154045; AAF73826.1;
EMBL: AF154045; AAF73826.1;
InterPro: IPR001899; Gram_pos_anchor.

Fram: PF00746; Gram_pos_anchor.

PRINTS: PR01217; PRICHEXTENSN.

PROSITE: PS00343; GRAM POS_ANCHORING; UNKNOWN_1.

SROUENCE 580 AA; 64957 MW; 272A0DB307A3E94C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2; Length 584; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2; Length 580;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arreptococcus pneumoniae.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF154044; AAF73821.1;
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00746; Gram_pos_anchor; 1.
PRINTE; PR01217; PRICHERYENSN.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 584 AA; 65449 WW; D309081C74A24D08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UT-2001 (TrEMBLrel. 17, Last annotation update)
SURFACE PROTEIN PCPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            62.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.0
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRLSYSRRRFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 REMRYSIRKFSVGV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRLSYSRRFFSVSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SURFACE PROTEIN PSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1313;
```

Q9KK12 O9KK12;

ID DTT NAME OF THE NAME OF T

RESULT Q9KK12

g

ò

ö

Gaps

ö

ö

Gaps

ö

SEQUENCE

RESULT Q9KK45

qq δλ

.

us-09-485-571-24.rspt

ì

```
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peradorcas concinna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RELSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=69272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 RRRGYSRRRYS
                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09GLQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09GLQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q9GLQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GLQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
    RA
RA
RA
RA
RA
DR
RT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and characterization of CDEP, a novel human protein containing the ezrin-like domain of the band 4.1 superfamily and the Dbl homology domain of Rho guanine nucleotide exchange factors."; Blochem. Blophys. Res. Commun. 241:369-375(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN—C57BL/6J; TISSUE—MEDULLA OBLONGATA;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
MEDLINE—21085660; PubMed=11217851;
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburnor M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                              Koyano Y., Kawamoto T., Shen M., Yan W., Noshiro M., Fujii K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 4; Length 1045;
Pred. No. 28;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OE8B2D61C0F58417 CRC64;
                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) 6330406115RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AA.
                     PRT; 1045 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00660; BAND_41_1; UNKNOWN_1.
PROSITE; PS50057; BAND_41_3; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                   TISSUE-CARTILAGE;
MEDLINE-98086358; PubMed-9425278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; PPR000299; Band_4.1.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
Fram; PF00373; Band_41; 1.
Pfam; PF00169; PH; 2.
Pfam; PF00169; PH; 2.
Pfam; PF00169; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1045 AA; 118632 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blochem. Blophys. Res. Commun.
EMBL; AB008430; BAA24267.1; -.
HSSP; P08567; 1PLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.68;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00295; B41; 1.
SMART; SM00233; PH; 2.
SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.6
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||: |:|| ::|
267 RKLSFKRKRFLIKLR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRLSYSRRRFSVSVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6330406I15RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                        Q9Y4F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9CU47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
09Y4F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09CU47
                        SO DE REPRENTATION OF THE SECOND OF THE SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Burk A., Springer M.S.;

Burk A., Springer M.S.;

Burk A., Springer M.S.;

J. Manmal. Evol. 0:0-0(2000).

J. Manmal. Evol. 0:0-0(2000).

I. FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 60 AA; 8436 MW; B0F0943F6F8BF58B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Peradorcas.
                                                                                                                                                                                                                                                                                                    'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 11; Length 299;
Pred. No. 12;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 6; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AA; 34095 MW; C81170399A6F2882 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).

-1- SIMILARITY: TO THE PROTAMINE P1 FAMILY.

EMBL; AR187538; AG27955.1; -1

InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                Nature 409:685-690(2001).
EMBL; AK018128; BAB31084.1; -.
MGD; MGI:1917967; 6330406115Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GLQ5;
01-MAX-2001 (TrEMBLrel. 16,
01-MAX-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 60...
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || |:| |:|||:||
244 RRSSFSDRKFSVTSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRRFSVSVR 15
```

Length 61;

```
1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 RRRGYSRRYS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                   1 RRLSYSRRRFS 11
                                                                                                                                   54
                                                                                                                                                                                                                                                                                                                                                                            SPERM PROTAMINE P1
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=38598;
                                                                                                                       44 RRRGYSRRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GLP8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9GLP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                             RESULT 11
Q9GLP9
                                                                                                                                                                                                                                                               Q9GLP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                  Óλ
                                                                                                                                           pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BUTK A., Springer M.S.;
Butk A., Springer M.S.;
Butk A., Springer M.S.;
J. Mammal. EVO. 10.0 (2000).
J. Mammal. EVO. 10.0 (2000)
J. PUNCTION: PROTABULINES UNSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING THE HAPLOID PHASE OF STABLE AND INACTIVE COMPLEX (BY SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY STERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY STABL
                                                                                                                                                                                                                                                                                                                          J. Mammal. Evol. 0:0-0(2000).

-i- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROWATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DURING THE HAPLOID PHASE OF STABLE AND INACTIVE COMPLEX (BY SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 61 AA; 8500 MW; A07F5C8LC4664B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onychogalea fraenata (bridled nail-tailed wallaby).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
NCBI_TaxID=114227;
                                                                                                               Macropus parryi (Whiptail wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA; 8454 MW; CBB8EFC966E44B6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
--- SUBCELLUTAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL: API87542: AAG27959.1:
Interpro; IPR000221; Protamine_Pl.
               "J" AT 18 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                          STEMICARITY).

-1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1. TISSUE SPECIFCITY: TESTIS (BY SIMILARITY).

-1. SIMILARITY: TO THE PROTAMINE P1 FAMILY.

EMBL: AF187533; AAG27950.1;

EnterPro: IPR000221; Protamine_P1.

Pfam: PF00260; protamine_P1.

PROSITE; PS00048; PROTAMINE_P1.

PROSITE; PS00048: PROTAMINE_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 6;
Pred. No. 3.7;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 RRRGYSRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9GLQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09GLQ3
```

g ò

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Burk A., Springer M.S.;

Burk A., Springer M.S.;

The Chronicle of Kangaroo Evolution.";

J. Mammal. EVO. 0:0-0(2000).

J. Mammal. EVO. 0:0-0(2000).

SPERM DIAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIAMINTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY SPERM DURING THE MAPLOID PHASE OF STABLE AND INACTIVE COMPLEX (BY STABLE AND INACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promit Pr00260; protamine_P1; 1.
PROSTIE: PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potcous longipes (long-footed potoroo).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aepyprymnus rufescens (rufous rat-kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Aepyprymnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 6; Length 61;
Pred. No. 3.7;
1; Mismatches 2; Indels
                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA; 8576 MW; 7B324691290717AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
--- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
---- STHILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF187547; AAG27964.1; ---
INTERPRO! IRRONO221; Protamine_P1.
DB 6;
3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AA.
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burk A., Springer M.S.;
Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).
EMBL, FX187548, AAG27965.1; -
InterPro; IPR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl: 1.
     Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequent Jun-2001 (TrEMBLrel. 17, Last annumentation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.78;
72.78;
          57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
```

ö

```
Search completed: February 12, 2002, 12:38:40 Job time: 753 sec
[1]
SEQUENCE FROM N.A.
MEDLINE-99310778; Pubmed-10381317;
                                                                                                                                                                                                                                                                                                                                                    1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                  || ||||||||||| 46 RRGYSRRRYS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRLSYSRRFFS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I, |||||:|
RRGYSRRRYS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTAMINE P1
                                                                                                                                                                                                                                                                                                                                                                                                                                         09GL07
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
09GLQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45
 ò
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                            ö
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES-O.unguifera, D.goodfellowi, and S.brachyurus;
SPECIES-O.unguifera, D.goodfellowi, and S.brachyurus;
Burk A., Springer M.S.;
The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:-0-0(2000).
J. Mammal. Evol. 0:-0-0(2000).
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                         Onychogalea unguifera (northern nail-tailed wallaby),
Dendrolagus goodfellowi (Goodfellow's tree kangaroo), and
Setonix brachyuus (guokka).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sminthopsis longicaudata (long-tailed dunnart).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
NCBI_TaxID=90764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                            ö
                                  Score 41; DB 6; Length 61;
Pred. No. 3.7;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 6; Length 61; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA; 8546 MW; F0D55C81C4664B62 CRC64;
D745F1F638DDBCDC CRC64;
                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                         61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequ
01-UNY-2001 (TrEMBLrel. 17, Last anno
SPERM PROTAMINE PL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF187541; AAG27958.1; -. Pro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF187537; AAG27954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.78;
72.78;
                                  Query Match 57.7%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF187543; AAG27960.1;
8431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRRFS 11
                                                                                                  1 RRLSYSRRRFS 11
                                                                                                                                                                                                                                      SPERM PROTAMINE P1.
61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
SEQUENCE
                                                                                                                                                                                      096301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09TUC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9TUC2
                                                                                                                                                                         096301
                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096701
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                    ò
                                                                                                            g
                                                                                                                                                                                      ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                         Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 62 AA; 8640 MW; A9EEA7D7C77964A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Petrogale xanthopus (Ring-tailed rock wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria; Diprotodontia, Macropodidae; Petrogale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0.0-0 (2000).
J. Mammal. Evol. 0.0-0 (2001).
InterPro; IPR000221; Protamine_P1.
Pfam. PF0020; protamine_P1.
PROSTE: FS00048; PROTAMINE_P1 UNKNOWN 1.
SEQUENCE 62 AA; 8656 MW; BEBEG85C8089D007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                           SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL: AF089881; AAD55340.1; -.
InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 6;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 6
Pred. No. 3.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                 Pfam; PF00260; protamine_P1; 1.
PROSTE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.78;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 72...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 57.7
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
```

antimicr antimicr antimicr PG-1. S

Cationic, Cationic, Protegrin

Cationic,

Protegrin peptide
Antimicrobial prot
Antimicrobial prot
Antimicrobial prot
Cationic, antimicr
Cationic, antimicr
Cationic, antimicr
Cationic peptide
Protegrin peptide
Protegrin peptide
Protegrin peptide
Protegrin peptide
Protegrin peptide
Antimicrobial prot
Antimicrobial comp
Antimicrobial comp
Antimicrobial protegrin
Protegrin peptide
Antimicrobial comp
Antimicrobial protegrin
Protegrin peptide

Post-processing:

Database

sed

Minimum DB Maximum DB

Title: Perfect score:

Sequence:

protein

ĕ

Run on:

Scoring table:

Searched:

Cationic, antimicr Cationic, antimicr Cationic, antimicr Tachytegrin and/or Tachytegrin and/or Tachytegrin and/or Cationic, antimicr Cationic, antimicr

- nsed

Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells

Σ

Kaczorek

ď

Grassy

Ř

щ

Calas

Query Match

Score

Result Š.

1000.0 1000.0 1000.0 1000.0 89.0 89.0 73.6 72.5 72.5

2 3 4 4 7 7 110 110

WPI; 1999-190034/16

```
containing at least 5, protegrin, and are mining and are mining at least 7 consecutive as from (a). Containing a side chain that includes a basic group; be Trp; each B is an acontaining a side chain that includes a basic group; and each X is an aliphatic or aromatic as. The linear peptide may be and each X is an aliphatic or aromatic as. The linear peptide may be critically at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 5, preferably at least 7 consecutive as from (a)-(c). Containing at least 7 consecutive as from (a)-(c). Containing perfects and are termed peptide antibiotics. They fall into 3 main containing bends due to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of with no major structure but containing bends due to the presence of the innear peptide antibiotic categories defined above: (a)-peptides of the innear peptide designed on peptides able to cross to protegrins; and (c)-peptides are based on tachyplesins. This sequence contragrines and is conjugated to a doxorubicin molecule by a succinate the BBB and is conjugated to a doxorubicin molecule by a succinate the BBB and allowed linker. The peptide may also be linked to a benzylpenicillin molecule of contingates of the linear peptide the peptide may also be linked to a benzylpenicillin molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugates of the linear peptides and the active agent are particularly conjugates of the linear or diagnose brain cancer, Alzheimer's or used to treat, prevent or diagnose brain and meningitis, but also for parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93179 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200032236-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                        88888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1- X16;
                                                                                      This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 91; DB 20;
100.0%; Pred. No. 3.5e-08;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protegrin-like peptide antibiotic Doxo-SynB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example I; Page 13; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93177 standard; peptide; 18 AA.
                                                              Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98FR-0015074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                          18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93177;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY931
```

Gaps

;

Length 18; Indels

100.0%; Score 91; DB 21; 100.0%; Pred. No. 3.5e-08; ive 0; Mismatches 0;

A);

ŏ g

^note= "cross-links to a molecule of dalargin via a disulphide linker"

Temsamani J;

98FR-0015074 99WO-FR02938

Location/Qualifiers

3

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                         ö
                                                                                                                                                    coupled to an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                      vectors for active ingredients, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used to treat, prevent or diagnose brain cancer, Alzheimer's or
Parkinson's diseases, depression, pain and meningitis, but also for
studying drug behaviour in BBB models.
                  Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 91; DB 21; Length 18; 100.0%; Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                  invention relates to the use of linear peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93615 standard; peptide; 18 AA.
                                                                                                       Example II; Page 20; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-FR02939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 rggrlsysrrrfststgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
AAY93615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE STATE OF THE S
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics for the peptide antibiotisc family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the
                                                                                                                                                     comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, particularly that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; ribozyme; antitumour agent; antiviral; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                     New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - nsed
                                                                                                                                            specification describes a pharmaceutical composition, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derivatives of antibiotic peptides lacking disulfide bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 91; DB 21;
100.0%; Pred. No. 3.5e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99403 standard; peptide; 18 AA
                                                                                                Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rggrlsysrrfststgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-190034/16.
WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                      18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9907728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW99403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AAW99403
```

SSSSSSSX

```
1 RGGRLSYSRRFFSTSTGR 18
                                                 1 rggrlsysrrrfsvsvgr 18
                                                                                                                                                                                                                             AAW18153
                                δλ
                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, marticularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81; DB 21; Length 18; pred. No. 1.5e-06; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                         JB 47.
.5e-06;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                               Score 81; DB 20;
Pred. No. 1.5e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93616 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                      89.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-FR02939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 rggrlsysrrrfsvsvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-412166/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93616;
                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93616

IID AAY9.

XX XX AAX9.

XXX AAX9.

XXX AAX10.

XX AAX10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
```

g δ

```
The present sequence is a specifically claimed example of a peptide, crecombinantly produced, corresponding to the generic formula: recombinantly produced, corresponding to the generic formula: an abasic amino acid; A2 and A3 = a small amino acid; A4 = a where A1 = a basic amino acid; A2 and A3 = a small amino acid; A1 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, conternial products and its N-terminal acylated and/or C-terminal amidated or estarlied forms, all of which may contain a disulphide bond to give a cystine residues are replaced by a hydrophobic, small or the cystine residues are replaced by a hydrophobic, small or the content of anti-fungal agents in plants and are useful as anti-bacterial, anti-viral and designated protegrins and are useful as anti-bacterial, anti-viral and continuous and are virus or microbial or viral infection in plants by preventing the residues are replaced disease caused by microorganisms e.g. treatment of sexually transmitted disease caused by microorganisms of candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and septivatives for food. The protegrins are more effective under a spreservatives for food. The protegrins are more effective under a spreservatives for food. The protegrins are more effective under a persibility products and are non-toxic to the cells of serum) than certain
                                                                                                                                                          Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                  Cationic, antimicrobial, virus-neutralising protegrin PC-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCA-) UNIV CALIFORNIA LOS ANGELES.
AAW18153 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 64; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0499523.
                                                                                 11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                      WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                             28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                              Synthetic.
                                              AAW18153;
```

ö

Gaps

; 0

89.0%;

Conservative

Query Match Best Local Similarity Matches 16; Conserv

ò g

```
AAY22007 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-385321/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA;
                                                                                                                                                                                                                                                                                                                                                                                   03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                     01-DEC-1998;
                                                                                                                                                                                                                                                                                      WO9927945-A1
                                                                                                                                                                                                                                                                                                                      10-JUN-1999.
                                                                                                           23-AUG-1999
                                                                                                                                                                                                                                                        Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang CC,
                                                                            AAY22007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW36429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
                               AAY22007
                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention, and comprises 10.30 amino acid residues based on a naturally-occurring protegrin peptide. The antimicrobial peptide is useful in environmental composition for application to plants or plant environments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by Staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antibiotic-resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gram-negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for anaterials such as foodstuffs, cosmetics, medicaments or other materials containing nutrients for organisms. The peptides exhibit decreased haemolytic activity against human red blood cells as compared with native for and melittin. They have improved serum compatibility and therefore improved uses as systemic antibiotics. At the same time the peptides
                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide: protegrin: microbe growth inhibitor; Pseudomonas; microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy; antibiotic-resistant bacterium; disinfectant composition; preservative; haemolytic activity; systemic antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents an example of an antimicrobial peptide (I) of
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   provide broad spectrum activity with a low frequency of resistance
                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
Score 67; DB 18; Length 10
Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 20; Lengtn Lo
Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                 Antimicrobial peptide derivative of protegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial threonine-containing protegrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehrer RI, Radel PA;
                                                                                                                                                                                      AAY22005 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INTR-) INTRABIOTICS PHARM INC
              73.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US25458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0984294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 rggrlcycrrfctcvqr 18
                                                                          1 RGGRLSYSRRRFSTSTGR 18
                                                                                                          1 rggrlayarrrfavawgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.5
Best Local Similarity 72.2
Matches 13; Conservative
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-385321/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen J,
         Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                W09927945-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1998;
                                                                                                                                                                                                                                                     23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang CC,
                                                                                                                                                                                                                      AAY22005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                        œ
```

```
materials such as foodstuffs, cosmetics, medicaments or other materials containing nutrients for organisms. The peptides exhibit decreased haemolytic activity against human red blood cells as compared with native PG-1 and melittin. They have improved serum compatibility and therefore improved use as systemic antibiotics. At the same time the peptides provide broad spectrum activity with a low frequency of resistance.
                                                                                                                                                                    Antimicrobial peptide; protegrin; microbe growth inhibitor; Pseudomonas; microbial infection; Staphylococcus aureus; Helicobacter pylori; therapy; antibiotic-resistant bacterium; disinfectant composition; preservative; haemclytic activity; systemic antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an example of an antimicrobial peptide (I) of the invention, and comprises 10-30 amino acid residues based on a naturally-occurring proceptin peptide. The antimicrobial peptide is useful in environmental composition application to plant environmental composition to application to plant environments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antiblotic-resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gram-negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.5%; Score 66; DB 20; Length 18; 72.2%; Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                  Antimicrobial peptide derivative of protegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial threonine-containing protegrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen J, Lehrer RI, Radel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW36429 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0984294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 72.2
Matches 13; Conservative
```

ö

a

ò

Cationic, antimicrobial, virus-neutralising protegrin IB-288. Antibacterial; antiviral; antifungal; antibiotic; endotoxin;

(first entry)

11-AUG-1997

AAW09084;

AAW09084 standard; peptide; 18 AA.

11

RESULT

AAW09084

/note= "results in bullet form peptide"

Location/Qualifiers

/note= "Acylated"

Disulfide-bond

WO9637508-A1

28-NOV-1996

(UYCA-) UNIV CALIFORNIA LOS ANGELES.

95US-0499523. 95US-0451832. 96WO-US07594

24-MAY-1996;

```
Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; saxually transmitted disease; oral mucositis; praminegative sepsis; endocarditis; pneumonia; blocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Stephylococcus aureus; systemic candidiasis.
   Antimicrobial protegrin peptide (229).
                                                                                                                                                                                                                     21-NOV-1996;
22-NOV-1995;
                                                                                                                                                                                  29-MAY-1997
                                                                                                                                             Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                      Synthetic
```

```
Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                Synthetic,
                                                                                                                                                                 food.
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faacium or faecalis, penicillin resistant streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MSGA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 18; Length 18;
Pred. No. 0.00056;
;; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        (INTR-) INTRABIÓTICS PHARM INC. (REGC.) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
66.78;
                                                                                                                                                                                                                                                                                                             96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                    96WO-US18544,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 AA;
                                                                                                                                                                                                                         WO9718826-A1
                                                                                                                                                                                                                                                                                                                                              17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                  22-NOV-1996;
```

```
The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

CC A1 = a basic amino acid; A2 and A3 = a small amino acid; A3. A12 and A16 = a hyprophobic amino acid; A17 and A14 = a hydrophobic amino acid; A18 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; hydrophobic or small amino acid; neutral/polar, hydrophobic or small amino acid; This has a charge of a centrified forms, all of which may contain a disulphide bond to give a esterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cesterified in a minals. The protegrins confer resistance to microbe viral infection in plants by preventing the growth of a virus or microbe are particularly useful for the treatment of sexually transmitted are particularly useful for the treatment of sexually transmitted are particularly rependent pallidum and Neisserial gonorrhoese. They can also the used in each are particularly mand Neisserial gonorrhoese. They can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                          Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 65; 106pp; English.
            Kokryakov VN,
                                                                                                                        WPI; 1997-033984/03.
                         Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sednence
```

-

1 RGGRLSYSRRRFSTSTGR 18 

> ò a

ö

Gaps

;

9 9

```
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW18151;
                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food
                                                                                                                                                                                                                                                                                                                                                        AAW18151
ò
                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysteine bridge. Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

Al-A2-A3-A4-A5-A4-A7-Cys-A3-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where Al = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may be absent or a basic, neutral/polar or small amino acid or proline; A17 may be absent or a basic, neutral/polar, hydrophobic or small amino acid and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; This has a charge of at
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                       care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                               ö
                                                                                                                                                                                                                                                                                       Cationic, antimicrobial, virus-neutralising protegrin IB-289
                                                                                                                                                                                                                                                                                                                     Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                    Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preser
           Length 18;
                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "results in bullet form peptide"
           DB 18;
                                               Mismatches
             Score 65;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCA-) UNIV CALIFORNIA LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehrer
                                                                                                                                                                                         AAW09085 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 65; 106pp; English.
             71.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0499523
95US-0451832
                                                                                              Kokryakov VN,
                                                                           1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                        (first entry)
          Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995;
                                                                                                                                                                                                                                                       11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                          12
```

```
and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Basic cr small amino acid; A5, A7 and A1 = a hydrophobic amino acid; A1 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A18 may be absort or a basic, hydrophobic or small amino acid; and A18 may be absort or a basic, neutral/polar, hydrophobic or small amino acid; A14s has a charge of at least +3 and its N-terminal acidited and adisulphide bond to give a cysteine bridge. This peptide is in snake form where all the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin PC-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 65; DB 18;
Pred. No. 0.00056;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW18151 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0499523
95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1996
```

```
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cyg-A7-Cyg-A9-A10-A11-A12-Cyg-A14-Cyg-A16-(A17-A18) where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic amino acid; A5 A and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may be absent or a basic, neutral/polar,
cystine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotroxin of graminegative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic, antimicrobial, virus-neutralising protegrin PC-56.
                                                                                                                                                                                                                                                                                                                                     Score 64; DB 18; Length 18;
Pred. No. 0.00081;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harwig SSL, Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18152 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0499523
95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US07594
                                                                                                                                                                                                                                                                                                                                             70.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 rggrlawarrrfavavgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                 Query Match 70.3
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                          18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW18152;
                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW18152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XX
                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                        5555555555555555
```

```
ö
hydrophobic or small amino acid; and Al8 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysterine bridge. This peptide is in snake form where all the cystine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and an anti-bacterial, anti-viral and resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-
                                                                                                                                                                                  negative bacteria. The protegilns are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Trepromem pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; antiviral; antifungal; antiblotuc; endocoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin PC-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 18; Length 18;
Pred. No. 0.00081;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "results in kite form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18150 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0499523.
95US-0451832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                   70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||:|:|||: | ||
| rggrlayarrrwavavgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-033984/03
                                                                                                                                                                                                                                                                                                                                     18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW18150;
                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW18150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                     $$$$$$$$$$$$$$$$$$$$$$$$$$$$$
```

```
The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-A17-A18)

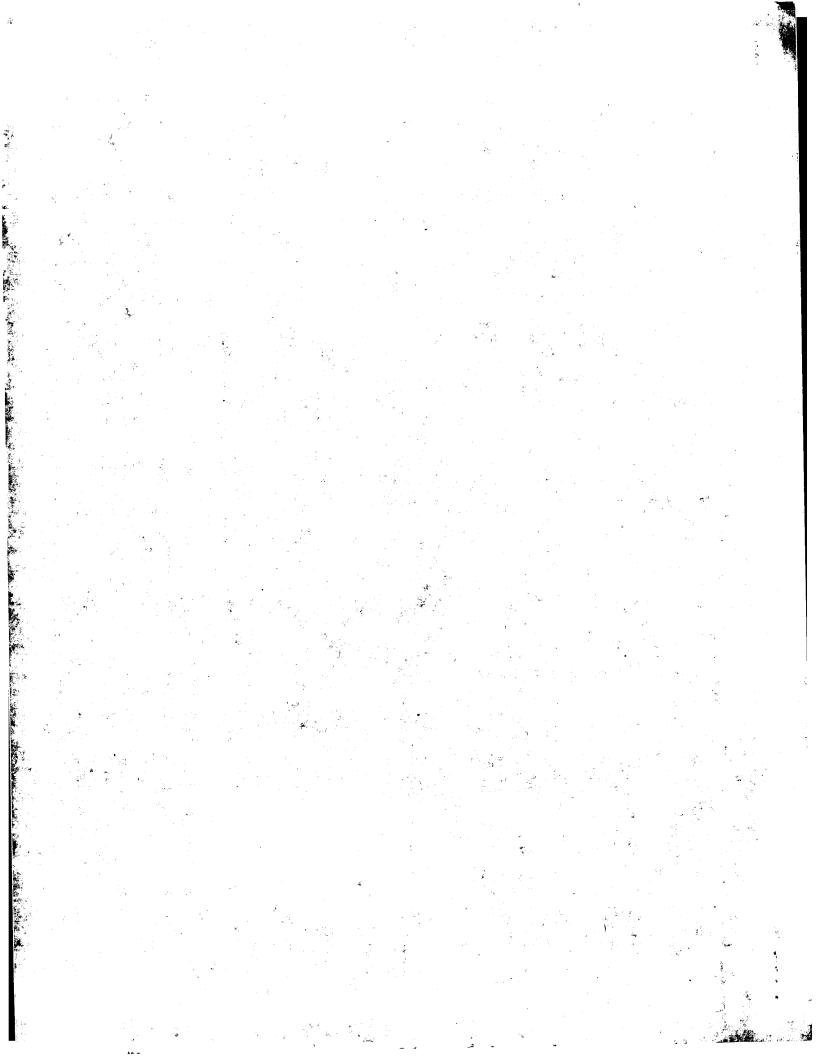
where A1 = a basic amino acid; A2 and A3 = a small amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A9, A12 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysteine bridge. Peptides of this formula are designated protegrins and create state and animals. The protegrins confer resistance to microbel or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia transmins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the
useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                 Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the presence of serum) the cells of higher organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
```

Score 63; DB 18; Length 18; Pred. No. 0.0012; 2; Mismatches 4; Indels Search completed: February 12, 2002, 12:30:32 Job time: 365 sec 1 RGGRLSYSRRFFSTSTGR 18 Query Match
Best Local Similarity 66.7'
Matches 12; Conservative g ò

69.2%; 66.7%;

ö

0; Gaps



OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result Š

Searched:

16, Appl 48, Appl 36, Appl 2, Appl 10, Appl 10, Appl 17, Appl 17, Appl 16, Appl 16, Appl 25, Appl 37, Appl 37, Appl

Appli Appli Appl

```
Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1
                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                     Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence Sequence
                                                                                                                                                Sequence
                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 3; Length 18;
Pred. No. 0.00017;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert I.
TITLE OF INVENTION: THREONINE-CONTAINING PROFECRINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
US-08-752-853-1

US-08-752-853-1

US-08-984-294-1

US-09-128-345-11

US-09-128-345-16

US-09-128-345-16

US-09-128-345-33

US-09-128-345-33

US-09-128-345-3

US-08-23-3

US-08-499-523-10

US-08-128-345-2

US-08-128-345-2

US-08-128-345-10

US-08-128-345-10

US-08-128-345-10

US-08-128-345-10

US-08-128-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16

US-08-138-345-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZUP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOGTWARE: FastESQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/984,294
FILING DATE: 03-DEC-1997
CLASSIFICATION SATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-984-394-6; Sequence 6, Application US/08984294; Patent No. 6043220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 00
TELECONMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6043220e
US-08-984-294-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.5%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.5
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
        000000000000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appli
                                                                                                                                                                                                                          (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           February 12, 2002, 12:32:23; search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTuS_COMB.pep:*
                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-499-523-11
US-08-499-523-16
US-08-499-523-33
US-08-499-523-48
US-08-752-852A-1
US-08-752-852A-9
US-08-752-852A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08 499-523-63
US-08 499-523-67
US-08 499-523-67
US-09-128-345-67
US-09-128-345-67
US-08-499-523-58
US-08-499-523-58
US-08-128-345-58
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-128-345-59
US-08-182-483A-2
US-08-243-879A-1
US-08-243-879A-1
US-08-243-879A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                              US-09-485-571-25
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
```

ö

Gaps

```
NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: Small, or a large polar amino acid"

US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                       COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION .514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.24
REFERENCE/POCKET NUMBER: 2000-0540.24
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-150
TELEPHONE: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEO ID NO: 63:
SEQUENCE CHARACTERISTICS:
TENGTH: 18 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORRYTON: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%; Score 65; DB 1; 1
66.7%; Pred. No. 0.00024;
tive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 67, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2000 Pen
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                STREET: ZOUV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 3; Length 18; Pred. No. 0.00017;
                                                                                                                                                                            Sequence 8, Application US/08984294
; Sequence 8, Application US/08984294
; Patent No. 6043220
; GENERAL INFORMATION:
    APPLICAMT: Chang, Jie
    APPLICAMT: Lehrer, Robert I.
    APPLICAMT: Lehrer, Robert I.
    APPLICANT: Lehrer, Sedmonds LLP
    APPLICANT: New York
    APPLICANT: New York
    APPLICANT: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008067-0049-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE ASSETTE MEDIUM TYPE: DISKETTE COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSCO VOESION 2.0 CURRENT APPLICATION DATA: US/08/984,294 APPLICATION NUMBER: US/08/984,294 FILING DATE: 03-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 63, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAWE: Coruzzi, Laura A
REGISTRATION UNDRER: 30,742
REFERENCE/DOCKET NUMBER: 00806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELERX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-DEC-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: No. 6043220e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLCYCRRRFCVCTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.5%
Best Local Similarity 72.2%
Matches 13; Conservative
                                           RGGRLSYSRRFFSTSTGR 18
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-984-294-8
                                                                                                                                                       RESULT 2
US-08-984-294-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                    ŏ
```

0; Caps

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: group(6, 8, 13, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a
GTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-63
                                                                                                                                                 71.4%; Score 65; DB 2; Length 18; 66.7%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 4; Length 18;
Pred. No. 0.00024;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDUNT TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/POCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.48;
66.78;
                                                                                                                                                                                                                                     1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                          1 RGGRLCYARREFAVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME, KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGGRLXYXRREXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 71.4 Best Local Similarity 66.7 Matches 12; Conservative
                                                                                                                                                                                            12; Conservative
                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
      TYPE: amino acid STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                    Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New YOR
                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-128-345-63
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                 COCATION: group(6, 8, 13, 15)
CTHER INFORMATION: /note= "X is a hydrophobic, a cother information: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 65; DB 1; Length 18; 66.7%; Pred. No. 0.00024; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FIRE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRAX: (202) 887-150
TELERAX: 90-4030
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATA:
APPLICATION NUMBER:
FILING DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: COTUZZI, LAUTA A. REGISTRATION NUMBER: 30,742 REGISTRATION NUMBER: 8067-034-999 TELECHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 230, Application US/08752852A Patent No. 5994306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIF: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: group(6, 8, 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.4
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212-869-9741
                                                                                                                                                                                                                                                    TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

```
NAME/KEY: Modified-site
LOCATION: group(6,15)
OTHER INFORMATION: /note= "X is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 63; DB 1; Length 18;
Pred. No. 0.00051;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58, Application US/08499523
; Sequence 58, Application US/08499523
; Patent No. 5804558
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEHRER. ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
ADDRESSEE: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
EDDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/499,523
FILING DATE: O7-JUL-1995
CLASSIFICATION NUMBER: US/08/499,523
ATTORREY/AGENT INRORMATION:
NAME: MURRASHIGE, KATE H.
REGISTRATION NUMBER: 2900-0540.24
REGISTRATION NUMBER: 2000-0540.24
TELEFRA: (202) 887-1500
TELEFRA: (202) 887-1500
TELEFRA: (202) 887-1500
TELEFRA: (202) 887-1503
TELER: 90-4030
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
wvpr: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE PORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLXYCRRRFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a oTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 4; Length 18;
Pred. No. 0.00024;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:

STATE:

COUNTEY:

USA

21P: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                           Sequence 67. Application US/09128345
; Sequence 615936
; Patent NO. 615936
; Patent NO. 615936
; PAPLICANT: LEBRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEHRER, STLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/08499523
Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.4;
Best Local Similarity 66.7;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000 Penn
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-499-523-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                       US-09-128-345-67
                                                         RESULT
```

δλ g

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                   LOCATION: group(6, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: group(8, 13);
; OTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-58
                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 63; DB 4; Length 18;
Pred. No. 0.00051;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                   Score 63; DB 4; I
Pred. No. 0.00051;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: ROKRYRAWOV, VLADIMIR N.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULER, A.
REGISTRATION NUMBER: 30,742
REFERENCE/OOCKET NUMBER: 8067
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.2%;
66.7%;
                                                                                                                                                                                                                                                   69.28;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond 6..15
                                 FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLXYCRRRFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENG'TH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO:
SEQUENJE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
           8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME,/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-128-345-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site

LOCATION: group(8, 13)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 1; Length 18;
Pred. No. 0.00051;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY.

STATE: New
COUNTRY: USA
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-40G-1998
CLASSIFICATION NUMBER: 30,742
ATTONNEY/AGENT INFORMATION:
NAME: COPICAL', LAUEA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELECHNUME: (212) 790-9090
TELECHNUME: (212) 869-9741
TONEY CANNOT C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEHREN, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
     2000-0540.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 53, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                   Disulfide-bond
6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                       LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-128-345-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
Score 62; DB 1; Length 18;
Pred. No. 0.00073;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "X is a hydrophobic, a small, or a large polar amino acid"
                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-195
CLEASIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, RATE H.
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, RATE H.
TELEPHONE: 2000-0540.24

TELEPHONE: (202) 887-0763

TELEFA: 90-4030

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
FEACTHER B AMIND ACIDS

INFORMATION FOR SEQ ID NO: 59:
FEACTHER B AMIND ACIDS

INFORMATION CALBERTICS:
FEACTHER B AMIND ACIDS

FEACTHER B AMIND ACIDS

FEACTHER B AMIND ACIDS

FEACTH B B AMIND ACIDS

FEATTH B B AMIND ACIDS

                                                                                  E: MORRISON & FOERSTER
2000 pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54, Application US/09128345; Sequence 54, Application US/09128345; Patent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STRIET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TITLE OF INVENTION: PROTEGRINS NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.1%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond LOCATION: 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLCYXRRFFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: group(8, 13)
; OTHER INFORMATION: /no
; OTHER INFORMATION: sma
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.1'
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                              Washington
                                                                                               ADDRESSEE:
STREET: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-128-345-54
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: group(6, 15)
CTHER INFORMATION: /note= "x is a hydrophobic, a offer information: small, or a large polar amino acid" US-08-499-523-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 62; DB 1; Length 18; 66.7%; Pred. No. 0.00073; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Date: PC-DOS/MS-DOS
COFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
NAME: WIRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 2000-0540.24
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELERAX: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR EGD ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                      Sequence 54, Application US/08499523;
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: POKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-499-523-59; Sequence 59, Application US/08499523; Patent No. 5804558; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLXYCRRRFCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                             RGGRLSYSRRFSTSTGR 18
                                                                 1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                      US-08-499-523-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                               q
```

Gaps

```
οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: group(6, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a corner information: small, or a large polar amino acid" US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62; DB 4; Length 18;
Pred. No. 0.00073;
0; Mismatches 6; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUBER: US/09/128,345 FILING DATE: CLASSIFICATION: 514
                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 867-0054-999
REPERENCE/DOCKET NUMBER: 867-0054-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY-AGENT INFORMATION:
NAME: COFUZZI, Laura, A. 7.2
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 867-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.1%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site LOCATION: group(6, 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLXYCRRFCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
; INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
NAME/KEY: Disulfide-bond
LOCATION: 6.15
NAME/KEY: Modified-site
LOCATION: 6.15
NAME/KEY: Modified-site
COCATION: 6.15
NAME/KEY: Modified-site
NAME/KEY: Modified-site
COCATION: 6.15
NAME/KEY: Modified-site
NAME/KEY: No. 0.00073;
Matches 12: Conservative
NAME/KEY: Modified-site
NAME/KEY: Modifi
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:34:40 ; Search time 126.85 Seconds
(without alignments)
10.809 Million cell updates/sec Run on:

1 RGGRLSYSRRFFSTSTGR 18 US-09-485-571-25 91 Perfect score: Sednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pir1:* pir2:* pir3:* pir4:* . . . . .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SHIMMARTES

		dF			SUMMAKIES	
Result No.	Score	Ouery Match	Length	DB	ID	Description
1	61	67.0	149	7	857607	protegrin 1 precur
7	52	•	147	7	0060NF	7
m	54	59.3	149	7	S57609	Ŋ
7	54	6	149	7	A53895	٣
Ŋ	47	51.6	94	Н	B48549	cid
ø	47	51.6	447	~	S53982	hypothetical prote
7	46	50.5	231	7	T32047	
80	45	49.5	191	٦	QQAG6T	
σ	44	48.4	1	7	A30832	_
10	44	48.4	293	7	D81896	c
11	44	48.4		7	T03240	FLO/LFY protein ho
12	44	48.4	53	~	H72730	probable acyl-CoA
13	43	47.3	107	7	JQ1251	hypothetical 12.6K
14	43	47.3	108	<del>, -</del>	WMVYP5	nucleic acid-bindi
15	43	47.3	108	~	S12976	12K protein - pota
16	42	46.2	118	~	C72642	1
17	42	46.2	386	7	A41950	Φ
18	42	46.2	747	~	T42599	minor capsid prote
19	42	46.2	1016	~	T30942	aminopeptidase (EC
50	42	46.2	1016	7	T30943	aminopeptidase (EC
21	41	45.1	201	~	B72739	hypothetical prote
22	41	45.1	310	~	T43147	hypothetical prote
23	41	45.1	325	7	T38308	
24	41	45.1	547	7	S53920	
25	41	45.1	619	7	A85958	glutathionylspermi
56	41		619	7	A57538	glutathionylspermi
27	40.5	44.5	464	7	A56600	intermediate filam
28	40	44.0	217	7	36	hypothetical prote
29	40	44.0	352	7	D96597	

hypothetical prote	sceloid 1/dipha-mo hypothetical prote	NADH dehydrogenase	keratin 9, type I,	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	ribosomal protein	hydroxymethylgluta	hydroxymethylgluta	conserved hypothet	hypothetical prote	glycosylphosphatid	hypothetical prote
C85022	T02002	A70414	137984	E71432	T16114	T26377	T00057	G70154	S42214	S42213	D82387	T05656	A48024	C84888
2.	7 7	7	~	7	7	7	7	~	7	7	~	~	7	7
499	513	622	622	743	1030	1224	1696	51	105	105	119	159	188	211
44.0	44	44.0	44.0	44.0	44.0	44.0	44.0	42.9	42.9	42.9	42.9	42.9	42.9	42.9
40	4 4	40	40	40	40	40	40	39	38	39	39	39	39	39
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
A; Molecule type: DNA
A; Residues: 1-149 < CHA>
A; Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
A; Cross-references: EMBL:X84094; NID:9887642; PIDN:CAA58890.1; PID:9887643
A; Critic: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: $45712; MUID:94283613
A; Recession: $45712
A; MOLECULE type: MRNA
A; Residues: 1-149 < CAH2>
A; Residues: 1-149 < CAH2>
A; Residues: 1-149 < CAH2>
A; Residues: GB:X79868; NID:9603035; PIDN:CAA56251.1; PID:9603036
B; Rimigorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; E9
FEBS Lett. 330, 339-342, 1993
A; Fille: Primary structure of three cationic peptides from porcine neutrophils. Seq
A; Reference number: $36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: $36820
A; Molecule type: protein
A; Residues: 131-148 <MIR>
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort
A; Reference number: $34585; WUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Gene: NPG...
A.Introns: 16/3; 102/3; 126/3
A.Introns: 16/7: 102/3; 126/3
A.Introns: 16/7: 102/3; 126/3
A.Introns: 16/7: 102/3; 126/3
A.Introns: 16/7: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/0: 102/
Protegrin : precursor - pig
NyAlternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S66284; S45712; S36820; S34585; S57607
FEBS Lett. 368, 197-202, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB 2; Length 149
Pred. No. 0.0069;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The structure of porcine protegrin genes. A;Reference number: S66283; MUID:95354835 A;Accession: S66284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.0%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S34585
A; Molecule type: protein
A; Residues: 131-148 <KOK>
```

ö

Gaps

```
F;22-129/Domain: cystatin homology <CYS.
F;30-130/Domain: propeptide #status predicted <PRO>
F;31-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protegrin 3 precursor - pig
protegrin 3 precursor - pig
protegrin 3 precursor - pig
N; Alternate names: neutrophil peptide 2
N; Alternate names: neutrophil peptide 2
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sus scrofa domestica (domestic pig)
C; Species: Sec286; As3895; S3450; S36821; S57608
R; Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 386, 197-202, 1995
A; Title: The structure of porcine protegrin genes.
A; Reference number: S66283; MUID:95354835
A; Molecule type: DNA
A; Residues: 1-149 <213>
A; Ross references: EMBL: X84095; NID:9887644; PIDN:CAA58891.1; PID:9887645
A; Cass references: EMBL: R: I.
FEBS Lett. 346, 288-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID:94283613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A;Residues: 131-148 <KOK>
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egr
FEBS Lett. 330, 339-342, 1993
A;Fille: Primary structure of three cationic peptides from porcine neutrophils. Seq.
A;Reference number: S36820; MUID:93387466
C;Keywords: amidated carboxyl end; antibacterial F;1-29/Domain: signal sequence #status predicted <SIG> F;22-129/Domain: cystatin homology <CYS> F;30-130/Domain: propeptide #status predicted <PRO> F;131-148/Product: protegrin 5 #status predicted <MAT> F;131-148/Product: protegrin 5 #status predicted <MAT> CAMPORATE CAMPORATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
A;Ratus: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-149 <ZHA>
A;Cross-references: GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:g603038
A;Cross-references: GB:X83267; NID:g603047; PIDN:CAA58240.1; PID:g603038
B;Rokryakov, V. N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Protegins: leukocyte antimicrobial peptides that combine features of cort. A;Reference number: S34585; MUID:93327946
A;Accession: S34587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c.Superfamily: carbelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status_predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 2;
Pred. No. 0.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                       59.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 RGGRLCYCRPRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.1'
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 66/3; 102/3; 126/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 131-148 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S36821
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                              NANOSOO
JANOSOO
JANOSOO
JANOSOO
JANOSOO
JANOSOO
JANOSOO
JANOSOO
JANOSOO
JALCENTER names: cathelin-like protein precursor; neutrophil peptide 3
N.Alternate names: cathelin-like protein precursor; neutrophil peptide 3
C.; Species is sa scrord demestica (domestic pig)
C; Dete: 19-May-1694 #sequence_relision 19-May-1994 #text_change 16-Jul-1999
C; Dete: 19-May-1694 #sequence_relision 19-May-1994 #text_change 16-Jul-1999
C; Accession: NOOSOO; SASE2; S34586
R; Storici, P.; Zanetti, M.
A; Title: A novel CDNA sequence encoding a pig leukocyte antimicrobial peptide with a cather an interpretation of the sequence encoding a pig leukocyte antimicrobial peptide with a cather an interpretation of the sequence encoding a pig leukocyte antimicrobial peptide with a cather and the sequence encoding a pig leukocyte antimicrobial encodex and the sequence of three cationic peptides from porcine neutrophils. Sequence A; Restactor and the sequence and antibacter and antibacter and sequence and antibacter and sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protegrin 5 precursor - pig
Nichternate names: cathelin-associated antimicrobial peptide
Nichternate names: cathelin-associated pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
C;Accession: S66283; S57609
FRIADO, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X84096; NID: 9887646; PIDN: CAA58892.1; PID: 9887647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 2; Length 147; pred. No. 0.067; 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: The structure of porcine protegrin genes. A;Reference number: S66283; MUID:95354835 A;Accession: S66283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Experimental source: leukocytes C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.4%;
64.7%;
                                                                                                                                                   131 RGGRLCYCRRFFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 RGGRLCYCRRFFCICVG 147
                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRFFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-149 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: NPG5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                  δ
                                                                                                                                                                                                   q
```

```
Wypothetical protein 6 - Agrobacterium tumefaciens plasmids
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agro-1986 #sequence_revision 13-Aug-1986 #text_change 16-Jul-1999
C;Accession: Ad4498; S28691
R;Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, EMBO J. 3, 835-846, 1984
A;Title: The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefa A;Reference number: A91001; MUID:84207942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Wolecule type: DNA
A; Residues: 1-191 GOTES
A; Cross-references: GB:X00493; GB:J05108; GB:X00282; NID:g39062; PIDN:CAA25171.1; P
A; Experimental source: plasmid priAch5
B; Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1983
A; Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens
A; Reference: number: $28683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A30832
hypothetical protein 6a - Agrobacterium tumefaciens plasmid pT1T37
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: Agrobacterium tumefaciens
C; Accession: Agrobacterium tumefaciens
R; Vanderleyden, J; Desair, J; De Meirsman, C; Michiels, K; Van Gool, A.; Jen, G
Plant Mol. Eiol. 7, 33-41, 1986
A; Title: Nucleotide sequence of the T-DNA region encoding transcripts 6a and 6b of
A; Reference number: A93763
                        A;Cross-rèferences: EMBL:AF016678; PIDN:AAB66149.1; GSPDB:GN00020; CESP:K07E8.3
A;Experimental source: strain Bristol N2; clone K07E8
C;Genetics:
A;Gene: CISP:K07E8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X00493; NID:939062; PIDN:CAA25171.1; PID:939071
A;Experimental source: plasmid pTil5955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 191;
                                                                                                                                                                                                                                   Length 231;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core 45; DB 1;
red. No. 3.9;
Mismatches 2
                                                                                                                                                                                                                                   Score 46; DB 2;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No.
                                                                                                                                A;Map posítion: 2
A;Introns: 69/3; 104/1; 171/3; 203/3
                                                                                                                                                                                                                                   50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 49.5
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GGRINYSKNEYSSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: T-6b protein
C; Keywords: crown gall tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGRLSYSRRFFSTS 15
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-191 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-186 <VAN>
     A; Residues: 1-231 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S28691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mypothetical protein 447 - actinophage RP3

hypothetical protein 447 - actinophage RP3

hypothetical protein 447 - actinophage RP3

c.Specias: actinophage RP3

c.Bate: 28-cot-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

c.Accession: 553982

R.Gabriel, K.; Schmid, H.; Schmidt, U.; Rausch, H.

Nucleic Acids Res. 23, 58-63, 1995

A.Title: The actinophage RP3 DNA integrates site-specifically into the putative tRNA(Arg A; Reference number: 553981; MUID:95175370

A.Status: preliminary

A.Status: preliminary

A.Residues: 1-447 <GAB>
                                                                                                                   C. Species: potato virus S
C. Species: potato S
C. Accession: B48549
N. Title: The 3'-nucleotide sequence of an ordinary strain of potato virus S.
A. Title: The 3'-nucleotide sequence of an ordinary strain of potato virus S.
A. Reference number: A48549, MUID:93033173
A. Molecule type: genomic RNA
A. Residues: 1-94 eros.
A. Cross-references: GB:S45593; NID:g256417; PIDN:AAB23462.1; PID:g256419
A. Note: sequence extracted from NCBI backbone (NCBIN:114637, NCBIP:114639)
C. Superfamily: potato virus nucleic acid-binding protein
C. Keywords: DNA binding: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein K07EB.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Accession: T32047
R:Jones, K.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid K07E8.
A:Reference number: Z21116
A:Accession: T32047
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 2;
Pred. No. 4.1;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1;
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.6%;
larity 47.1%;
Conservative
131 RGGGLCYCRRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: EMBL:X80661
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ::|: :| ||: |
9 RGGSVAYAEKRVSTAKG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :|:|:| : | ||
38 GGRSTYARKRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S:
Matches 8;
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
```

G

qq ò

```
Ricession: J01251
Ricession: J01251
Ricession: J01251
Ricession: J01251
A. Tavil. 72, 2333-2337, 1991
A. Title: Nucleotide sequence and gene organization of the 3'-terminal region of chry A. Reference number: J01246; MJID: 92013948
A. Reference number: J01251
A. Molecule type: genomic RNA
A. Residues: J-107 CAEVA
A. Residues: J-107 CAEVA
A. Residues: GESO150; NID: 9237315; PIDN: AAB20081.1; PID: 9237321
C. Superfamily: potato virus nucleic acid-binding protein
                              probable acyl-CoA dehydrogenase, short-chain specific APE0385 - Aeropyrum pernix (st c; Species: Aeropyrum pernix
C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Date: 30-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
R; Kawarabayasi, Y; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; T.
DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropaston: H72730
A; Accession: H72730
A; Accession: H72730
A; Accession: H72730
A; Attack Perliminary
A; Molecule type: DNA
A; Doctorie type: DNA
A; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-532 < KAW>
A; Residues: 1-532 < KAW>
A; Cross-references: DDBJ: AP000059; NID: g5103911; PIDN: BAA79340.1; PID: d1043126; PID
A; Experimental source: strain Kl
C; Genetics:
A; Gene: APE0385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid-binding protein - potato virus M (strain Russian)
nucleic acid-binding protein - potato virus M (strain Russian)
A;Note: host Lycopersicon esculentum (tomato)
A;Note: host Lycopersicon esculentum (tomato)
C;Date: 31-Max-1990 #sequence_revision 23-Mar-1995 #text_change 29-Oct-1999
C;Accession: F54333; PN0006; PN0095; S21606
B;Zavriev, S.K.; Kanyuka, K.V.; Levay, K.E.
J, Gen. Virol. 72, 9-14, 1991
A;Ritle: The genome organization of potato virus M RNA.
A;Ritle: The genome organization of potato virus M RNA.
A;Reference number: A54333; MUID:91116326
A;Accession: F54333
A;Nolecule type: genomic RNA
A;Residues: 1-108 <ZAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical 12.6K protein - chrysanthemum virus B
hypothes: chrysanthemum virus B
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-108 <ZAV>
A;Cross-references: EMBL:X53062; NID:g61291; PIDN:CAA37237.1; PID:g61297
R;Rupasov, V.V.; Morozov, S.Y.; Kanyuka, K.V.; Zavriev, S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2; Length 107;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2;
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.48;
52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || ||:||| : ||
40 GRSSYARRRRALELGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10

D81896

Neisseria meningitidis hypothetical protein NMA1282 - Neisseria meningitidis (strain 224 c; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C; Accession: D81896
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, J. Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2020
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Residues: L-1293 ARN>
A; Cross-references: GB:AL162755; GB:AL157959; NID:g737942; FIDN:CAB84534.1; PID:g737995
A; Cross-references: GB:AL162755; GB:AL167959; NID:g737912; FIDN:CAB84534.1; PID:g737995
A; Conerine NWA1282
C; Superfamily: Neisseria meningitidis hypothetical protein NMA1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Accession: T03240
R.Kelly, A.J.: Bonnlander, M.B.; Meeks-Wagner, D.R.
Plant Cell 7, 225-234, 1995
A.Title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally expres A; Reference number: 214855; MUD:95276463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introns: 154/1; 288/3
Introns: 154/1; Arabidopsis thaliana LFY floral meristem identity control protein Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLO/LFY protein homolog NFL1 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Residues: 1-413 <KEL>
|Cross references: EMBL:U16172; NID:9561681; PIDN:AAC48985.1; PID:9561683
|Experimental source: cultivar Samsun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                   Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-413 <KEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2;
Pred. No. 8.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2
Pred. No. 12;
2; Mismatches
                                                                                               5;
                                                                                       Score 44; DB 2;
Pred. No. 5.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.4%;
ilarity 52.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GGRMKQRRRKKVVSTGR 202
                                                                                                   Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                  107 GGRINYSRNEHSSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RLSYSRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || || || || || || || || || 38 RLGYSRKNFAEQTG 51
                                                                                                                                                                                                                                                2 GGRLSYSRRFFSTS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
C; Superfamily: T-6b protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ò

ö

Gaps

ö

Gaps

```
J. Gen. Virol. 70, 1861-1869, 1989

A; Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvi
A; Reference number: A92800; MUID:89293091
A; Reference number: RPAD MUID:89293091
A; Residues: 1-79, 'LVSLTMCAMRNLLMKE' < RUP>
A; Note: this sequence has been corrected
A; Note: this sequence has been corrected
A; Title: The complete nucleotide sequence of potato virus M genomic RNA.
A; Reference number: PN0093; MUID:92049299
A; Recession: PN0095
A; Molecule type: genomic RNA
A; Reference sombler: PN0093; MUID:92049299
A; Accession: PN0095
A; Molecule type: genomic RNA
A; Residues: 1-108 & ZAZ>
A; Cross references: GB: X53062; NID:961291; PIDN:CAA37237.1; PID:961297
A; Cross references: GB: X53062; NID:961291; May 1990
A; Reference number: S21601
A; Reference number: S21601
A; Reference number: S21601
A; Reference number: S21604
A; Residues: 1-19-1, LVSLTMCAMRNLLMKE' < ZA3>
A; Cross references: EMBL:X53062
A; Cross references: EMBL:X53062
A; Cross references: EMBL:X53062
A; Experimental source: Russian wild type
C; Superimental source: Russian wild ing; nucleotide binding; zinc finger
F; 57-78/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: potato virus M
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: S12976
C;Accession: S12976
R;Gramstat, A.; Courtpozanis, A.; Rohde, W.
FEBS Lett. 276, 34-38, 1990
A;Title: The 12 KDa protein of potato virus M displays properties of a nucleic acid-bind
A;Reference number: S12975; MUID:91092429
A;Accession: S12976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Status: preliminary
A:Wolecule type: genomic RNA
A:Wolecule type: genomic RNA
A:Residues: 1-108 <GRA>
A:Cross-references: GB:X57440; NID:g61400; PIDN:CAA40689.1; PID:g61402
C;Superfamily: potato virus nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.3%; Score 43; DB 2; Length 108; 52.9%; Pred. No. 4.9; tive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
47.3%; Score 43; DB 1; Length 108;
Best Local Similarity 52.9%; Pred. No. 4.9;
Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.9*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 GGRSKYARRRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| |:||| : | |
40 GGRSKYARRRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12K protein - potato virus M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
S12976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: February 12, 2002, 12:34:40 Job time: 558 sec

·	
*1	
	_m in
i, g	
A Company of the Comp	
3 2 marie 1 m	

4

Run on:

SwissProt_39:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P32194 sus scrofa P32195 sus scrofa P32195 sus scrofa P42196 sus scrofa P42192 macropus ru P42131 caenolestes P42137 macropus ag O18768 parantechinus P42137 macropus ag O18768 parantechinus P42130 antechinus P42130 doservent P42130 doservent P42130 doservent P42130 doservent P42130 doservent P46950 saccharcmyc P43675 e bifunctio O04948 branchisosto O95718 homo sapien P29220 borrelia bu P29320 borrelia bu P29320 borrelia bu P29320 borrelia bu P2933 sus scrofa P49933 sus scrofa P49933 sus scrofa P49933 sus scrofa
SU	PG1_PIG PG2_PIG PG2_PIG PG3_PIG PG3_PIG HSP1_MACRU HSP1_CAEFU HSP1_CAEFU HSP1_DACYI HSP1_DACAU HSP1_DACAU HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_ANTSA HSP1_CAERU CATE_STASP VNBP_CVB VNBP_CVB VNBP_CVB VNBP_CVB KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN VNBP_LSV VNBP_LSV VNBP_LSV FG4_PIG KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN KICI_HUMAN
DB	
Length	149 147 147 148 149 149 147 147 161 161 161 161 161 161 161 161 161 16
ry	
Ma Vo	। ὑοῦΛοῦ ਚੰਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚੇਚ
Score	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Result	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

013286 homo sapten	Q50715 mycobacteri	P13647 homo sapien	P57429 buchnera ap	Q9w705 xenopus lae	Q9z0y8 rattus norv	P51817 homo sapien	P42145 pseudochiro	P80015 sus scrofa	028756 archaeoglob	P24647 autographa
CLN3_HUMAN	IMDH_MYCTU	K2C5_HUMAN	RNE_BUCAI	NCO2_XENLA	CCAI_RAT	PKX1_HUMAN	HSP1_PSECU	CAP7_PIG	SFSA_ARCFU	VIEN_NPVAC
٦,		Н	-1	-	-	-	-	-	-	-
438	529	290	902	1516	1835	358	99	219	219	408
41.8	41.8	41.8	41.8	41.8	41.8	41.2	40.7	40.7	40.7	40.7
38	38	38	38	38	38	37.5	37	37	37	37
34	36	37	38	39	40	41	42	43	44	42

## ALIGNMENTS

RESULT 1  RECLPIG STANDARD; PRT; 149 AA.  D POL_PIG STANDARD; PRT; 149 AA.  D POL_PIG STANDARD; PRT; 149 AA.  D 10-CCT-1993 (Rel. 27, Created)  DT 10-CCT-1993 (Rel. 37, Created)  DT 10-CCT-1993 (Rel. 36, Last annotetion update)  DT 10-LCCT-1996 (Rel. 36, Last annotetion update)  DT 10-LCCT-1996 (Rel. 36, Last annotetion update)  DT 15-UL-1998 (Rel. 36, Last annotetion update)  DR NGLTAXID-9923;  RN PRIME PRESON NA.  RN MEDLING-4283613; Pubmed-8013647;  RA FIGHER FROM NA.  RT 15SUB-Bone marrow;  RN MEDLING-4283633; Pubmed-7628604;  RN FIGHER SEQUENCE FROM NA.  RY TISSUB-Bone marrow;  RN MEDLING-933833; Pubmed-7628604;  RN FIGHER SEQUENCE FROM NA.  RN FIGHER SEQUENCE ROWN NA.  RN FIGHER SEQUENCE PROWN NA.  RN FIGHER SEQUENCE PROWN NA.  RN FEBS Lett. 346:285-288(1994).  RN FEBS Lett. 368:197-202(1995).  RN FIGHER SEQUENCE OF 131-18.  RN FEBS Lett. 368:197-202(1995).  RN FEBS Lett. 368:197-202(1995).  RN FIGHER SEQUENCE OF 131-148.  RN FEBS Lett. 377:231-236(1993).  RN FEBS Lett. 377:231-236(1993).  RN FEBS Lett. 377:231-236(1993).  RN Aleshina GW. Shamova O.V., Konrewa H.A., Lehrer R. I.;  RN FEBS Lett. 377:231-236(1993).  RN Aleshina GW. Shamova O.V., Konrewa H.A., Lehrer R. I.;  RN FEBS Lett. 377:231-236(1993).  RN ALERS Lett. 377:231-236(1993).  RN ALERS Lett. 377:231-236(1993).  RN HERS Lett. 377:231-239(1993).  RN HERS Lett. 377:231-239(1993).  RN HERS Lett. 377:231-239(1993).  RN HERS Lett. 377:231-239(1993)	
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	--

```
Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PG3_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          αq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Bone marrow;
MEDLINE-94071898; PubMed-8250892;
Storici P., Zanetti M.;
A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
                                                                                                               peptide from porcine leukocytes.";
Chem. Biol. 3:543-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION (G-149 PROVIDE AMIDE GROUP). 6EFBA98429CD6EC4 CRC64;
                                                       Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                           Feigon J.;
"Solution structure of protegrin-1, a broad-spectrum antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; X79868; CAA56251.1; -.
EMBL, X84094; CAA58890.1; -.
PIR, S34585; S34585.
PIR, S36820; S36820.
PIR, S36820; S6820.
PIR, PR001894; Cathelicidin.
Propom; PD001838; Cathelicidins; 1.
Probom; PD001838; Cathelicidins; 1.
PROSTER; PS00946; CATHELICIDINS_1; 1.
PROSTER; PS00941; Amidation; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 1; Length 149;
Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                     MONOCYTOGENES AND C.ALBICANS, IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.00
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEGRIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                 STRUCTURE BY NMR OF PROTEGRIN 1. MEDLINE=97113279; PubMed=8807886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last seq
01-NOV-1997 (Rel. 35, Last and
PROTEGRIN 2 PRECURSOR (PG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 RGGRLCYCRRFFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 66.7
es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
148
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136
138
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PG2_PIG
P32195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PG2_PIG
AC PPG2_PIG
AC PPG2_PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).
- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.
-- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-147 PROVIDE AMIDE GROUP).
698429DFFEC40466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata, Craniata, Vertebrata, Euteleostomi,
Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao C., Liu L., Lehrer R.I.; "Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEGRIN 2.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB 1; Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PRO0666; Cathelicidins; 1.
Probom; PRO01838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
Antibiotic; Signal; Amidation; Multigene family. SIGNAL 1 29
PROPEP 30 130 PROTEGRIN 2.
CHAIN 131 146 PROTEGRIN 2.
MOD_RES 30 30 PYRROLIDONE CARBOXYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-077-1993 (Rel. 27, Created)
01-077-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L24745; AAA31061.1; -.
HSSP; P32194; 1PG1.
InterPro; IPR001894; Cathelicidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Bone marrow;
MEDLINE-94283613; PubMed-8013647;
Zhao C., Liu L., Lehrer R.I.;
                           IISSUE=Leukocyte;
MEDLINE=93327946; Pubmed=8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16478 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEGRIN 3 PRECURSOR (PG-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett. 346:285-288(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.48;
64.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 RGGRLCYCRRRFCICVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRFFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity .
SEQUENCE OF 131-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
```

07:52:39 2002

Wed Feb 13

```
147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : |:|| :||
147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone F39B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                           |||||| | : |
252 KWAFRTLYEQVAY 264
                1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: F39B2.4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: F39B2.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Addid:

hypothetical protein Vng0013c [imported] - Halobacterium sp. NRC-1

c;Species: Halobacterium sp. NRC-1

c;Species: Halobacterium sp. NRC-1

c;Species: Halobacterium sp. NRC-1

c;Accession: A84161

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Neithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Vng0026c [imported] - Halobacterium sp. NRC-1
C; Species: F84162
R: NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. T. 2176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483
A; Accession: F84162
A; Status: preliminary
                               C;Comment: The peptide is one of the antimicrobial peptides in the American horseshoe C;Keywords: amidated carboxyl end F;4-17,8-13/Disulfide bonds: #status predicted F;18/Modified site: amidated carboxyl end (Arg) #status experimental
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <STO>
A;Cross-references: GB:AE004437; NID:g10579674; PIDN:AAG18666.1; GSPDB:GN00138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004437; NID:q10579658; PIDN:AAG18653.1; GSPDB:GN00138 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 307
                                                                                                                                                                         52.2%; Score 47; DB 2; Length 18;
Llarity 53.8%; Pred. No. 0.095;
Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 2;
Pred. No. 7.1;
1; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB :
Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 48.9
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 KWAFRTLYEQVAY 193
                                                                                                                                                                                                                                                                        1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                1 KWAFRVAYRGIRY 13
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-378 <STO>
A; Residues: 1-18 <MIY> C; Comment: The first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: VNG0013C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: VNG0026C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
A;Map position: 1
A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
A;Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 670/3; 835/1; 906/2; 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
S76323
hypothetical protein s110310 - Synechocystis sp. (strain PCC 6803)
hypothetical protein s110310 - Synechocystis sp.
G.Species: Synechocystis sp.
A.Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C.Accession: S76323
R.Kaneko, T.: Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima
                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1661 <WIL>
A;Cross-references: EMBL:292834; PIDN:CAB07385.1; GSPDB:GN00019; CESP:F39B2.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1663 <WIL>
A;Cross-refarences: EMBL:292834; PIDN:CAB07394.1; GSPDB:GN00019; CESP:F39B2.4b
A;Experimental source: clone F39B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F39B2.4b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999
C;Accession: T21993
R;Dobson, R.
submitted to the EMBL Data Library, March 1997
A;Reference number: 219498
                       C;Species; Caenorhabditis elegans
C;Date: 1:-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21986
R;Dobson, R.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19498
A;Accession: T21986
A;Accession: T21986
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
hypothetical protein F39B2.4a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2
Pred. No. 33;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ore 44; DB;
ed. No. 33;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
```

Gaps

.; 0

Indels

Length 611;

2;

```
A;Gene: CESP:F48E3.1
A;Introns: 22/1; 81/3; 130/3; 156/3; 234/3; 290/3; 311/3; 343/2; 382/3; 422/1; 448/2,
C;Keywords: glycosyltransferase; hexosyltransferase
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil. A; Reference number: A69580; MUID:98044033
A; Accession: G69860
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Mesidues: 1-611 CKUN>
A; Cross-references: GB:299110; GB:299111; GB:AL009126; NID:92633699; PIDN:CAB13213.1
A; Ederimental source: strain 168
C; Genetics: A; Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-702 - CPAU>
A;Cross-references: EMBL:U28735; NID:g860708; PID:g860709; PIDN:AAA68263.1; CESP:F^A
A;Experimental source: strain Bristol N2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.8%; Score 43; DB
53.8%; Pred. No. 20;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 2 Pred. No. 17; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: February 12, 2002, 12:34:42 Job time: 560 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 41.27
Fig. 2. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 KWALDKAFKGFRY 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G69860
kyothetical protein ykou - Bacillus subtilis
cj69860
c; Species: Bacillus subtilis
C; Species: Bacillus subtilis
C; Species: G5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Species: G5060
C; Accession: G6960
R; Kunst, F: Ggasawara, N: Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Accession: G6960
R; Kunst, F: Ggasawara, N: Enuschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChG
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Fabret, C.; Ferrari, E.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A.; Winters 900, 249-256, 1997
A.; William, S.; Galizzi, A.; Galler
A.; Milbert, P.; Koningstein, G.; Krogh, S.; Kunmano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; M.; Parro, V.; Pohl, T. M.; Portetelle
A.; Authors: Schleich, S.; Schroeter, B.; Rocke, M.; Sadale, Y.; Sato, T.; Sarollon, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, E.; Sekjquchi, J.; Sekowska, A.; Serollon, R.; Winters, P.; Munters, P.; Topanoi, A.; Tosato, V.; Uchiyama, akeuchi, M.; Tanaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Voshida, R.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .Superfamily: alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase;Keywords: glycosyltransferase; hexosyltransferase
                                                o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasudd
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-302 <KAN>
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10175.1; PID:g100154
A;Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAA10175.1; PID:g100154
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T43341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mnMA
A;Residues: 1-467 <CHE>
A;Cross-references: EMBL:AF082011; NID:g3420841; PIDN:AAD03023.1; PID:g3420842
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                   S. Reference number: S74322; MUID:97061201
A;Accession: S76323
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 2; Length 467;
pred. No. 13;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%; Score 43; DB 2; Length 302; 60.0%; Pred. No. 8.4; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%; Score 43;
ilarity 53.8%; Pred. No.
Conservative 2; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRYLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 KWALDKAFKGFRY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: X
C; Superfamily: alp
C; Keywords: glycos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gly-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   С
```

ö

Gaps

; 0

Indels

Length 702

2;



```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

February 12, 2002, 12:39:54; Search time 67.2 Seconds OM protein - protein search, using sw model Run on:

(without alignments)
9.275 Million cell updates/sec

US-09-485-571-32 90 1 KWAFRVAYRGIRYLLRL 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq'length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMARIES		
Result		Query					
NO.	Score	Match	Length	8	ΩI	Description	on
Н	57	63.3	17	Н	TAC1_TACGI	P23684 tac	tachypleus
7	57	63.3	17	~	TAC3_TACGI	~	tachypleus
м	57	63.3	77	7	TAC1_TACTR	6	tachypleus
4	54	•	77	7	TAC2_TACTR		tachypleus
Ŋ	20		18	-	PPM1_LIMPO		limulus pol
9	47		18	7	PPM2_LIMPO		limulus pol
7	44	48.9	1587	7	SUR2_CAEEL	_	caenorhabdí
ω	42.5	47.2	752	٦	HYSA_PROAC		propionibac
σ	42		90	Н	IATP_SCHPO		schizosacch
10	41	45.6	174	٦	CSF3_SHEEP	_	ovis aries
11	41	45.6	195	٦	CSF3_BOVIN	_	bos taurus
12	40	44.4	173	-	CRGA_HUMAN		homo sapien
13	40	44.4	304	٦	TUA3_AGRVI		agrobacteri
14	40	44.4	507	-	YCGC_ECOLI	_	escherichia
15		44.4	529	-	Y632_CHLTR	084637 chl	chlamydia t
16	40	44.4	529	-	Y921_CHLMU		chlamydia m
17	39	43.3	184	-	MPL_MPLV		myeloprolif
18	39	•	516	П	GLPD_MYCTU	_	mycobacteri
19	39	•	553	-	GLPD_SYNY3		synechocyst
20	39	43.3	625	П	TPOR_MOUSE	_	mus musculu
21	38	42.2		7	WCAF_ECOLI	_	escherichia
22	38	42.2		-	ARBB_ERWCH	_	erwinia chr
23	37.5	41.7		П	Y561_CHLMU	-	chlamydia m
24	37		174	-	CRGA_BOVIN	P02527 bos	s taurus
. 52	37		174	-	CRGB_BOVIN	P02526 bos	s taurus
56	37		174	-	CRGB_MOUSE	P04344 mus	s musculu
27	37		174	-	CRGB_RAT	S	rattus norv
28	37		201	-	MGF_CHICK		gallus gall
29	37	41.1	263	Н	TRUA_PYRAB	Q9uzz3 pyr	pyrococcus
30	37		326	-	AA1R_BOVIN		oos taurus
31	37	41.1	326	-	AA1R_CANFA	_	canis famil
32	37	41.1	326	-	AA1R_CAVPO	<u>.</u>	cavia porce
33	37	41.1	326		AA1R_HUMAN	P30542 homo	mo sapien

P25099 rattus norv P34970 oryctolagus	003424 streptomyce 014197 schizosach	012556 aspergillus 027597 drosophila	070157 mus musculu P52965 synechocyst	O24585 zea mays (m O74021 pyrococcus	Q03740 mus musculu
AA1R_RAT AA1R_RABIT	SFA1_STRFR YDQ4_SCHPO	AMO1_ASPNG NCPR_DROME	TP3A_MOUSE NIFJ_SYNY3	CRI4_MAIZE RS13_PYRHO	CRGF_MOUSE
	- A -		.i -i	- ~	7
326	357 452	67.	119	14.	15
41.1	41.1	4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	41.1	40.6	40.0
37	37	37	37	36.5 36	36
34 35	36	0 8 4 0 0 0	41	44	45

## ALIGNMENTS

	0;
oce ;	Gaps
ab). Xiphos (orses) a	 0
nd hoe cr mata; sian h igas): , and	gth 17; Indels
ub), an increase irostos irostos east A eeus gens gens gens gens gens gens gens gen	ren ;
date) date) date) eshoe cra exhoe cra t Asian h erata; M of Southe d Tachypl achyplesi or."; ESIN/POLY	DB 1; 0.00089; thes 3
updat on updat on updat on poses h east A licera licera and T r tach ursor. rPLESI	ore 57; DB ed. No. 0.0 Mismatches
STANDARD; PRT; 17 AA.  (Rel. 20, Created) (Rel. 22, Last sequence update) (Rel. 22, Last annotation update) (Rel. 32, Last annotation update) (Figes Southeast Asian horsesho metazoa: Arthropoda; Chelicerata; Merostoma Tachypleus.  (1952, 6848; Metazoa: Arthropoda; Chelicerata; Merostoma Resorbelus.  (195357; PubMed-2229025; Metajan H., Iwanaga S.; Insolated from hemocytes of Southeast Asinoscorplus rotundicauda and Tachyplesin III, insolated from hemocytes of Southeast Asinoscorplus rotundicauda and Tachyplesin III, intermediated from hemocytes of Southeast Asinoscorplus rotundicauda and Tachyplesin III, intermediate of its precursor.";  108.261-266(1990).  ITY: BELONGS TO THE TACHYPLESIN/POLYPHEWUSI;  ANABATION.  Amidation.  3 16 7 12 7 12 17 AA; 2269 MW; E9E09BD9D2923C94 CRC64;	ត្រ
Created) Last sectors and Last and theast As through a control of throug	.; * * * O
STANDARD; 1. 20, Cr. 1. 20, La. 2	vat 13 13
STANDAR (Rel. 20, (Rel. 20, (Rel. 32, 17. Rel. 20, 17. Re	Similarity 76. O. Conservative PRVARGIRY 13
TACGI TACCI	Simi O; FRV? 
TACGI TACCI TACCI TACLIACGI STANDARD; PRT; 17 AA.  17 AA.  17 AC.  17 AC.  17 AC.  17 AC.  17 AC.  18 AC.  18 AC.  18 AC.  18 AC.  18 AC.  19 G.  10 -NCV-1991 (Rel. 20, Created)  10 -NCV-1991 (Rel. 20, Last sequence update)  10 -NCV-1995 (Rel. 32, Last annotation update)  10 -NCV-1995 (Rel. 32, Last annotation update)  17 ACHYPLESIN I.  18 ACHYPLESIN I.  19 ACHYPLESIN I.  10 -NCV-1995 (Rel. 32, Last annotation update)  10 -NCV-1995 (Rel. 30, Last annotation update)  10 -NCV-1995 (Rel. 30, Last annotation and Cachyplesin III, and a processing intermediate of its precursor.";  19 ACHYPLESIN I.  10 -NCV-1995 (Rel. 30, Last annotation of a new tachyplesin, tachyplesin III, and a processing intermediate of its precursor.";  10 -N - Biochem. 108:261-266 (1990).  11 - SIMILANITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.  11 AN 19824; A38824.  12 AMIDATION.  13 AMIDATION.  14 AND AND RES.  17 AMIDATION.  17 AMIDATION.  18 AMIDATION.  19 AMIDATION.  10 AMIDATION.  10 AMIDATION.  11 AM: 2269 MW; E9E09BD9D233C94 CRC64;	Query Match Best Local Matches 1 Matches 1 KWA
RESULT TACL_TACGI TACL_TACGI TACL_TACGI DD TACHY DD 01-NO	Que Bes Mat Qy Db

RESULT 2
TAC3_TACGI

TAC3_TACGI

DT TAC3_TACGI

STANDARD; PRT; 17 AA.

AC P18252:
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DT 01-

```
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6853;
                                  [5]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tridentatus).";
                                                                                                                  components.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAC2_TACTR
P14214;
                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAC2_TACTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-89031158; Pubmed=3144410; Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S., Nakamura T., Furunaka H., Miyata T., Tokunaga F., Muta T., Iwanaga S., Niwa M., Takao T., Shimodishi Y.; antimicrobial peptide from the hemocytes of the horseshoe crab (Tachypleus tridentatus). Isolation and chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDDINE=93257488; Pubmed=8490053; Tammamura H., Kuroda M., Masuda M., Otaka A., Funakoshi S., Tammamura H., Kuroda M., Waki M., Matsumoto A., Lancelin J.-M., Nakashima H., Yammoto N., Waki M., Matsumoto A., Lancelin J.-M., Kohda D., Tate S., Inagaki F., Fujii N.; Tate S., Inagaki F., Fujii N.; A comparative study of the solution structures of tachyplesin I and
                                                                                                                                                                                                                                                                                                                                                                                                                                      Tachypleus tridentatus (Japanese horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                         Gaps
            Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
Muta T., Fujimoto T., Nakajima H., Iwanaga S.;
"Tachyplesins isolated from hemocytes of Southeast Asian horseshoe
crabs (Carcinoscorpius rotundicauda and Tachypleus gigas):
identification of a new tachyplesin, tachyplesin III, and a
processing intermediate of its precursor.";
J. Blochem. 108:261-266(1990).
-:- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Antimicrobial peptide, tachyplesin I, isolated from hemocytes of horseshoe crab (Tachypleus tridentatus). NMR determination of the beta-sheet structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.; "Antimicrobial tachyplesin peptide precursor. cDNA cloning and cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                                                         ;
                                                                                               GRAM-POSITIVE BACTERIA.
-1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 24-40.
MEDLINE-90368729; PubMed-2394727;
Kawano K., Yoneya T., Miyata T., Yoshikawa K., Tokunaga F.,
Terada Y., Iwanaga S.;
                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
AMIDATION.
E9E08CE9D2923C94 CRC64;
                                                                                                                                                                                                                                    Score 57; DB 1; 1 Pred. No. 0.00089;
                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 13, Created)
(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   77 AA.
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 24-40, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chem. 265:15365-15367(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 265:21350-21354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 263:16709-16713(1988).
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91065956; PubMed=2250028;
        MEDLINE=91035357; PubMed=2229025;
                                                                                                                                                                                                                                                             ·
0
                                                                                                                                                                                                                                      63.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 24-40.
                                                                                                                                                                                                    2241 MW;
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TACHYPLESIN I PRECURSOR
                                                                                                                                       PIR; JX0125; JX0125.
Antibiotic; Amidation.
DISULFID 7 12
                                                                                                                                                                                                                                                                                    1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                    1 KWCFRVCYRGICY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                    17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tridentatus).
                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (
01-NOV-1991 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                     TAC1_TACTR
P14213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol.
                                                                                                                                                                                          MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              TAC1_TACTR
                                                                                                                                                                                                                                                                                                                                                                                     a
              ò
```

ij

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tachypleus tridentatus (Japanese horseshoe crab).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
Limulidae; Tachypleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
a novel anti-HIV synthetic peptide, T22 ([Tyr5,12, Lys7]-polyphemusin II), determined by nuclear magnetic resonance.";
Biochim. Biophys. Acta 1163:209-216(1993).
                                                                                                                                                                                                                                                                                                                     J. Biochem. 114:307-316(1993).
-1- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 24-40.
MEDLINE-90110066; PubMed-2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
B940CAA4A641335F CRC64;
                                                                                                                                             MEDLINE-94110249; PubMed-8282718;
Shigenaga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage on pair of basic residues; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A.
MEDLINE-91065956; PubMed-2250028;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Shigenaga T., Muta T., Toh Y., Tokunaga F., Iwanaga S.;
Antimicrobial teorpplesin peptide precursor. CDNA cloning and
cellular localization in the horseshoe crab (Tachypleus
                                                                                                                                                                                                                           "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: HEMOCYTES.
-1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 1; Length 77;
Pred. No. 0.0042;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TACHYPLESIN II PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACHYPLESIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 265:21350-21354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: S-GRANULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M57242; AAA63538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9349 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
40
77
39
35
40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibiotic; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1| ||| ||| ||| |
24 KWCFRVCYRGICY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A30068; A30068.
PIR; A38345; A38345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KWAFRVAYRGIRY
                                                                                                                                                                                                                     Iwanaga S.;
```

ó

```
2 RWCFRVCYRGFCY
          Query Match
Best Local Similarity
Matches 8; Conserv
                                                1 KWAFRVAYRGIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                      POLYPHEMUSIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUR-2 PROTEIN.
                                                                                                                                       01-JAN-1990
01-JAN-1990
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUR2_CAEEL
Q10669:
                                                                                                                     PPM2_LIMPO
P14216;
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                  RESULT 6
PPM2_LIMPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
SUR2_CAEEL
                                                                  Db
                                                                                                                      g
                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biochem. 106:663-668(1989).
-I- FUNCTION: SIGNIFICANTLY INHIBITS THE GROWTH OF GRAM-NEGATIVE AND GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Chelloerata; Merostomata; Xiphosura;
Limulidae; Limulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=90110066; PubMed=2514185;
Miyata T., Tokunaga F., Yonega T., Yoshikawa K., Iwanaga S., Niwa M. Takao T., Shimonishi Y.;
Takao T., Shimonishi Y.;
Antimicrobial peptides, Isolated from horseshoe crab hemocytes, tachyplesin II, and polyphemusins I and II: chemical structures and biological activity.
      tachypiesin II, and polyphemusins I and II: chemical structures and biological activity.";
J. Blochem. 106:663-668(1989).
                                                                  MEDLINE-94110249; PubMed-8282718; Silgenga T., Takayenoki Y., Kawasaki S., Seki N., Muta T., Toh Y., Ito A., Iwanaga S.; "Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) hemocytes and characterization of their
                                                                                                                                                                                                                                                              BY SIMILARITY.
AMIDATION (G-41 PROVIDE AMIDE GROUP).
ASP/GLU-RICH (ACIDIC).
6EBES/A4A652AEFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE TACHYPLESIN/POLYPHEMUSIN FAMILY.
PIR: JU0124; JU0124.
                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                         Score 54; DB 1; Length 77;
Pred. No. 0.013;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION.
FB3FA109D2923504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
POLYPHEMUSIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limulus polyphemus (Atlantic horseshoe crab).
                                                                                                                                                                                                                                 TACHYPLESIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                      18 AA.
                                                                                                                                                                                                                                                     BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: HEMOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
2459 MW;
                                                                                                                                                                                                                                                                                                                          60.0%;
69.2%;
                                                                                                                                                                                                                                                                                             9335 MW;
                                                                                                                                                                                                                                                                                                                         Query Match 60.0
Best Local Similarity 69.2
Matches 9; Conservative
Shimonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibiotic; Amidation.
                                                                                                                                                                                                                                                                                                                                                                            1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 AA;
                                                         CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PPM1_LIMPO
P14215;
Takao T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            PPM1_LIMPO
                                                                                                                                                                                                                                                                                                                                                                                     쉽
 ò
```

```
Gaps
                          Gaps
                                                                                                                                                                                                          Limulus polyphemus (Atlantic horseshoe crab).
Eukaryota; Metazoa; Arthropoda; Chellcerata; Merostomata; Xiphosura;
Limulidae; Limulus.
NCBI_TaxID=6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_rexID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Singh N., Han M.; "sur-2, a novel gene, functions late in the let-60 ras-mediated signaling pathway during Caenorhabditis elegans vulval induction."; Genes Dev. 9:2251-2265(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION.
E402A109D2923504 CRC64;
 Score 50; DB 1;
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 1;
Pred. No. 0.047;
2; Mismatches
                                                                                                                                                              (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                       Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1587 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
                           Mismatches
                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=90110066; PubMed=2514185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=96018822; PubMed=7557379;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.2%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 AA; 2431 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.2
Best Local Similarity 53.8
Matches 7; Conservative
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
13
18
                                                  13
                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RWCFRVCYKGFCY 14
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=95102116; PubMed=7528579; Mood P.R.; O'Brien P.M., Seow H.F., Rothel J.S., Wood P.R.; Cloning and sequencing of an ovine granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Wood V., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FORMS A ONE-TO-ONE COMPLEX WITH ATPASE TO INHIBIT THE
--- STRIVER ACTIVITY COMPLETELY (BY SIMILARITY).
-!- SUBGELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ATPASE INHIBITOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%; Score 42; DB 1; Length 90;
44.4%; Pred. No. 1.7;
Live 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Mitochondrion; Transit peptide.
TRANSIT 7 90 PUTATIVE ATPASE INHIBITOR.
SEQUENCE 90 AA: 10674 MW; F4C4DF852E3E6909 CRC64;
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR.
SPCC70.02C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
GRANULOCYTE COLONY-STIMULATING FACTOR (G-CSF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 AA.
                                                                                                                                                              90 AA
                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL023794; CAA19352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: || ::||||::
3 KYCFRKPACISYRGIRFM 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWAFR----VAYRGIRYL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                               :||:| : :|:||||
450 EWAYRTS-QGMRYLL 463
                                                                                                                                                                   STANDARD;
       KWAFRVAYRGIRYLL 15
                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSF3_SHEEP
Q28746;
                                                                                                                                                                IATP_SCHPO
074523;
20-AUG-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSF3_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                               IATP_SCHPO
              <del>, |</del>
                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οp
                                                                                                                                                                       δŏ
                                                         qq
                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Can. J. Microbiol. 43:315-321(1997).

-i. CATALYTIC ACTIVITY: HYALURONATE = N 3-(4-DEOXY-BETA-D-GLUC-4-I-GARLYTIC ACTIVITY: HYALURONATE = N 3-(4-DEOXY-BETA-D-GLUC-4-I-GRUGONOSYL)-N-ACETYL-D-GLUCOSAMINE.

-i. SUBBUIT: MONOMER.
-i. SUBCELLUIAR LOCATION: CELL-ASSOCIATED.
-i. SUBCELLUIAR LOCATION: CELL-ASSOCIATED.
-i. SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 8.
-i- FUNCTION: FUNCTIONS IN THE LET-60 RAS SIGNALING PATHWAY; ACTS DOWNSTREAM OF LET-60 DURING C.ELEGANS VULVAL INDUCTION.
-i- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN EMBRYOS AND LARVAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYALURONATE LYASE PRECURSOR (EC 4.2.2.1) (HYALURONIDASE) (HYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.2%; Score 42.5; DB 1; Length 752; 53.3%; Pred. No. 12; Live 5; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Propionibacterineae; Propionibacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDIJNE-97270208; PubMed-9115089;
Steiner B.M., Romero-Steiner S., Cruce D., George R.;
"Cloning and sequencing of the hyaluronate lyase gene from
                                                                                                                                                                                                                                                                                                                                                                                                         48.9%; Score 44; DB 1; Length 1587; 40.9%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                1405 1587 GLN/HIS-RICH.
1587 AA; 183906 MW; Al25FCA74922B11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYALURONATE LYASE.
60D5DCAA691C41A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                      ACIDIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || | :: |:|| :|
147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 H
81910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003159; Lyase_8.
Pfam; PF02278; Lyase_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U15927; AAA51650.1; -
                                                                                                                                                                                                                                                                            EMBL; U33051; AAA85507.1; -.
DOMAIN 1387 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes
                                                                                                                                                                                                                                                                                                      1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 752 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyase; Signal.
```

HYSA_PROAC

HYSA_PROAC

g ολ

SIGNAL

Matthes

SEQUENCE

DOMAIN

SSSSSSSSSSEEES

1;

Gaps

4

١

```
EMBL; AF092533; AAD16102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00433; ILGGCSFMGF.
ProDom; PD008388; GCSF_MGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.68;
77.88;
  CSF INDUCES GRANULOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                           SUBUNIT: MONOMER.
PTM: O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195
953
953
944
60
60
71
75
76
85
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 LAYRGLRYL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VAYRGIRYL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
85
85
93
32
65
70
72
76
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRGA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P11844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELIX
TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRGA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELIX
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lovejoy B., Cascio D., Eisenberg D.;
"Crystal structure of Canine and bovine granulocyte-colony
"Crystal structure of Cash."
J. Mol. Biol. 234:640-653(1933)
-1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CYTOKINES THAT ACT IN HEMATOPOLESIS BY CONTROLLING THE PRODUCTION.
DIFFERENTIATION AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
                DNA Seq. 4:339-342(1994).

-1- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOEISES BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLADOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS CSF INDUCES GRANULOCYTES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte colony stimulating factor."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

O-LINKED (GALNAC. . .) (BY SIMILARITY).

BASAA8F8D23ACDIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P35833; Q9TV89;
01-JUN-1994 (Rel. 29, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GRANULOCYTE COLONY-STIMULATING FACTOR PRECURSOR (G-CSF).
                                                                                                                                                                                                     PTM: O-GLYCOSYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00254; INTERLEUKIN_6; 1. Cytokine; Growth factor; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE-94076341; Pubmed-7504736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003573; IL6_MGF_GCSF. Pfam; PF00489; IL6; 1.
SMART; SM00126; IL6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L07939; AAA68006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidari M., Kehrli M.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae; Bos
                                                                                                                                                                                  SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||||:|||
163 LAYRGLRYL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P35833; 1BGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VAYRGIRYL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-HOLSTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSF3_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
CSF3_BOVIN

CSF3_BOVIN

DT 20-JUN

DT 20-JUN

DT 20-AUG

DE GRANUIC

CO EUKATY

CO MAMMALIA

RN [1]

RP STRAIN

RR Heldar!

RR STRAIN

RR LOUGH

RR STRAIN

CC C - i - FUI

CC DDII

CD DDII

CC DDII

CD DDII

C
STITE TENT TO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDIAGE 3670288; MEDLINE-88033805; PubMed=3670288; MEDLINE-8033805; PubMed=3670288; Medekin S.O., Du R.P., Tsui L.-C., Breitman M.L.; "Gamma-crystallins of the human eye lens: expression analysis of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O-LINKED (GALNAC. . .) (BY SIMILARITY).
TS -> RG (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRANULOCYTE COLONY-STIMULATING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00126; IL6; 1.
PROSITE; PS00254; INTERLEUKIN_6; 1.
Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; 8C06119E4ADFBA73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1;
Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CRYGA OR CRYSTALLIN A (GAWMA CRYSTALLIN 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       members of the gene family.";
Mol. Cell. Biol. 7:2671-2679(1987).
                                                                                                                                                                                                                                                                                                                                                                           PDB; 1BGC; 31-OCT-93.
InterPro; IPR003573; IL6_MGF_GCSF.
Pfam; PF00489; IL6; 1.
```

```
EcoGene; EG13888; ycgG
                                                                                                                                                                                                                                                                                          YCGG_ECOLI
P75995;
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                   YCGG_ECOLI
                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                             this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salomone J.-Y., Crouzet P., de Ruffray P., Otten L.; "Characterization and distribution of tartrate utilization genes in the grapevine pathogen Agrobacterium vitis."; Mol. Plant Microbe Interact. 9:401-408(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i - FUNCTION: TRANSCRIPTIONAL REGULATOR OF THE TTUABCDE TARTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS. OF THE VERPEBRATE EYE LENS.
SUBUNIT: MONOMER (BY SIMILARITY).
DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UTILIZATION OPERON.
SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                   VERY SIMILAR GREEK KEY MOTIFS.
SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     44.4%; Score 40; DB 1; Length 173; 80.0%; Pred. No. 7.4; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
PROBABLE TARTRATE UTILIZATION TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                                                                                                                                                                                                                                     2B4325FEC0E7B070 CRC64;
                                                                                                                                                                                                                                     InterPro; IPR001064; Crystallin.
pfam; PF00030; crystall; 2.
SMART; SM00247; XTALbq; 2.
PROSITE; PS00225; CRYSTALLIN_BETAGAMWA; 4.
Ey elens protein; Multigene family; Duplication.
INIT_MET
                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 AA.
                                                                                                                                                                                                                                                                                                               MOTIF 1. MOTIF 2.
                                                                                                                                                                                                                                                                                                                                                 MOTIF 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96252899; PubMed-8672817;
                                                                                                                                                                                  EMBL; M17316; AAA52108.1; -.
EMBL; M17315; AAA52108.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                         20761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobiaceae; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium vitis.
                                                                                                                                                                                                          PIR; A26912; A26912.
HSSP; P02526; 1GCS.
MIM; 123660; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 YRGRQYLLRL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 YRGIRYLLRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pTrAB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUA3_AGRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AB3
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUA3_AGRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
        ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Hada C., Yamamoto Y.,
Yano M., Horluchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIA / MGIGES5;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.R., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
-- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
                                                                                                                                                                                   EMBL; U32375; AAB61621.1; -.
InterPro; IPR000847; HTH_LYSR.
Pfam; PF00126; HTH_1.1; 1.
PROSITE; PS00044; HTH_LXSR_FAMILY; 1.
Transcription regulation; DNA-binding; Plasmid.
DNA_BIND 18 H-TH MOTIF (BY SIMILARITY).
SEQUENCE 304 AA; 33903 MW; D75979BDD919588F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 1;
Pred. No. 13;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN YCGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000215; AAC74252.1; ALT_INIT.
EMBL; D90750; BAA36000.1; ALT_INIT.
EMBL; D90751; BAA36004.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.48;
42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| |:| |:|13
245 QWTARLAVSGVRYV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGIRYL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCGG OR B1168.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
```

ì

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lb.ch).
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-759(198).
-I- SIMILARITY: BELONGS TO THE UPF0159 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                        ö
                                                                                                                                  Score 40; DB 1; Length 507;
Pred. No. 22;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.4%; Score 40; DB 1; Length 529; 35.3%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
InterPro; IPR001633; DUF2.
Pfam; PF00563; DUF2; 1.
SMART; SM00552; DUF2; 1.
Hypothetical protein; Complete proteome.
DOMAIN 245 492 DUF2.
SEQUENCE 507 AA; 56905 MW; D144600B361285D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome.
SEQUENCE 529 AA; 60915 MW; 35BFF03D77AD2D1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHEFICAL PROTEIN CT632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001334; AAC68236.1; -.
                                                                                                                                     Ouery Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | : ||:::| | RWLFHINARGLQWLCEL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.3
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                          | | :|:||:||:
157 ALNVPLKGVRYVLRV 171
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                      3 AFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                                                                                                                        Y632_CHLTR
O84637;
                                                                                                                                                                                                                                                                                         RESULT 15
Y632_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460
                                                                                                                                                                                                                                     q
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                          g
      DR
DR
FT
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
```

Search completed: February 12, 2002, 12:39:54 Job time: 807 sec

Ą					
			5		-
. iš					. v 4
					: : :
P.					
	•				
:#					
BCA.					T.
* * *			Property of the second		
v. Us					
eky L	•				
e ^{te}		$\frac{du}{dt}$ $\frac{dt}{dt}$ $\frac{dt}{dt}$ $\frac{dt}{dt}$ $\frac{dt}{dt}$ $\frac{dt}{dt}$	• Section 1 and 1 an		
				The second secon	
*					
	<b>₩</b>				. The second second
* *:					
t,	7 (4) (5)				
2					<b>4</b>
-					
	1 to 4				
					•
	*** ***			5 mag	
÷					y 10
6 67 5c		- 1	in the second of		

```
099pul hecrodera
097180 drosophila
024818 entamoeba h
024860 entamoeba h
099t37 heterodera
02653 oryctolagus
097791 oryctolagus
010466 homo sapien
09kma2 vibrio chol
09km32 drosophila
050898 myxococcus
091444 streptomyce
02149 caenorhabdi
025546 naegleria
025546 naegleria
09511 streptomyce
09559 qrosophila
09559 qrosophila
09559 mycobacteri
006559 mycobacteri
006559 mycobacteri
006559 mycobacteri
006559 mycobacteri
006559 mycobacteri
                O91qe8 arabidopsis
O9yxe5 sphaeropsis
O9vxk4 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Redenbach M., Ikeda K., Yamasaki M., Kinashi H.;
"Cloning and physical mapping of the EcoRI fragments of the giant
linear plasmid SCP1".
J. Bacteriol. 180:2796-2799(1998).
Hypothetical protein
SEQUENCE 724 AA, 79705 MW; F16E675DF39F77A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 53.3%; Score 48; DB 2; Length 724; Similarity 53.3%; Pred. No. 12; 8; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=A3(2);
Brown N.P.P., Harris D.;
Stownitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 79.7 KDA PROTEIN.
                Q9LQE8
Q9YXE5
Q9VXK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                   Q9GFU1
097180
024818
0248618
096737
096737
09078633
090788
0910466
095789
091091
021991
                                                                                                                                                                                                                                                                                                                                                                                         09C8F4
 020533
                                                                                                                                                                                                                                                                                                                                                       Q9VRI8
                                                                                                                                                                                                                                                                                                                                                                       Q9RJU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=43(2);
MEDLINE=98241550; PubMed=9573173;
441
767
767
789
949
954
1162
11165
11174
1802
2000
2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces coelicolor.
                                                                                                                                                                                                              665
975
225
225
267
307
330
357
563
1132
571
868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KWAFRVAYRGIRYLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                            39.5
39.5
39
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9AD25
   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AD25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09ephl rattus norv
09bsz halobacteri
09bsz halobacteri
045497 caenorhabdi
025655 synechocyst
076777 cudp-n-ace
09pgs acenorhabdi
09lgs arabidopsis
091498 bacillus su
00662 salmonella
073419 synechocyst
099ag8 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9x564 enterococcu
O9a531 caulobacter
O9v1q8 drosophila
O9b112 caenorhabdi
O56836 amoeba prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ad25 streptomyce
                                                                                                                                          (without alignments)
10.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      February 12, 2002, 12:38:43; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9GPA3
Q9LQE3
Q34398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9AD25
Q9EPH1
Q9HSY4
Q9HSZ6
O45497
Q9U3G5
Q55655
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                            1 KWAFRVAYRGIRYLLRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-485-571-32
90
                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPTREMBL 17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553.3

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

56
```

Total number of

Database

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

ö

40.5 40 40

55 60 70 111 113 114 118 118 118 118

Score

Result

Gaps

ö

Length 307;

DB 1;

Score 44; DB Pred. No. 22;

Mismatches

g

```
48.9%;
                                                                           Conservative
                                                                                                                                  1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                              Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              045497
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                               9ZSH6Ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             045497
                                                                                                                                                                                                                                                                              RESULT
Q9HSZ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TID DIT DIT DIT SEED OF SEED O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The SEQUENCE FROM N.A.

The SEQUENCE SECTION S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alphalB-glycoprotein.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYRAIN-SPRAGE DANLEY; TISSUE-LIVER; GATAIN-SPRAGE DANLEY; TISSUE-LIVER; Gardino C., Mode A.; "Cloning of a novel GH regulated rat cDNA homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 11; Length 513;
Pred. No. 26;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 AA; 34492 MW; AB92A26FFF80AF39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0991BF67031DAA83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                 01-MAR-2001 (TIEMBLIEL 16, Created)
01-MAR-2001 (TIEMBLIEL 16, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
PUTATIVE ALPHA 1B-GLYCOPROFIEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AA
                                                                                                                               513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ^- N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AJ302031; CAC19029.1; -.
Interpro; IPR003599; IG.
Interpro; IPR03600; Ig_like.
Interpro; IPR03006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 24 N
513 AA; 56478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 2.
SMART; SM00409; IG; 3.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                     PRELIMINARY;
541 RWAFRLAARAVRSIL 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| || ||: ||||
154 RVAMRGVTYLLR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HSY4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HSY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
Q9HSY4
                                                                                                                                                                  Q9EPH1;
                                                                                                                                           Q9EPH1
                                                                                       RESULT
Q9EPH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP
                                                                                                                                           ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE_2050483; PubMed=11016950;
Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.P., Baliga N.S., Thorsson V., Shrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freites T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION WITH SECTION WITH STREET AND ACTION OF THE SECTION OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodae;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halobacterium sp. (strain NRC-1).
Archaea: Buryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 AA; 41710 MW; 9D3334B29435FD33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1;
Pred. No. 27;
                                                                                                                                                                                                                                                                             378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1661 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequ 01-JAN-1999 (TrEMBLrel. 09, Last anno SUR-2 PROTEIN.
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||| | : |
252 KWAFRTLYEQVAY 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KWAFRVAYRGIRY 13
181 KWAFRTLYEQVAY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
```

```
Query Match
                                   Tabata S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen S
                                                                                                                                                                                                                                                                                                                                                                                                                                                            076777
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
076777
                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                               ij
                                             <u>بر</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoldea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latteille P.,
Lightning J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                              9
                                                                                                                                                         Length 1661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                               Score 44; DB 5; Length Low-
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                 14; CAB07385.1; -.
1661 AA; 192896 MW; 36AACA0C7CD86F81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E2FD5A4D2D6FAA23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 33.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 5; 1
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AA
                                                                                                                                                                                                                                                                         PRT; 1663 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z92834; CAB07394.1; -. SEQUENCE 1663 AA; 193108 MW;
                                                                                                                                                                                                            147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 KWKFINDCIPKIDYKGIRNILR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                  1 KWAF-----RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.9%;
                                                                                                                                                                                                                                                                                           (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 16, I
                                                                                                                                                         48.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                       Nature 368:32-38(1994)
EMBL; 292834; CAB07385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
'..haq 9; Conserva
                                                                                                                                               Query Match
Best Local Similarity
'.^^c 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              01-MAR-2001 (Trem
F39B2.4B PROTEIN.
F39B2.4B.
                                                                                                                                                                                                                                                                                            01-MAY-2000
                                                                                                                                                                                                                                                                                                       01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                             elegans."
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Dobson R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLL0310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q55655
Q55655;
                                                                                                                                                                                                                                                                        0903G5
                                                                                                                                                                                                                                                   RESULT
Q9U3G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
    ò
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                          ò
```

```
MEDLINE-97061201: PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TEMBLEEL. 08, Last sequence update)
01-MAR-2001 (TEMBLEEL. 16, Last annotation update)
UDP-N-ACETYLGLUCOSAMINE:A-3-D-MANNOSIDE B-1,2-N-
ACETYLGLUCOSAMINULTRANSFERASE I (EC 2.4.1.101) (ALPHA-1,3-MANNOSYL-
GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE) (N-GLYCOSYL-
OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I).
                                                                                                                                                                                          Sugiura M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-96127529; Pubmed-8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome.
62D74D7F5B74564E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02585159B0F9B21D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schachter H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen S., Zhou S., Sarkar M., Spence A., Schach'
"Expression of three Caenorhabditis elegans N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D64000; BAA10175.1; -.
InterPro; IPR00182; Acetyltransf_GCN5.
Pfam; PF00583; Acetyltransf; 1.
Hypothetical protein; Complete proteome
SEQUENCE 302 AA; 33760 WW; 62D74D7F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Glycosyltransferase,
SEQUENCE 467 AA; 54363 MW; 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.8%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.v.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EWAFRVAYRGIRYLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                       Submitted (AUG-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 AA;
                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                          STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998
```

DB 5;

Score 43;

47.88;

F48E3.1

09GPA3 Q9GPA3

RESULT

δλ qq

```
KEDLINE-98044033; Pubbwed-9384377;

RA KURST F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Borriss R., Bourseler C.V., Caldwell B., Capueno V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galider D.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Caradi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Notaysahi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Persecan B., Pujic P., Purnelle B., Ropenort G., Rey M., Reynolds S.,

RA Rosenlan E., Schleich S., Schroetter R., Scoffone F.,

RA Schiguchi J., Sekowska A., Serror P., Shin B.S., Soldo B.,

RA Schiguchi J., Sawahara S., Vandehol M., Vannier F., Vassarotti A.,

RA Sorokin A., Tanakoshi A., Tanaka T., Takahashi H., Takematu A.,

RA Sorokin A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Sorokin A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Wipat A., Yanamaco H., Yanne K., Yasahikawa H., Danchin A.,

RA Winters P., Wipat A., Yanaka H.F., Sonkitan E., Yashikawa H., Danchin B.,

RY The complete genome sequence of the gram-positive bacterium Bacillus
                                  RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Ra Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Ra Cheuk R., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Chon L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., RA Chon L., Conway A., Gonzalez A., Liu J., Liu S., Mukharsky N., RA Lée J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., RA Theologis A., Ecker J., E.
R. Jubmitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R. Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R. Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R. Prems. PF02362; B.3; 1.

R. Sequence 570 AA; 65041 MW; E64A987BA713DF7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 10; Length 570;
Pred. No. 62; 2; Indels
4; Mismatches 2; Indels
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   611 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:|| :||| |:||
175 QWSFRHSYRGTPQRHLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KWAFRVAYRGI--RYLL 15
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.8
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKOU PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 034398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           034398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
034398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                      ö
                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update)
F1504.42.
Arabidopsis thaliana (Mouse-ear cress)
Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotylodons; core eudicots; Rosidae;
Spermatophyta; Magnollophyta; eudicotylodons; core eudicots; Rosidae;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 5; Length 471;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U28735; AAF99958.2; -. SEQUENCE 471 AA; 54905 MW; 6CEE1D36791D6AE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid F48E3.";
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                 471 AA.
                             Pred. No. 50;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STŘAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.8%;
                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, F48E3.1 PROTEIN.
                                  Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWAFRVAYRGIRY 13
                                                                                                                                                   153 KWALDKAFKGFRY 165
                                                                                                        1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pauley A.;
```

Q9LQE3; Q9LQE3 RESULT 10

O9LOE3

g δ

```
MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000
01-JUN-2001
                                                                                           Tabata S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VAQ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
09VAQ8
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2; Length 276;
Pred. No. 41;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                              Length 611;
                                                                                                                                                                                                                                                                                                                                   Indels
                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 299110; CAB13197.1; -.
InterPro; IPR000977; DNA_11gase.
Pfam: PF01068; DNA_11gase.
PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei Y., Miller C.G.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U89718; AAB53420.1; -.
HSSP: P09373; 1CM5.
                                                                                                                                                                                                                                         611 AA; 70204 MW; 5CB06797A2C955C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 AA; 32455 MW; BAC87EBD1F926757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 31.8 KDA PROTEIN.
SLL1469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL PYRUVATE FORMATE-LYASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                            Score 43; DB 2;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 AA
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.78;
                                                                                                                                                                                                                                                                                              47.88;
                                                                                                                                                                                                                                                                                                                                                                                          :| : | | | ; ||:
18 EWRYEVKYDGYRCILRI 34
                                                                                                                                                                                                                                                                                                                                                                     1 KWAFRVAYRGIRYLLRL 17
Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 RVALYGIRYLVR 198
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
T; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 RVAYRGIRYLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lyase; Pyruvate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-LT2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P73419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 006962
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
006962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC DOTA PLANT REPARATE PRESENTATION OF THE PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
RA Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.E.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Basu A., Baxendale J., Bayraktaroglu L., Basley E.M.,
RA Ballew R.M., Gawles P., Berman B.P., Bhandkoch C., Baldwin D.,
RA Ballew R.M., Cawles P., Berman B.P., Bhandari D., Botther P.,
Borkove D., Botchan M.R., Bouck J., Brokstein P., Botcher P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkove D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Davis S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Bortis M.J., Evangelista C.C., Ferriaz C., Ferriaza S., Filalschmann W.,
RA Fosler C., Gabriellian A.E., Garrell J.H., Gu Z., Guan P., Harris M.,
Alush K.A., Hewland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Hewland T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alasi M. M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Malush P.,
RA Liu X., Matteil B., McIntosh T.C., McLeod M.D., McPherson D.,
RA Markel B. McIntosh T.C., McLeod M.D., McPherson D.,
RA Markel W. M., Waller M. M., Waller M. M., Maloch M. M., Maloch
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson B.R., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Resee M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosopila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000182; Acetyltransf_GCN5.
Pfam. PF00583; Acetyltransf, 1.
Hypothetical protein; Complete proteome.
Hypothetical 285 AA; 31778 WW; OEFALE207532B5E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2
Pred. No. 63;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAINEBERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D90906; BAA17459.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :||| |||
117 KSGFHLAYRNIRY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KWAFRVAYRGIRY 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG14517 PROTEIN.
```

us-09-485-571-32.rspt

```
ó;
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

A Enen X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,

A Sheng X.H., Zhong F.N., Zhong W., Zhong G., Zhao Q., Zheng L.,

A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

The genome sequence of Drosophila melanogaster.";

B EMBL, AE003768; AAF56843.1, -

R FlyBase; FBGN0039625; CG14517.

R FlyBase; FBGN003859; Galactosyl_T_2.

R Fire Prop. 1PR003859; Galactosyl_T_2.

R Ffam; PF02709; Galactosyl_T_2.

R Ffam; PF02709; Galactosyl_T_2.

SEQUENCE 323 AA; 37826 MW; A70251F8888A9DBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Franz C.M.A.P., Worobo R.W., Ostillinger U.,
Holzapfel W.H., Vederas J.C., Stiles M.E.,
"Atypical genetic locus associated with constitutive production of
enterocin B by enterococcus faecium BFE 900.";
Appl. Environ. Microbiol. 65:2170-2178(1999).
EMBL; AF121254; AAD28227.1;
HSSP: P11546; 1PBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faecium (Streptococcus faecium).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nicerpro; 17 PR001360; Glyco_hydro_1.
Pfam; PF00232; Glyco_hydro_1; 2.
PRINTS; PR00131; GLHYDRLASE1.
PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; UNKNOWN_1.
PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
SEQUENCE 475 AA; 54617 MW; D36A3EA8CBF8F12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PHOSPHO-BETA-GLUCOSIDASE BGLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.6%; Score 41; DB 5;
60.0%; Pred. No. 72;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BFE 900;
MEDLINE-99240446; PubMed=10224016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 WAFRVAYRGI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ||: |||:
208 WRFRLPYRGL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9X564
Q9X564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
09X564
10 09X564
10 01-00V
DT 01-00V
DT 01-10V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                           RA
RA
RA
RA
RA
DR
DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

ö Gaps ö Score 41; DB 2; Length 475; Pred. No. 1.1e+02; 3; Mismatches 5; Indels 45.6%; Query Match 45.6 Best Local Similarity 46.7 Matches 7; Conservative

1 KWAFRVAYRGIRYLL 15

δ

14 : : |:|||| 344 KWGWTIDPTGLRYLL 358 g Search completed: February 12, 2002, 12:38:44 Job time: 757 sec

```
February 12, 2002, 12:30:34; Search time 242.57 Seconds (without alignments) 5.191 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2. /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1992.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
//SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522463
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KYAWRVAHRGIRWLLRX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-485-571-33
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                             Run on:
```

	Description	Tachyplesin deriva	Tachyplesin deriva	Antimicrobial pept	Antimicrobial pept	Antimicrobial pept	Antimicrobial pept	Human polypeptide	Plant viral moveme	Antimicrobial pept	Antimicrobial pept	Human protein sequ
	ID	AAW99417	AAW99416	AAW47706	AAY32548	AAW47695	AAY32629	AAM41298	AAB44510	AAW47690	AAY32624	AAB95059
	DB	20	20	13	20	13	20	22	21	19	20	22
	Query Match Length DB ID	17	17	20	20	27	27	337	202	27	27	125
æ	Query Match	6.86	66.7	48.4	48.4	48.4	48.4	48.4	47.8	47.3	47.3	47.3
	Score	92	62	45	45	45	45	45	44.5	44	44	44
	Result No.		7	e	4	2	9	7	œ	6	10	11

SUMMARIES

		444444444444444444444444444444444444444		22 22 22 23 23 23 23 23 23 23 23 23 23 2	481880080808080		A murine cholester Antimicrobial tach Tachyplesin analog Antimicrobial pept
	22222222222222222222222222222222222222	11111 10111 101111 1010000000000000000	444444444	5508 5508 5508 5508 571 571 572 572 572 573 573 574 575 577 577 577 577 577 577 577 577	75555555555555555555555555555555555555	AAW92995 AAW99953 AAW89953 AAW873908 AAB173008 AAB173006 BAAB0044 AAW57899 BAAR5811 AAR75813 AAR75813 AAR75814 AAR75814 AAW32638 AAW47694 BAAW32638 AAW47694 BAAW32638 AAW47694 BAAW32638 BAAW47694 BAAW32638 BAAW32638 BAAW32638 BAAW32638	Human 1a.pha hydro Human 25-hydroxyvi Human 25-hydroxyvi Human 25-hydroxyvi Human 08FX ORF670 Protein of clone C Amino acid sequenc Human C11480_9 pr Protein involved i Thrombospondin pep Antimicrobial tach Antimicrobial tach Antimicrobial pept Antimicrobial pept Antimicrobial pept Antimicrobial pept Antimicrobial pept Antimicrobial pept Antimicrobial pept Human EST encoded Human EST encoded
RESUI AAW99 ID XX	.T 1 9417 AAW994	17	standard;	peptide	e; 1	ALIGNMENTS 7 AA.	
XX DXX OX	AAW99417; 08-JUN-19 Tachyp.les	17; -1999 Lesin d	(first  erivati	ent	ry) peptid	le SM2192.	
KW K	Linear: disulphi anti-inf nucleus; Syntheti	Linear: tachyplesin disulphide bridge; anti-inflammatory; nucleus; blood-brai Synthetic.	plesin; idge; a tory; m	; pe anti mamm n ba	ide au dy; r ; cel ier.	antibiotic; beta-sheet; se ribozyme; antitumour agent 11 membrane; passive trans	econdary structure; ; antiviral; sport; cytoplasm;
X	Key Modifite W099077 18-FEB- 06-AUG- 12-AUG- (SYNT-)	ed-s 728- -199 -199 -199 ) SY B,	9 9 9 van	ation bel= -FR01	Oua 1e 57. 97.	lifiers Sy G, Kaczorek M;	
XX DR	WPI; 1	999	-190034/16				

```
This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents,
                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear; tachyplesin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                    This peptide represents a linear derivative of the tachyplesin family of peptide antibiotics. Tachyplesin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridges. The newel derivatives are used to deliver active agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
      nseq
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                 Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Score 92; DB 20; 1 Pred. No. 9.3e-08; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaczorek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tachyplesin derivative peptide SM2191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW99416 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 28; 37pp; French.
                                                                  8; Page 28; 37pp; French
                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                         98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                   17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Calas B,
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW99416;
                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW99416
```

g

δ

```
The invention relates to new antimicrobial peptides which correspond to amino acid sequences in the transmembrane proteins of lentiviruses, in particular HYV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high tructural amphipathicity and hydropholic moment. Also disclosed are structural and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to marcroorganisms (bacteria, fungi, viruses and protozoa) but significantly is demonstrated against Gram positive and negative bacteria including pseudomonsa seruginosa, Staphylococcus aureus, Enterococcus faecalis and presents and precoccus faecalis and
                                                                                                                                                       0;
antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of 169 disclosed specific examples of the present sequence. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                       Gaps
                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 20;
                                                                                                                             DB 20; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                          Indels
                                                                                                                        Score 62; DB 20; LP Pred. No. 0.0034;
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide SLP1 analogue.
                                                                                                                                                                                                                                                                                                AAW47706 standard; peptide; 20 AA.
                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0786748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0010634.
                                                                                                                                66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                             (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                               Conservative
                                                                                                                                                                                          1 KYAWRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-158352/14.
                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIV strain MM239.
                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mietzner TA,
                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                              26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5714577-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                               AAW47706;
                                                                                          Sequence
                                                                                                                                                                                                                                                                                      AAW47706
                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                   δŏ
                                                                                                                                                                                                                          Db
                   SSSSX
```

```
The invention relates to new antimicrobial peptides which correspond to amino acid sequences in the transmembrane proteins of lentiviruses, in particular HIV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high amphipathicity and hydrophobic moment. Also disclosed are structural and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly is demonstrated against Gram positive and negative bacteria including Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis and
                                                                                                                                                                                                                                                                                     Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serratia marcescens. The present some of 169 disclosed specific examples of the present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 19; Length 27; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                  Antimicrobial peptide SLP1 analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY32629 standard; peptide; 27 AA.
                                                                                                                        AAW47695 standard; peptide; 27 AA
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0786748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0010634.
97US-0786748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montelaro RC,
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.4
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WFVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11: || ||:|
2 wrllrrggrwil 13
                 2 wrllrrggrwil 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-158352/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIV strain MM239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1997;
                                                                                                                                                                                                           26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                      US5714577-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY32629;
                                                                                                                                                                   AAW47695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AAY32629
ID AAY3:
XX
AC AAY3:
                                                                                                      AAW47695
                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents an antimicrobial peptide of the invention, and used for treating infections caused by Staphylococcus aureus.

C used for treating infections caused by Staphylococcus aureus.

C methicillin resistant s. aureus, Pseudomonas aeruginosa, Enterococcus faecalis, S. marcescens Escherichia coli, fungi, protozoa and viruses in acrocoganisms such as bacteria, fungi, protozoa and viruses in acrocoganisms such as bacteria, fungi, protozoa and viruses in acrocoganisms such as production of intibit unwanted microbial growth, particularly for the production of recombinant proteins or vectors for gene therapy. They can also be used in preventing infections through the trainisation of wounds prior to suture and to sterilise surgical instruments. The unique structure of these antimicrobial peptides inparts high potency while selectivity is maintained, they are concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing it more difficult for a microorganism to develop a mechanism of testistance against this type of antiblotic. Their small size makes them relatively simple to prepare by standard synthetic peptide chemistry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                     ó
                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial peptides useful for treating microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 20; Length 20;
Pred. No. 1.5;
2; Mismatches 3; Indels
                     Indels
                     3;
  Pred. No. 1.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tencza SB;
                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide SLP-1 analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Column 107; 62pp; English
                                                                                                                                                                                                               AAY32548 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0010634.
97US-0786748.
97US-0932682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0932682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montelaro RC,
                                                                                                                                                                                                                                                                                              21-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.37
                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYPI-) UNIV PITTSBURGH.
                                                                                   ||: || ||:|
2 wrllrrggrwil 13
                                                               4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-508189/42.
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          sterilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5945507-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 - JAN-1997
```

Synthetic.

AAY32548;

RESULT AAY32548

6 qq ö

Gaps

;

3; Indels

Sequence

us-09-485-571-33.rag

peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

nootropic; immunosuppressant; cytostatic; gene therapy;

Human polypeptide SEQ ID NO 6229.

```
methicillin resistant S. unaced. Pseudomonas acruginosa, Enterococcus faccalis, S. marcescens, Escherichia coli, fungi, protozoa and viruses in amammalian host. They can be used to inhibit growth of diverse microorganisms such as bacteria, fungi, protozoa and bNa and kNa viruses of microorganisms such as bacteria, fungi, protozoa and bNa and kNa viruses and can be used in tissue culture to inhibit unwanted microbial growth, particularly for the production of recombinant proteins or vectors for gene therapy. They can also be used in preventing infections through the sterilisation of wounds prior to suture and to sterilise surgical instruments. The unique structure of these antimicrobial peptides imparts high potency while selectivity is maintained, they are moderately haemolytic but only lyse red blood cells at high concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing little selectivity. The peptides target a membrane structure which makes it may be added to a mechanism of resistance against this type of antibiotic. Their small size makes them resistance against this type of antibiotic. Their small size makes them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                         Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production; sterilisation.
                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents an antimicrobial peptide of the invention, and is an analogue of the peptide SLP-1 (see AAX32551). The peptides can be used for treating infections caused by Staphylococcus aureus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptides useful for treating microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 20
Pred. No. 2.1;
2; Mismatches
                                                                                                                                                                                                                                                                                                 Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                        62pp; English.
                                      Antimicrobial peptide SLP-1 analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM41298 standard; Protein; 337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                            Simian immunodeficiency virus.
                                                                                                                                                                                                                          96US-0010634.
97US-0786748.
97US-0932682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.48;
                                                                                                                                                                                                   97US-0932682.
                                                                                                                                                                                                                                                                                                  Montelaro RC,
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                           (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: || ||:|
2 wrllrrggrwil 13
                                                                                                                                                                                                                                                                                                                        WPI; 1999-508189/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AA;
               21-OCT-1999
                                                                                                                                                                                                   18-SEP-1997;
                                                                                                                                                                                                                                       24-JAN-1997;
18-SEP-1997;
                                                                                                                                                                                                                                                                                                  Mietzner TA,
                                                                                                                                                                                                                           26-JAN-1996;
                                                                                                                                                    US5945507-A.
                                                                                                                                                                            31-AUG-1999
                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM41298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXX
     δy
```

ä

Wang

Ren F, W Zhang J;

Qian XB, Yang Y,

Ma Y, Xue AJ,

Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ Goodrich R, Drmanac RT;

Liu C, Wang Z, V

Tang YT, Wang J, V Zhao QA,

2000US-0488725. 2000US-0552317. 2000US-0598042.

25-APR-2000; 09-JUL-2000; 19-JUL-2000; 03-AUG-2000;

WO200153312-A1.

26-DEC-2000; 21-JAN-2000;

26-JUL-2001

Homo sapiens.

leukaemia.

2000US-0620312. 2000US-0653450. 2000US-0662191. 2000US-0693036.

14-SEP-2000;

19-OCT-2000; 2000US-0693036. 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC

Novel nucleic acids and polypeptides, useful for treating disorders

such as central nervous system injuries

WPI; 2001-442253/47. N-PSDB; AAI60454.

```
ö
                                                                                                                              in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2
Pred. No. 29;
4; Mismatches
Example 2; SEQ ID NO 6229; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB44510 standard; Protein; 202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : |: :||:|
250 wiiphkavrwil 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB44510
ID AAB44
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

(first entry)

22-OCT-2001

7

AAM41298;

- Wed Feb 13 07:52:42 2002

```
Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LL. SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                             Synthetic.
Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.38;
                                                                                                                                                                        97US-0786748.
                                                                                                                                                                                                                                                                                      Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.3%;
                                                                                                                                                                                                                        97US-0786748
                                                                                                                                                                                                        96US-0010634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                        (UYPI .. ) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                   WPI; 1998-158352/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 wrtlrrggrwil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AA;
                                                                                                                                                                                                                                                                                       Mietzner TA,
                                                                                                                                                                        24-JAN-1997;
                                                                                                                                                                                                        26-JAN-1996;
                                                                                                                                                                                                                        24-JAN-1997;
                                                                                                           US5714577-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5945507-A
                                                                                                                                           03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY32624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY32624
   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences AAC79348-C79375 encode plant viral movement proteins AAB4494-B44520. Some plant viruses have been shown to be able to establish systemic infections via movement proteins that utilise existing plant pathways to traffic macromolecules to surrounding cells. Proteins such as those of the invention are similar to viral movement proteins are useful for obtaining a nucleic acid fragment encoding a viral movement protein. Polynucleotides cell: The plant viral movement proteins are useful for obtaining a nucleic acid fragment encoding a viral movement protein. Polynucleotides cenceding the plant viral movement proteins are useful in the field of plant molecular biology, and in the preparation of antibodies against the proteins. The proteins are also useful in the field of proteins. The proteins from the same or other plant species, and to create transgenic plants in which the protein is presented at higher or lower levels than normally found. The proteins and nucleotide sequences may be used to control cosuppression and engineer plant virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                Novel viral movement polypeptides and polynucleotides useful in field of plant molecular biology, for producing transgenic plants, to prepare antibodies and in immunological screening of CDNA expression libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 202;
                                                                                              protein; transport; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44.5; DB 21;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 21;
                                                             Plant viral movement protein SEQ ID 34.
                                                                                                                                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptide SLP1 analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 52; .62pp; English.
                                                                                                           viral resistance; cosuppression
                                                                                                                                                                                                                                                                                                                                      Weng Z, Cahoon RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW47690 standard; peptide; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                       06-APR-2000; 2000WO-US09110.
                                                                                                                                                                                                                                                                       99US-0128092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KYAWRVA-----HRGIRWLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || :||| :||| 35 kypwrvglglsrnrgvffllr
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                              movement
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-638467/61.
N-PSDB; AAC79364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AA;
                                                                                                                                                                        WO200060088-A2
                                                                                                                                                                                                                                                                       07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1998
                                                                                            Plant viral
                                                                                                                                                                                                                                                                                                                                      Krebbers E,
                               06-FEB-2001
                                                                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance
AAB44510;
                                                                                                                                            Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW47690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW47690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
```

Tencza SB;

ö The invention relates to new antimicrobial peptides which correspond to particular HIV and SIV. These peptides comprise arginine rich sequences which, when modelled for secondary structure, display high amplicational analogues and homologues of these peptides are structural and furcional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly is demonstrated against Gram positive and negative bacteria including Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis and Antimicrobial peptide; LLP1; SLP-1; LLP2; SLP2A; SLP2B; ELP; infection; growth inhibitor; microorganism; virus; gene therapy; vector production; sterilisation. Gaps The present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of SIV strain MM239. ő Score 44; DB 19; Length 27; Pred. No. 3; 1; Mismatches 4; Indels Retroviral TM peptides - useful as antibacterial agents Disclosure; Column 10; 59pp; English. Antimicrobial peptide SLP-1 analogue. AAY32624 standard; peptide; 27 AA. Simian immunodeficiency virus.

XX EX SE

à a 99JP-0300253

```
27-AUG-1999;
           11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY84945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                              Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY84945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
 This sequence represents an antimicrobial peptide of the invention, and is an analogue of the peptide SIP-1 (see AAY2551). The peptides can be used for treating infections caused by Staphylococcus aureus, used for treating infections caused by Staphylococcus aureus, used for treating infections. Peaudomonas aeruqinosa, Enterococcus faecalis, S. marcescens, Escherichia coli, fungi, protozoa and viruses in a mammalian host. They can be used to inhibit growth of diverse in cororganisms such as bacteria, fungi, protozoa and DNA and RNA viruses and can be used in tissue culture to inhibit unwanted microbial growth, particularly for the production of recombinant proteins or vectors for gene therapy. They can also be used in preventing infections through the sterilisation of wounds prior to suture and to sterilisas surgical instruments. The unique structure of these antimicrobial peptides instruments. The unique structure of these antimicrobial peptides instruments high potency while selectivity is maintained, they are concentrations unlike melittin, a peptide extracted from bee venom, which is highly active against bacteria and lyses red blood cells showing the moreorganism to develop a mechanism of the mesistance against this type of antibiotic. Their small size makes them concentratively simple to prepare by standard synthetic peptide chemistry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                          Antimicrobial peptides useful for treating microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:16879.
                                                                                                                                                          Tencza SB;
                                                                                                                                                                                                                                          Disclosure; Column 11; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB95059 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0248036
                                                                        96US-0010634.
97US-0786748.
97US-0932682.
                                            97US-0932682.
                                                                                                                                                          Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                              (UYPI-) UNIV PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || || || ||:|
2 wrtlrrggrwil 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WRVAHRGIRWLL 15
                                                                                                                                                                                      WPI; 1999-508189/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                            Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001
                                               18-SEP-1997;
                                                                           26-JAN-1996;
                                                                                                     18-SEP-1997;
                                                                                       24-JAN-1997,
                   31-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB95059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of
the 5602 nucleotide sequences defined in the specification, where the
complementary strand of a polynucleotides; or (b) a combination
complementary strand of a polynucleotides; or (b) a combination
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
complementary strand of a sequence is selected comprises a 5'-end
coligonucleotide which comprises a 3'-end sequence, where the
coligonucleotide comprises a 1'-end sequence, where the
coligonucleotide primers are useful for synthesising polynucleotides,
the specification. The primers are useful for synthesising polynucleotides,
che fall-length cDNAs. The primers are also useful for the
complementary without any specialised methods are also useful for the
complementary and an expecialised methods. And 1365 to AAH13632
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
complementary full-length cDNAs and a useful in the exemplification
conference and and a man amino acid sequences; and AAH13632 to AAH13632
complementary full-length cDNAs and a useful in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                               Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cholesterol 25-hydroxylase; serum cholesterol; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                      Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A murine cholesterol 25-hydroxylase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 8; SEQ ID 16879; 2537pp + Cp ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%; Score 44; DB 22;
38.5%; Pred. No. 15;
Live 3; Mismatches 5
                                                                                                                                                                                                                                                    Ishii S, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                  Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84945 standard; Protein; 298
                                                                                                                                                                                                                  Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US24873.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 WRVAHRGIRWLLR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::| | |: | 37 wkichlgfnwirr 49
                                                                                                                                                  (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200023596-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000
                                                                               39-JUN-2000;
```

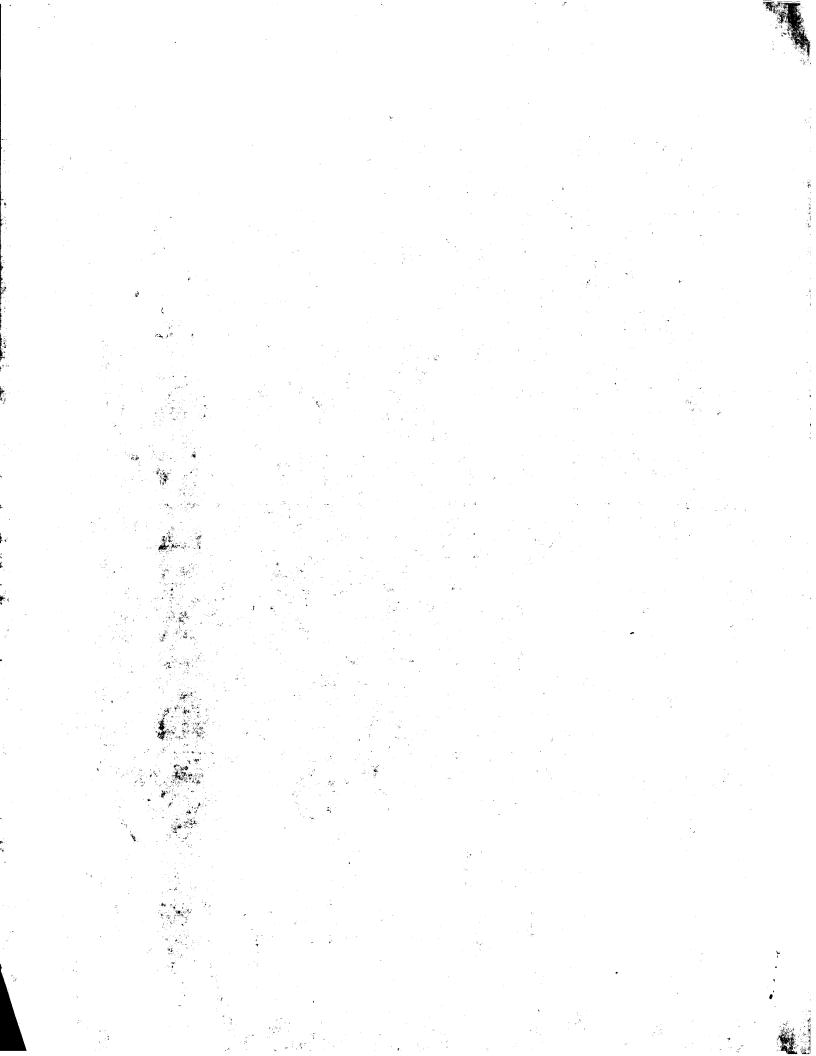
```
Claim 1; Page 29; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-1997;
                                                                                                                                                                                                                                                                                                   08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  US6015941-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                               AAY69630;
                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rao AG:
                                                                                                                                                                                                                                                   AAY69610
                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                The present sequence represents a murine cholesterol 25-hydroxylase polypeptide. The polypeptides and polynuclectides can be used to regulate cholesterol 25-hydroxylase activity and therefore serum cholesterol in a mammalian host. The polypeptides, polynucleotides and the cholesterol 25-hydroxylase-specific binding agents are useful in diagnosis (e.g. genetic hybridization screens for cholesterol 25-hydroxylase transcripts), therapy (e.g. cholesterol 25-hydroxylase inhibitors to modulate serum cholesterol) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating natural 25-hydroxylase genes and transcripts, reagents for screening chemical libraries for lead pharmacological agents).
                                                                                               New cholesterol 25-hydroxylase polypeptides, useful for regulating cholesterol 25-hydroxylase activity and therefore serum cholesterol in a mammallan host, have cholesterol 25-hydroxylase-specific structure
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide derivs. of tachyplesin - having antimicrobial activity, used against plant pathogenic fungi or human or animal infections
                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachyplesin; inhibitor; antimicrobial; plant pathogen; fungi; infection.
                                                                                                                                                                                                                                                                                                                    Score 44; DB 21; Length 298; Pred. No. 37; Alsmatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial tachyplesin peptide derivative.
                                                                                                                                                Claim 1; Page 47-48; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75806 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                       47.38;
         98US-0177419.
                                                                                                                                                                                                                                                                                                                                40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US14619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0168809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rao A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                            (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                         :|| : | : || |
140 fawhllhhkvpwlyr 154
                                                                                                                                                                                                                                                                                                                                                             2 YAWRVAHRGIRWLLR 16
                                               Lund EG;
                                                                   2000-339695/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-231570/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rao AG,
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                         298 AA;
                                                                            N-PSDB; AAA15142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-1994;
                                                                                                                            and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09516776-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1993;
        22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1995.
                                               Russell DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putman RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR75806;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75806
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
à
```

```
Sequences AAY69610-Y69611 and AAY69617 represent tachyplesin analogues used in an exemplification of the present invention, in which the native tachyplesin cysteine residues are replaced with Ala, Leu and Asp, respectively. Tachyplesin (AAX69608) is a naturally occurring antimicrobial peptide which contains two disulphide bonds which halp to maintain its tertiary structure. The invention relates to novel peptide analogues of tachyplesin (Y69612-AAX69614, AAX69616) in which the cysteine residues at positions 3, 7, 12 and 16 of the native tachyplesin are replaced by the hydrophobic amino acids isolaucine, valine, methionine, phenylalanine or tyrosine, the same amino acid being
AAR75802-04 and AAR75806-22 are peptide derivatives of tachyplesin (AAR75805) a small peptide isolated from japanese horseshoe crab hosmocyctes which has antimicrobial properties. The peptide derivatives also have antimicrobial activity and can be used for killing and inhibiting fungl, in particular for fungl pathogenic to plants e.g. Fusarium graminearum, Fusarium monilforme, Sclerotinia scleroticum, sclerotinia trifoliorum and Aspergillus flavus. The peptides can also be used for treating and preventing infection in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tachyplesin analogs useful for controlling fungal and bacterial activity in agricultural and medical applications and for controlling plant viruses have four cysteine substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tachyphesin analogue; generic; antimicrobial; disulphide bond; antifungal; antiviral; antimicrobial; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 16; Length 17; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY696:10 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page -; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0962034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tachypiesin analogue, TPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
E.c. 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-126327/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KYAWRVAHRGIRW
                                                                                                                                                                                                                                                                                                                                                         17 AA;
```

us-09-485-571-33.rag

```
ö
                                                                                                               fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences in the transmembrane proteins of lentiviruses, in which, when modelled for secondary structure, display high amphichty and hydrophobic moment. Also disclosed are structural and functional analogues and homologues of these peptides which also display antimicrobial activity. The peptides are highly inhibitory to microorganisms (bacteria, fungi, viruses and protozoa) but significantly less toxic to red blood cells and other normal mammalian cells. Activity is demonstrated against Gram positive and negative bacteria including pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; transmembrane protein; TM; lentivirus lytic peptide; LLP; SLP; amphipathic; antibacterial; antifungal; antiviral; antiprotozoal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to new antimicrobial peptides which correspond to
present at all four positions. Despite being unable to form intramolecular disulphide bonds, the analogues are functional as antimicrobial agents. The tackipplesin analogues are useful for controlling fungal and viral activity in agricultural and medical applications and for controlling plant viruses. They can also be expressed in transgenic plants, preferably wheat, sorghum, sunflower, soya or especially maize plants to provide resistance to pathogenic fand viruses. Note: The present sequence is not shown in the specification, but is derived from the generic tachyplesin analogue sequence given in column 23.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of 169 disclosed specific examples of the new peptides. It is an analogue of the peptide designated SLP1 (see AAW47616) which is a peptide from the transmembrane protein of
                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                     46.2%; Score 43; DB 21; Length 17; 61.5%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retroviral TM peptides - useful as antibacterial agents
                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tencza SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Column 10; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptide SLP1 analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47701 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0786748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Montelaro RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0010634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0786748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                    Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYPI-) UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                             |:|:|||:||| :
| kwafrvayrgiay 13
                                                                                                                                                                                                                                                                                                                              1 KYAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-158352/14
                                                                                                                                                                                                   17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mietzner TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5714577-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-1998
                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW47701;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47701
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                              셤
 555555555555888
                                                                                                                                                                                                                                                                                                                              ð
```

```
ö
                                                                                 Gaps
                                                                               ;
0
                                                          DB 19; Length 20;
                                                                               Indels
                                                       Score 42; DB 1
Pred. No. 4.4;
1; Mismatches
                                                                                                                                                                         Search completed: February 12, 2002, 12:30:34 Job time: 367 sec
                                                       45.2%;
ilarity 50.0%;
Conservative
                                                                                                     4 WRVAHRGIRWLL 15
                                                                                                                 | || || || || wetlrrgcrwil 13
                                                                  Best Local Similarity
Matches 6; Conser
 SIV strain MM239.
                       Sequence
                                                          Query Match
SXS
                                                                                                     δy
                                                                                                                           g
```



Sequence Sequence Sequence

Sedineuce Sedine

OM protein

Run on:

```
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TILLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
               US-08-786-7488-73
US-08-786-7488-90
US-08-786-7488-90
US-08-786-7488-101
US-08-932-682-90
US-08-932-682-90
US-08-932-682-99
US-08-932-682-99
US-08-932-682-99
US-08-932-682-99
US-08-932-682-101
US-08-932-682-88
US-08-786-7488-78
US-08-786-7488-78
US-08-786-7488-79
US-08-786-7488-88
US-08-786-7488-79
US-08-786-7488-79
US-08-786-7488-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1;
Pred. No. 0.66;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTONNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 32,300
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-408-2500
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 97, Application US/08786748A; Patent No. 5714577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: NO. 5714577e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-786-748A-97
  (without alignments)
3.605 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76,
2,
10,
12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Beguence Beg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-932-682-97
US-08-786-748A-86
US-08-786-748A-81
US-08-932-682-81
US-08-932-682-81
US-08-932-682-81
US-08-932-682-92
US-08-786-748A-94
US-08-932-682-92
US-08-932-682-92
US-08-932-682-94
US-08-932-682-94
US-08-932-682-89
US-08-786-748A-80
US-08-932-682-89
US-08-932-682-89
US-08-932-682-89
US-08-932-682-89
US-08-98-932-682-89
US-08-98-932-682-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-111-730-7
US-08-168-809-10
US-08-168-809-12
US-08-168-809-13
US-08-786-740A-96
US-08-786-740A-85
US-08-932-682-85
US-08-931-682-85
US-08-971-937-2
                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                February 12, 2002, 12:32:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                 US-09-485-571-33
93
1 KYAWRVAHRGIRWLLRX 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match 1
                                                                                                                                                                                                                                                          Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                         Scoring table:
```

Minimum DB Maximum DB

Database

Result Š

Searched:

ö

Gaps

ö

Length 20; Indels

```
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
WUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          SOFTWARE: FastEED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                              AP30421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BAKER & BOTTS, L.L.P. STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY AGENT INFORMATION:
NAME: Rochelle K. Seide
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: RCOFFELE K. Seide
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 86, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFFINARE: FASTSEQ VERSION 2.0 CURRENT APPLICATION NUMBER: US/08/932. FITTER APPLICATION NUMBER: US/08/932.
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: AP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: No. 5714577e
                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-408-250
TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 WRLLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                   COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                         New York
                                                Y: USA
10112-0228
    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-786-748A-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-932-682-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.4%; Score 45; DB 2; Length 20; 58.3%; Pred. No. 0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Brumbaugh, Graves, Donohue & Raymond
30 Rockefeller Plaza
                                                                                                                                                                                                               APPLICANT: Tentald, Montelaro C.
APPLICANT: Tencas, Sarah B.
APPLICANT: Mictaner, Timochy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ANDERSS:
CORRESPONDENCE ANDERSS:
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86, Application US/08786748A
Patent No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVERTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: USA

ZIP: 10112-0228

COMPUTER READABLE FORM:
MEDLUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION UNDARA:
APPLICATION UNDARA:
APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: 32,300
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 212-765-5509
                                                                                                                                                   Sequence 97, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5945507e
US-08-932-682-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh
4 WRVAHRGIRWLL 15
                       11: || ||:|
2 WRLLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 WRLLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-786-748A-86
                                                                                                                          US-08-932-682-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                          RESULT
                                         g
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Gaps
48.4%; Score 45; DB 1; Length 27; 58.3%; Pred. No. 0.89; tive 2; Mismatches 3; Indels
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                   APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE C. FINVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 1.3;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP30421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30421-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-765-2519
INFORMATION FOR SEQ ID NO: 81:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rey, Michael
Golightly, Elizabeth
Klotz, Alan
Mathisen, Thomas Erik
Dambmann, Claus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/08943714; Patent No. 6187578
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blinkovsky, Alexander
Berka, Randy
                                                                                                                                                ; Sequence E1, Application US/08932682
; Patent No. 5945507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: No. 5945507e
US-08-932-682-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.3
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUMTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                       4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 WRTLRRGGRWIL 13
                 4 WEVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-943-714-10
                                                                                                              RESULT 6
US-08-932-682-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                   ŏ
                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 27;
Pred. No. 1.3;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                      DB 2; Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIF: 10112-0228

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEX Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN 1997
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION UNBER: 60/010,634
FILING DATE: 26-JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: ROCHelle K. Seide
REGISTRATION NUMBER: 32,300
REGISTRATION NUMBER: 32,300
REGISTRATION NUMBER: 32,300
RECISTRATION NUMBER: AP30421
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
             REFERENCE/OCCKET NUMBER: AP30421-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-705-5000
TELEFAX: 212-705-2519
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                      Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81, Application US/08786748A Patent No. 5714577
GENERAL INFORMATION:
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: No. 5714577e
                                                                                                                                                                                                                                                                                    48.48;
                                                                                                                                                                                                         , MOLECULE TYPE: NO. 5945507e
US-08-932-682-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                   212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                   11: || || || || 2 WRLLRRGGRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-786-748A-81
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Indels

DB 1; Length 17;

```
Score 43; DB Pred. No. 1.1; 4; Mismatches
   REGISTRATION NUMBER: 29,342
REERERENG-JOCKET NUMBER: 0173R US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-245-3595
TELEPRAX: 515-245-3634
INFORMATION FOR SEQ. ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.28;
61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 20 amino acids
                                                                                                                                                                                                                                                       LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.2
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-CONTROLLED TO A NOT CONTROLLED TO TO THE TOTAL THE TOTAL TO THE TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KYAWRVAHRGIRW 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-786-748A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-168-809-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                           No. 61875780 No. 6187578disk of No. 6187578th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08168809
Patent No. 5580852
GENERAL INFORMATION:
APPLICANT: Putnam, Rebecca J.
APPLICANT: Rao, Aragula G.
TITLE OF INVENTION: DERIVATIVES OF TACHYPLESIN HAVING
TITLE OF INVENTION: INHIBITORY ACTIVITY TOWARDS PLANT PATHOGENIC FUNGINUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 4; Length 481;
Pred. No. 22;
4; Mismatches 4; Indels
   Carboxypeptidases And Nucleic Acids
Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pioneer Hi-Bred International STREET: 700 Capital Square, 400 Locust Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,714
FILING DATE: 03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REEISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4990.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/168,809
                                                                                                                                                                        405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Roth, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 481 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| |||:|: |||:
460 QYQPRVAYRHLEWLLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KYAWRVAHRGIRWLLR 16
TITLE OF INVENTION: CA
TITLE OF INVENTION: EN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-943-714-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                CITY: New York
                                                                                                                                                                                                                                                                                    USA
                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-168-809-5
                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
```

```
DB 1; Length 20;
                                                                                                                                                                                                                                                          ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza CITY: New York STATE: New York
US-08-786-748A-92
Sequence 92, Application US/08786748A
Patent No. 5714577
GENERAL NO. F714577
APPLICANT: Ronald, Montelaro C. APPLICANT: Tencza, Sarah B. APPLICANT: Tencza, Sarah B. APPLICANT: Tencza, Sarah B. APPLICANT: Nietzner, Timothy A. TITLE CP INVENTION: NOVEL ANTIMICROBIAL PEPTIDES NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPUTE.
COMPUTER: IBM COMPUTE.
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
NAME: Rochelle K. Seide

NAME: Rochelle K. Seide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.2%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: AF
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFRAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: No. 5714577e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

```
Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 94, Application US/08932682
Patent No. 5945507
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timcthy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
UMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY ACCHOIN THORNAMION:
RAME: ROCHOINE K. Seide
REGISTRATION NUMBER: 32,300
REGISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RECISTRATION NUMBER: 32,300
RELECHONE: 212-705-500
                                                                                                                                                                                                                                                                                                                                                                                                                                     AP30421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                  ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: No. 5945507e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.2%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDALL
STREET: 30 ACC
CITY: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WETLRRGCRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE amino acid
STRANDEDNESS: sir
                                                       New York
New York
                                                                                              RY: USA
10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-932-682-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-932-682-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 1; Length 20; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Miectner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                        APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
50.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP30421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROCHELLE K. Seide
NAME: ROCHELLE K. Seide
REFERENCE/DOCKET NUMBER: 32,300
                                                                                                                                                                                             Sequence 94, Application US/08786748A Patent No. 5714577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92, Application US/08932682 Patent No. 5945507 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: NO. 5714577e
US-08-786-748A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.0
الا Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-765-2519
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New 10...
STATE: New York
COUNTRY: USA
71P: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 WRVAHRGIRWLL 15
                                                                                  | | || || 1
2 WETLRRGCRWIL 13
                                                                                                                                                                        US-08-786-748A-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-932-682-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                           ô
                                                                                              g
```

0; Gaps

Gaps

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó.
                     DB 1; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 21;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                  APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDESSE: ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-786-748A-80
Sequence 80, Application US/08786748A
Sequence No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
                  Score 42; DB 1
Pred. No. 2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.2%; Score 42; DB 50.0%; Pred. No. 2; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP30421-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,682
FILING DATE: 18-SEP-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                            Sequence 89, Application US/08932682
Patent No. 5945507
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/786,748
FILING DATE: 24-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: RCChelle K. Seide
REGISTRATION NUMBER: 32,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: AP TELECOMMUNICATION INFORMATION:
                     45.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: No. 5945507e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 212-705-5000
TELEFAX: 212-765-2519
Query Match
Best Local Similarity 50.0.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.2
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                   4 WRVAHRGIRWLL 15
                                                                                                                          4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 WETLRRGCRWIL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 30 Rockef
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                      RESULT 14
US-08-932-682-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-932-682-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                             ó:
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 89. Application US/08786748A
Patent No. 571457
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Tencza, Sarah B.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                           REFERENCE/DOCKET NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: AP30421-A
; TELECOMMUNICATION INFORMATION:
; TELEPAN: 212-705-5000
; TELEPAN: 212-765-2519
; INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; STRANDEDENESS: single
; TYPE: amino acid
; STRANDEDENESS: single
; TOPOLOCSY: linear
; MOLECULE TYPE: NO: 5945507e
US-08-932-682-94
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                   45.2%; Score 42; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 26-JAN-1996
ATTORNEY/ACENT INFORMATION:
NAME: ROCHELLE K. Seide
REGISTRATION UMBER: 32,300
REFERENCE/DOCKET NUMBER: AP90421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: No. 5714577e
US-08-786-748A-89
                24-JAN-1997
                                   ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-765-2519 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 WRVAHRGIRWLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | || || || 2 WETLRRGCRWIL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-786-748A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

g ŏ

ö

Gaps

```
NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
STATE: New York
COUNTRY: USA
2 IP: 10112-028
COMPUTER: EABDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: EASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
REGISTRATION NUMBER: 32,300
FELECOMMUNICATION INFORMATION:
TELEBHONE: AL2-408-2500
TELECOMMUNICATION INFORMATION:
TELEBHONE: AL2-408-2500
TELECOMMUNICATION INFORMATICS:
CHARCH: AMINO ACID
SEQUENCE CHARACTERISTICS:
CHARCH: AT AMINO ACID
STRUMBENESS: Single
TYPE: amino acid
STRUE TYPE: NO. 5714577e
US-08-786-748A-80
```

; 0 Gaps ö Query Match
Best Local Similarity 50.0%; Pred. No. 2.5;
Matches 6; Conservative 1; Mismatches 5; Indels

4 WRVAHRGIRWLL 15 | | | | | | | | 2 WETLRGCRWIL 13 ò

g

Search completed: February 12, 2002, 12:32:25 Job time: 453 sec

	est Control of the Control of the Co
	A
다 보고 있는 것이 되었다. 그는 것이 되었다. 그 경에 가장 하는 것이 되었다. 그 것이 그는 것이 되었다. 그 것이 되었다. 	
는 사람들이 되었다. 그는 사람들이 바다 바다 되었다. 그는 사람들이 되었다. 그런 사람들이 되었다. 그는 사람들이 되었다. 그는 사람들이 되었다. 그는 사람들이 되었다. 그는 사람들이 되었다. 그 	
	•
	•
	•
en de la composition de la composition Magnetica de la composition de la comp	

Page

```
February 12, 2002, 12:34:37 ; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                   219241
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                       US-09-485-571-20
33
1 xGGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                               Searched:
                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	iption	ici		N-acetylmuramoyl-L	hypothetical prote	transcription fact	transcription fact	sterol regulatory	acidic ribosomal p	19K antigen - Myco	chorion protein s3	beta-lactamase (EC	beta-1,3-glucanase	pre-B-cell leukemi	PBX2 protein - mou	phosphatidylinosit	paired box transcr	CAD ATPase (AAA1),	protein kinase sgg	se	hypothetical prote	AAA protein L4171.	major merozoite su	hypothetical prote	gene hindsight pro	44	tenascin-like prot	neuroglian, long c	hypothetical prote	
SUMMARIES	Ω	B33061	A54863	E86692	T33913	C34734	B34734	B54962	R5BYA1	S22630	808607	JN0520	T50563	A56002	T09061	T09084	S78502	B96835	S35327	S35423	T48805	T02831	A45532	T13594	T13893	A54148	S47008	РН0083	2	090690
	DB	7	~	7	7	4	4	~	-	~	~	~	7	~	~	~	~	7	~	~	~	7	7	7	7	~	~	7	7	7
	Query Match Length	•	347	361	605	742	825	1139	110	163	306	311	377	430	430	490	520	523	575	1067	1075	1541	1772	1891	1920	2406	2515	120	205	236
ď	Query Match	48.5	48.5	48.5	•	48.5	48.5	48.5	45.5	•	45.5		•	45.5				45.5							•	•	45.5	42.4	42.4	42.4
	Score	16	16	16			16		15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	14	14	14
	Result No.	-	7	m	4	'n	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	<b>5</b> 6	27	28	29

basigin precursor hypothetical prote	extradenticle prot	female-specific do	probable integral	glutamyl-tRNA amid	spore coat protein	male-specific doub	serine/threonine p	serine/threonine p	period clock prote	spore coat protein	hypothetical prote	basic protein, cyt
S65739 G85362	A48840 D83465	A32372	T36810	E71725	B33485	B32372	T42100	T36502	UMFF	507638	T39141	S47857
77	0 0	7 5	7	7	7	7	7	7	П	7	7	7
270	376 419	427	463	493	537	549	556	556	571	9	647	737
42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4	42.4
14 14	14	14	14	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
30 31	32 33	34	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT

	B33061
	homeotic protein prl - human
	C, Species: Homo sapiens (man)
	C; Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 17-Oct-1997
	100 cm
	N.NOCLISE, O., MELTEULLI, V.D., GALILLI, N., WILKINSON, V., SCANDILUGE, E., SHILLI, S. Submitted to the Protein Sequence Database, January 1990
	A; Reference number: A33061
•	A, Accession: B33061
	A;Status: preliminary; not compared with conceptual translation
	A postation of 1242 Andry
	7. Contaction in the Amount of Contaction in the Contaction in the Amount of Contactio
	A.Gono. CDR.DRY
_	A. Cross-references GDB-125351: OMIM-176310
	A: Map Dosition: 1923-1923
	C; Superfamily: unassiqued homeobox proteins; homeobox homology
_	C; Keywords: acute lymphoblastic leukemia; DNA binding; homeobox; nucleus; transcrip
	F;146-205/Domain: homeobox homology #status atypical <hox></hox>
	48.5%; Score 16;
	cal Similarity 17.6%; Pred. No. 5.6e+03;
	native 0; Mismato
	Qy 2 GGXXXXXXXXXXXX 18
	_
	Db 36 GGSAAAAAAAAAGGAG 52
	KESULT Z
	ACAGON ACADOS ACAGON
	Common Minuscon Incommon Common Commo
	C. Speciaes. Was insectuted findse include. C. Date: 02-1711 - 1996 #septienne regision 02-1711-1996 #text change 24-Sep-1999
	C; Accession: A54863
	R;Kaqawa, N.; Oqo, A.; Takahashi, Y.; Iwamatsu, A.; Waterman, M.R.
	J. Biol. Chem. 269, 18716-18719, 1994
	A; Title: A cAMP-regulatory sequence (CRSI) of CYP17 is a cellular target for the hc
	A; Reference number: A54863; MUID:94308119
	A; Accession: A54863
	A Status: preliminary; translated from GB/EMBL/DDBJ
	A) MULECULE LYDE: IIKNA
	A; Kesidues: 1-34/ <kes></kes>
	A;Cross-references: GB:LZ/453; NID:g455108; PIDN:AAAZ183Z.1; PID:g456109
	A.Cornettos:
	r.vene: Forth Transcrience homocher proteine. homocher homology
	C.Kevwords: DNA binding: homeobox: nucleus: transcription regulation
_	

```
transcription factor 3/homeotic protein prl mutant fusion protein II - human N'Alfernate names: BZA/prl mutant fusion protein II; EZA-Prl mutant fusion protein C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: 13-Jul-1990 #sequence_revision 17-Nov-1995 #text_change 22-May-1997 C.Saccession: C3474, B34733 E34733 Cell 60, 547-555, 1999
                                                                                                                                                                                                                                                                 A;Title: A new homeobox gene contributes the DNA binding domain of the t(1;19) trans:
A;Reference number: A34734; MUID:90150282
A;Accession: C34734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: GB:M31522; NID:g339894
R;Nourse, J.; Mellentin, J.D.; Gallii, N.; Wilkinson, J.; Stanbridge, E.; Smith, S.Di Cell 60, 535-545, 1990
A;Title: Chromosomal translocation t(1:19) results in synthesis of a homeobox fusion A;Reference number: A34733; MUID:90150281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapies: excypti mucual tusion, process to a sapies services man)
C; Date: 13-Jul-1990 #sequence_revision 17-Nov-1995 #text_change 20-Apr-2000
C; Accession: 134734, A34733
R; Kamps, M.P.; Murre, C.; Sun, X.; Baltimore, D.
Cell 60, 547-555, 1990
A; Title: A new homeobox gene contributes the DNA binding domain of the t(1;19) trans A; Reference number: A34734; MUD: 90150282
A; Feference number: A34734; MUD: 90150282
A; Reference number: B34734
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-825 < KAM>A; Residues: 1-825 < KAM>A; Residues: 1-825 < KAM>A; Corss references: GB: M31522; NID: 9339894; PIDN: AAA36764.1; PID: 9339895
R; Nourse, J.; Mellentin, J.D.; Galili, N.; Wilkinson, J.; Stanbridge, E.; Smith, S.D.
A; Title: Chromosomal translocation t(1;19) results in synthesis of a homeobox fusion
A; Reference number: A34733; MUD: 90150281
A; Molecule type: mRNA
A; Residues: 7-579, DEC, 582-825 < NOUS
A; Croment: This sequence is the chimeric product of a translocation mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 7-579, 'DE', 582-742 <NOU>
A):Cross-references: GB:M31222; NID:9181905
C; Comment: This sequence is the chimeric product of a translocation mutation.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcription factor 3/homeotic protein prl mutant fusion protein I - human N.Alternate names: E2A/prl mutant fusion protein I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16; DB 4; Length 742;
Pred. No. 1e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 4; Length 825;
Pred. No. 1.1e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-742 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 GGSAAAAAAAASGGAG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: TCF3/PBX1
C; Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: TCF3/PBX1
C,Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B34733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Оp
                                                                                                                                                                                                                                                                                                     **RESULT 3
**B6692
N-acctylautramoyl-L-alanine amidase (EC 3.5.1.28) [imported] - Lactococcus lactis subsp.
N.Alternate names: N-acetylmuramidase
C; Species: Lactococcus lactis subsp. lactis
C; Species: Lactococcus lactis
C; Marchard S; Noll
N; Malarme, K; Weissenbach, J; Ehrli
N; Reference number: A86625
A; Residues: 1-361 <STO>
A; Residues: 1-361 <STO
A; Reperimental source: strain IL1403
C; Genetics:
A; Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF125459; PIDN:AAD12833.1; GSPDB:GN00020; CESP:Y25C1A.3
A;Experimental source: strain Bristol N2; clone Y25C1A
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y25C1A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caecasion: T33913
R;Kalicki, J.; Smith, A.; Gibson, A.
Submitted to the EMBL Data Library, February 1999
A;Beference number: Z21437
A;Reference number: Z21437
A;Reference number: Z21437
A;Reference to the Lanslated from GB/EMBL/DDBJ
A;Relevence DA
A;Reference number: Lanslated from GB/EMBL/DDBJ
A;Relevence Lobal
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
       Score 16; DB 2; Length 347;
Pred. No. 5.7e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 361;
                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 2; Length 605
Pred. No. 8.8e+03;
); Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 2; Pred. No. 5.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
       48.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                           124 GGSAAAAAAAASGGAG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 GGTAVTTSSSASTNSAG 193
                                                                                                                                         2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 GGSTATTAAGGSTASTG 362
                                                                            3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: CESP:Y25ClA.3
A;Map position: 2
A;Introns: 392/3; 429/1; 567/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                         δλ
                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```

ö

ŏ

```
A; Experimental source: strain S288C (AB972)
R; Dietrich, F.S.
submitted to the EML Data Library, July 1995
A; Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and la
                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: U32274; NID: 9927313; PIDN: AAB64824.1; PID: 9927315; GSPDB: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: $22630
R; Nair, J.; Rouse, D.A.; Morris, S.L.
Mol. Microbiol. 6, 1431-1439, 1992
A; Title: Nucleotide sequence analysis and serologic characterization of the Mycobac A; Reference number: $22630; MUID: 92326626
A; Accession: $22630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chorion protein s38 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 0.2-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C;Accession: S08607,
E;Spradling, A.C.; de Cicco, D.V.; Wakimoto, B.T.; Levine, J.F.; Kalfayan, L.J.; Cc EMBO J. 6, 1045-1053, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Amplification of the X-linked Drosophila chorion gene cluster requires a 1 A;Reference number: S07193; MUID:87246506 A;Accession: S08607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A;Residues: 1-165 -<br/>KonI>-
A;Cross-references: EMBL:X65483; NID:944361; PIDN:CAA46469.1; PID:9581330<br/>A;Note: the authors translated the initiation codon GTG for residue 1 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 4R
C;Superfamily: rat acidic ribosomal protein Pl
C;Reywords: phosphoprotein; protein biosynthesis; ribosome
F;1-110/Product: acidic ribosomal protein P2.e.B #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate namas: gene MI22 protein
C;Species: Mycobacterium intracellulare
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-316 <SPR.
A;Cross.references: EMBL:X05245; NID:97725; PIDN:CAA28871.1; PID:97727
A;Note: the authors translated the codon TAC for residue 112 as Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 1; 1
Pred. No. 3.9e+03;
0; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15; DB 2; 1
Pred. No. 5.3e+03;
0; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: SGD:S0002790; MIPS:YDR382w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19K antigen - Mycobacterium intracellulare
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SGD: RPL45; RPLA4; MIPS: YDR382w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 GGASSAAAGAAGAAGG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 GGNKSGTSASSSASSSG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                  A; Accession: S69666
A; Molecule type: DNA
A; Residues: 1-110 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: MI22
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acidic ribosomal protein P2.e.B, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: acidic ribosomal protein P2.alpha; protein D9481.1; protein YDR382w;
C:Species: Saccharomyces cerevisiae
C:Dete: 31-064-1080 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C:Accession: A35109; A28104; A02776; S61177; S69666
R:Newton, C.H.: Shimmin, L.C.: Yee, J.; Dennis, P.P.
J:Bacteriol. 172, 579-588, 1990
A:Title: A family of genes encode the multiple forms of the Saccharomyces cerevisiae rib protein.
A:Reference number: A35109; MUID:90130289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Notecule type: DNA
A; Residues: 1-110 < REWY
A; Note: the authors translated the codon GAA for residue 28 as Ala
A; Note: the authors translated the codon GAA for residue 28 as Ala
B; Itoh, T.
Babothia. Blophys. Acta 671, 16-24, 1981
A; Title: Primary structure of an acidic ribosomal protein YPA1 from Saccharomyces cerevi.
A; Reference number: A02776; MUID: 82069169
A; Reference number: Protein
A; Residues: 1-74, GPAS', 79-85, 'G', 86-90, 92-110 < ITO>
B; Ding, H.
Submitted to the EMBL Data Library, June 1995
A; Description: The sequence of S. cerevislae cosmid 9481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: S61177
A,Molecule type: DNA
A,Residues: 1-110 <DIN>
A,Cross-references: EMBL:U28373; NID:g849184; PIDN:AAB64818.1; PID:g849203; GSPDB:GN0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-110 <NEW>
A; Residues: 1-110 <NEW>
A; Residues: 1-110 <NEW>
A; Cross-references: GB:MZ6505; NID:9171810; PIDN:AAA34732.1; PID:9171811
B; Remacha, M.; Saenz-Robles, M.T.; Vilella, M.D.; Ballesta, J.P.G.
J. Biol. Chem. 263, 9094-9101, 1988
A; Title: Independent genes coding for three acidic proteins of the large ribosomal subuna; Reference number: A92726; MUID:88243786
                                                                                                                                                                                                                                                                                                                                                                   C. Accession: B54962
R:Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
Genes Dev. 8, 1910-1919, 1994
A:Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A:Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A:Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A:Tatle: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A:Tatle: Sterol-resistant transcription in CHO cells caused by gene rearrangement that A:Accession: B54962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                     sterol regulatory element binding protein 2 precursor - Chinese hamster C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 04-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 2; Length 1139;
Pred. No. 1.4e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                           519 GGSAAAAAAAAASGGAG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 GGSSGSSSSSNSSSSSG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A35109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A28104
                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                   JN0520

JN0520

JN0520

JN0520

C;Species: Streptomyces cellulosae

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Jun-2000

C;Accession: JN0520

G;Sqavara, H.

Gene 124, 111-114, 1993

A;Title: Sequence of a gene encoding beta-lactamase form Streptomyces cellulosae.

A;Reference number: JN0520; MUID:93178958

A;Reference number: JN0520

A;Reference number: JN0520

A;Reference number: JN0520

A;Reference number: JN0520
                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
T50563
Cstart 12
Secies: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C;Accession: T50563
R;Romero, G.O.; Doan, M.; Rodriguez, R.L.
Submitted to the EMBL Data Library, September 1996
A;Description: Rice beta-1,3-glucanase, Gns9.
A;Accession: T50563
A;Accession: T50563
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:D12653; NID:g287453; PIDN:BAA02176.1; PID:g287454 C;Superfamily: beta-lactamase I C:Keywords: hydrolase F;86,184/Active site: Ser, Glu #status predicted
                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·,
                                                                                                                              Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 2; Length 377;
Pred. No. 1e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 311;
                                                                                                                                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                          ; DB 2; L
. 8.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB 2; Pred. No. 8.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U72255; PIDN:AAD10386.1
A;Experlmental source: strain M202
                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                          Score 15;
Pred. No.
C;Genetics:
A;Gene: Flybase:Cp38
A;Cross-references: Flybase:Fbgn0000360
A;Introns: 15/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: Gns9
A;Introns: 25/1
C;Superfamily: beta-1,3-glucanase
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%;
                                                                                                                          h 45.5%;
Similarity 17.6%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 GGNSLAAAAAARTTAG 369
                                                                                                                                                                                                       2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                            39 GGADAASAAAAAGGAG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GGALALGSTTASAASAG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-377 <ROM>
                                                                                                                                                                 Matches
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

```
A, Molecule type: DNA
A, Residues: 1-430 <AGU>
A, Molecule type: DNA
A, Residues: 1-430 <AGU>
A, Caross references: GB: 80700; NID:9625185; PIDN:CAA56717.1; PID:9634053
R; Monica, K.; Galili, N.; Nourse, J.; Saltman, D.; Cleary, M.L.
Mol. Cell. Biol. 11, 6149-6157, 1991
A; Title: PBX2 and PBX3, new homeobox genes with extensive homology to the human prot A; Reference number: S19009; MUID:92049345
A; Molecule type: mRNA
A; Residues: 1-392, IT, 394-430 <AMO>
A; Molecule type: mRNA
A; Residues: 1-392, IT, 394-430 <AMO>
A; Cross-references: EMBL: X5942; NID:935312; PIDN:CAA42503.1; PID:935313
R; Sugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, Genomics 23, 408-419, 1994
A; Title: Three genes in the human MHC class III region near the junction with the classiant of mouse mammary tumor gene int. 3.
A; Reference number: A55562; MID:99137587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T09061
R; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C. submitted to the EMBL Data Library, October 1997
A; Description: Sequence of the mouse major histocompatibility locus class III region A; Reference number: 216543
A; Accession: T09061
A; Accession: T09061
A; Accession: T09061
A; Accession: T09061
A; Molecule type: DNA
A; Residues: 1-430 < ROW>
A; Cross references: EMBL; AF030001; NID:92564945; PID:92564949
C; Genetics:
A; Aces PRZ
A; Map position: 17
A; Introns: 74/2; 99/1; 181/3; 245/2; 290/3; 342/1; 371/3; 400/3
                                                                         C;Species: Homo sapiens (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 24-Sep-1999
C;Accession: A56002; S19009; A55562
R;Aquado, B.; Campbell, R.D.
Genomics 25, 650-659, 1995
A;Title: The novel gene GI7, located in the human major histocompatibility complex, A;Reference number: A56002; MUID:95278934
A;Reference number: A56002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PBX2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:D28769; NID:9561657; PIDN:BAA05957.1; PID:9561658 C;Genetics: GB:PB2.2 G17
A;Cene: GDB:PB2.2 G17
A;Cross-references: GDB:306356; OMIM:176311
A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-6p21.3
C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;245-304/Domain: homeobox homology <a href="https://document.com/monology/">https://document.com/monology/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 2; 1
Pred. No. 1.1e+04;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
pre-B-cell leukemia transcription factor 2 - human
N;Alternate names: homeotic protein PBX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.5%;
Best Local Similarity 17.6%;
Matches 3; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 GGGSAAAAAAAASGGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-430 <RES>
```

```
RESULT 15
T09084
phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
C; Species: Chlamydomonas reinhardtii
C; Species: Chlamydomonas reinhardtii
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: T09084
R; Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998
A; Title: Inositide signalling in Chlamydomonas: Characterization of a phosphatidylinosit
A; Reference number: 216411; MUID:98281574
A; Accession: T09084
A; Status: preliminary: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule speciments: 1-490 AMOL>
A; Cross-references: EMBL:097663; NID:92109290; PIDN:AAC50018.1; PID:92109291
A; Experimental source: strain cw-15
C; Genetics:
C; Genetics:
A; Introns: 265/3; 331/3; 330/3; 455/1; 481/3
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;245-304/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.5%; Score 15; DB 2; Length 490; Best Local Similarity 17.6%; Pred. No. 1.3e+04; Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                          Query Match 45.5%; Score 15; DB 2; Length 430; Best Local Similarity 17.6%; Pred. No. 1.1e+04; Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                           133 GGGSAAAAAAAASGGG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 GGGAAAAAAAAAGAGG 438
                                                                                                                                                                                                                                                                                 2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

Search completed: February 12, 2002, 12:34:38 Job time: 556 sec

• 

Ì

```
Appl
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Appli
Appli
Appli
Appli
                                                                                                                                                            (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                      ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-240-712-29
US-08-443-890-29
US-08-2840-712-33
US-08-2840-712-33
US-08-443-890-33
US-09-105-349A-6
US-09-105-390-64
US-09-105-390-64
US-08-185-432-8
US-08-185-432-8
US-08-209-521-11
US-08-209-521-11
US-08-209-521-11
US-09-247-806-6
US-09-247-806-6
US-09-247-806-6
US-09-155-543-2
US-09-155-543-2
US-09-155-643-2
US-09-156-643-2
US-09-156-643-4
US-08-185-432-4
US-08-185-432-4
US-08-185-432-4
US-08-185-432-4
US-08-185-432-4
US-08-185-432-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                      February 12, 2002, 12:32:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                               US-09-485-571-20
33
1 XGGXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sed
                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                        OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠
ي
```

Sequence Seq

-08-556-978B-26 -08-556-978B-69 -08-556-978B-89

-08-317-844B-42 -08-317-844B-54

```
Sequence 20, Appl
Sequence 22, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= one or both of Gly residues 131 and 132 can be absent; one or both of Gly residues 147 and 148 can be absent
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEMS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIETCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
ANDER COMPREY APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                      US-09-247 806-3
US-09-247 806-3
US-09-247 806-7
US-08-301-162-10
US-09-135-994-12
US-08-209-747-8
US-08-218-686-2
US-08-218-686-2
US-08-460-242-2
S252556-1
US-08-556-978B-20
US-08-556-978B-22
US-08-556-978B-62
                                                                                                                                                                                  US-08-985-090-2
US-09-165-543-2
US-09-167-354-7
US-08-672-571A-1
                                                                                                                                                                                                                                            US-08-556-978B-63
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/08240712; Patent No. 5599907; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
COTHER INFORMATION:
US-08-240-712-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          US-08-240-712-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
```

```
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                           GENERAL INFORMATION:
APPLICANT: Kunio
                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-08-240-712-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues 131 and 132 can be absent; one or both of Gly residues 147 and 148 can be absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                      DB 1; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Indels
                                                                                                                                                                                                                                                   APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
                                      1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 1;
Pred: No. 1.4e+03;
); Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                   Score 17; DB 1
Pred. No. 1.4e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ANDERSON=6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                      Sequence 29, Application US/08443890 Patent No. 5739011 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28,005
                   51.5%;
17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.5%;
17.6%;
                                                                                                                 130 GGGAAAAAAAAAAAA 146
Ouery Match
Best Local Similarity 17.07
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 amino acids
                                                                                  2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 GGGAAAAAAAAAAAA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COOPER, IVER PREGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20004
                                                                                                                                                                      RESULT 2
US-08-443-890-29
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                 Db
                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
APPLICANT: Kunio NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBO,

TITLE OF INVENTION: 10 SAID POLYPEPTIDE

ONDMER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17; DB 3; Length 738;
Pred. No. 3.5e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/08240712
Patent No. 559907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STELER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAME/KEY: peptide
LOCATION: from 1 to 738
DENTIFICATION METHOD: E (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U5/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UF 8-184459
FILING DATE: 15-July 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE: mantle epithelial cell
Sequence 3, Application US/08864038A Patent No. 6001592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pinctada fucata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.5%;
17.6%;
                                                                                                                                                                                                                                                                                           812-5 Hirano
                                                                                                                                                                                                                                                                                                              STREET: Isshinden
CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 GGSAAAAAAAAAAGG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
```

ŀ

```
US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= one or both of Gly residues 2 and 3 can be absent; one or both of Gly residues 17 and 18 can be absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB 1; Length 18;
Pred. No. 4.9e+02;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Application US/08443890
Patent No. 5739011
GENERAL INFORMATION:
APPLICANT: MATHEMS, ANTONY JAMES
APPLICANT: MATHEMS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: 28,005
REGISTRATION NUMBER: ANDERSON-6
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.58;
17.68;
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGAAAAAAAAAGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-08-240-712-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                   CITY: Washir
STATE: D.C.
COUNTRY: US
                                                                                                                                             20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-443-890-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
Sequence 6, Application US/07906349A

Sequence 6, S44064

GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
APPLICANT: Schlessinger, Joseph
APPLICANT: Margolis, Benjamin L.
APPLICANT: Margolis, Benjamin L.
TITLE CF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINAS;
TITLE CF INVENTION: TARGET PROTEINS
NUMBER OF SEQUENCES: 16
CORRESCONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- one or both of Gly residues 2 and 3 can be absent; one or both of Gly residues 17 and 18 can be absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NOTA:
FILING DATE: 30-JUN-1992
    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1;
Pred. No. 4.9e+02;
0; Mismatches 14
                                                                       CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTONNEY, AGGNT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE, FOOR TOWNER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELECHHONE: 202-628-5197
        ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/643,237
FILING DATE: 18-JAN-1991
TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGXXXXXXXXXXXX 18
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGAAAAAAAAAAGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLÒGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
COTHER INFORMATION:
US-08-443-890-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino e
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C. COUNTRY: USA
                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20004
```

οp

202-628-5197

TELEPHONE:

```
APPLICANT: Busseau, Isabelle
APPLICANT: Diederlich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
APPLICANT: Matsuno, Kenji
APPLICANT: MATSUNO, ROBEREX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                  APPLICANT: ROdriquez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 4; I
Pred. No. 6.5e+03;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELLACOMPUTER: IBM COMPALLACOMPUTER: IBM COMPACE.

OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
TING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
APPLICANT: Artavanis_Tsakonas, Spyridon
                                                                                             US-09-105-390-64
Sequence 64, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           COUNTK1:
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
THEN COMPALIBLE
THEN COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.68;
                 325 GGNSLAAAAAAARTTAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 377 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 GGNSLAAAAAARTTAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.5
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-09-105-390-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-185-432-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                          48.5%; Score 16; DB 1; Length 801; ilarity 17.6%; Pred. No. 6.3e+03; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
45.5%; Score 15; DB 4; Length 349
Best Local Similarity 17.6%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FOLK.

MEDIUM TYPE: DISKELLE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKELLE
COMPUTER: TOWN
SOFTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455,30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            #ESO105-390-48
; Sequence 48, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 801 amino acids TYPE: amino acid STRANDENNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-07-906-349A-6
                                                                                                                                                                                                                                                                                                                                                                  457 GGTTGGATTTAAAAATG 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-105-390-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 350 Camb
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                            ð
```

ö

Gaps

ö

2 GGXXXXXXXXXXXX 18

οy

Length 377; 14; Indels Gaps

ö

```
Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Liskay, Robert M.
APPLICANT: Bronner, C. Eric
APPLICANT: Baker, Sean M.
APPLICANT: Baker, Sean M.
APPLICANT: BALlag, Roni J.
APPLICANT: Kolodner, Richard D.
TITLE CF INVENTION: MAMMALIAN DNA MISMATCH REPAIR GENES
TITLE CF INVENTION: MALHI AND hPMS1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: ADDRESSE: KOLISCH, HATTWell, Dickinson, McCormack 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 97204
COMPUTER READABLE FORM:
MEDITH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1;
Pred. No. 9.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Heuser
STREET: 520 S.W. Yamhill, Suite 200
CITY: Portland
STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: 0HSU 306A
TELECONMUNICATION INFORMATION: 1
TELEFENCE (503) 224-6655
ITELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OHSU 306A
                                        7326-006
                              REFERENCE/DOCKET NUMBER: 7326-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11, Application US/08209521
; Patent No. 5922855
; GENERAL INFORMATION:
          18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.4%;
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; POSITION IN GENOME:
; MAP POSITION: 3p21.3-23
US-08-209-521-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGSAASSCATMALSTAG 34
          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-185-432-5
                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-209-521-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNT'RY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Attavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
ADDRESSEE: PENNIE & EDMONDS
CORRESPONDENCE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14; DB 1; Length 204;
Pred. No. 7.5e+03;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                        CURRENTINS SISIEM: F. LUCKING BOTTON OF THE CONTROL OF THE CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible OPERATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-185-432-5
; Sequence 5, Application US/08185432
; Patent No. 5750652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.4%;
Best Local Similarity 17.6%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 GGSAASSCATMALSTAG 34
                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21 CLASSIFICATION:
                                                                                                    New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datem: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14; DB 3;
Pred. No. 1.1e+04;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MII-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09165543
Patent No. 6093545
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.48;
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 362 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 GGAAASPTSSSGSSSRG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.4
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-165-543-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIRES.
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Andrew
                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-165-543-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                   Sequence 5, Application US/08985090
Patent No. 5885893
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09165543
Patent No. 6093545
GENERAL INFORMATION:
APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
NUMBER OF SEQUENCES: 39
Score 14; DB 2; Length 341;
Pred. No. 1e+04;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 2; Length 362;
Pred. No. 1.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)727-7400
TELEFAX: (617)727-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
    42.48;
17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.48;
17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 362 amino acids
amino acid
                                                                               2 GGXXXXXXXXXXXX 18
Query Match
Best Local Similarity 17.6
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GGAAASPTSSSGSSSRG 230
                                                                                                                   17 GGAAAATGAGTAACATG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-985-090-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-165-543-32
                                                                                                                                                                                 RESULT 12
US-08-985-090-5
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

ó;

Length 362;

į

```
GENERAL INFORMATION: 0.2014

APPLICANT: PHILLIPPE, Michel

APPLICANT: GRASON, Jean-Claude

APPLICANT: GRASON, Jean-Claude

APPLICANT: GRASON, Jean-Pierre

TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT

TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN

TITLE OF INVENTION: ANALOG

FILE REFERENCE: 6388-0365-0

CURRENT APPLICATION NUMBER: US/09/247,806

CURRENT APPLICATION NUMBER: FR 98/01614

EARLIER FILING DATE: 1999-02-11

MUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

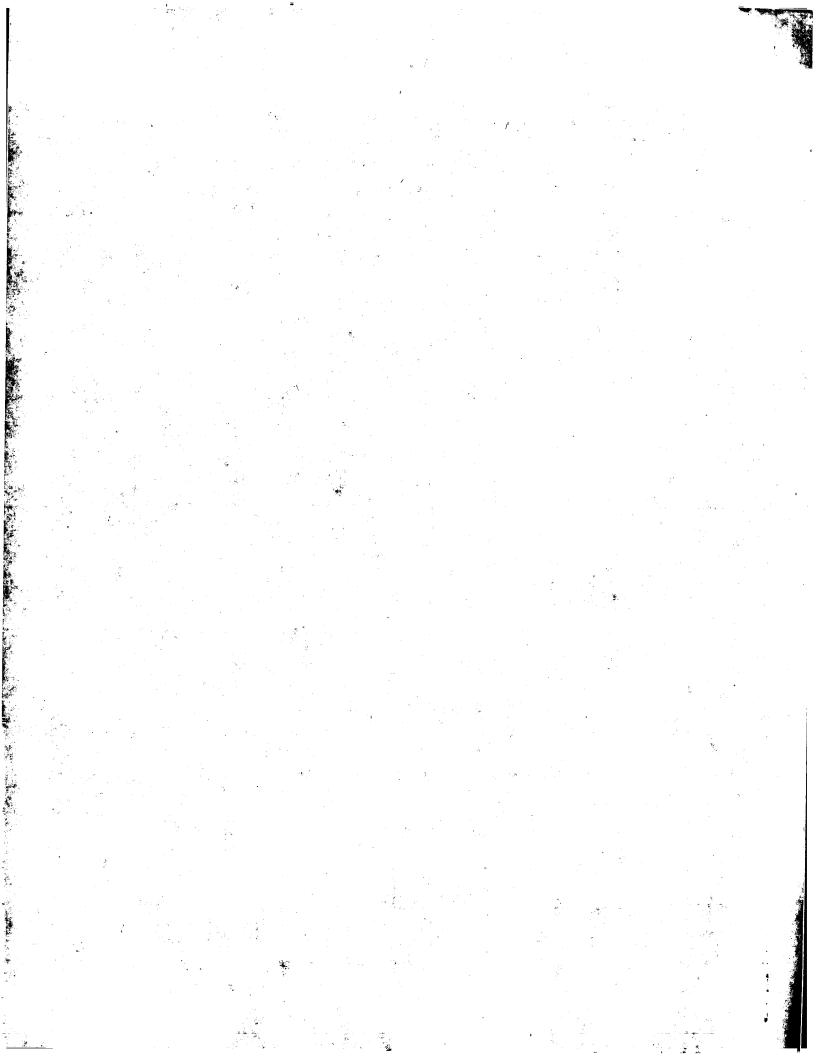
SEQ ID NO 6

LENGTH: 606

TYPE: PRT

ORGANISM: Nephila clavipes

US-09-247-806-6
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                        Query Match
42.4%; Score 14; DB 3; Length 445;
Best Local Similarity 17.5%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 42.4%; Score 14; DB 4; Length 606; Best Local Similarity 17.6%; Pred. No. 1.5e+04; Matches 3; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 12, 2002, 12:32:23 Job time: 451 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/09247806
; Patent No. 6280747
: INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-09-165-443-5
                                                                                                                                                                                                                                                                                                                                                                       297 GGAAASPTSSSGSSSRG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 GGGGAAAAAAAAGGAG 342
                                                                                                                                                                                                                                                                                                                         2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGXXXXXXXXXXXX 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-247-806-6
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
```



Database : A_Geneseq_1101:*

1: \SIDSB\gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: \SIDSB\gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: \SIDSB\gcgdata/geneseq/geneseqp/AA1981.DAT:*
4: \SIDSB\gcgdata/geneseq/geneseqp/AA1981.DAT:*
5: \SIDSB\gcgdata/geneseq/geneseqp/AA1981.DAT:*
6: \SIDSB\gcgdata/geneseq/geneseqp/AA1981.DAT:*
7: \SIDSB\gcgdata/geneseq/geneseqp/AA1985.DAT:*
8: \SIDSB\gcgdata/geneseqp/AA1986.DAT:*
9: \SIDSB\gcgdata/geneseqp/AA1981.DAT:*
10: \SIDSB\gcgdata/geneseqp/AA1981.DAT:*
11: \SIDSB\gcgdata/geneseqp/AA1991.DAT:*
12: \SIDSB\gcgdata/geneseqp/geneseqp/AA1991.DAT:*
13: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
14: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
15: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
16: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
17: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
18: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
22: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
22: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
22: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*
22: \SIDSB\gcgdata/geneseq/geneseqp/AA1991.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Opioid peptide SEO	Opioid peptide SEO	Opioid peptide SEO	Opioid peptide SEO	Opioid peptide SEQ	Polypeptide SEQ ID	Miscellaneous pept	Sequence of collag	Sequence encoded b	Synthetic peptide	Antiviral agent.
SUMMARIES	AAB91687	AAB91688	AAB91721	AAB91731	AAB91740	AAB92149	AAB92356	AAP30453	AAP81081	AAP91660	AAR04607
93	22	22	22	22	22	22	22	4	6	10	11
% Query Match Length DB ID		7	7	7	7	7	7	m	3	3	e
% Query Match	7.3	17.3	17.3	17.3	27.3	27.3	27.3	7.3	7.3	27.3	7.3
		(3)									
Score	9	9	9	9	9	9	9	9	9	9	9
Result No.	1	7	3	4	S	9	7	æ	σ	10	11

Modifying and attaching therapeutic peptides to albumin prevents

Thibaudeau K;

Holmes DL,

Milner PG,

Ezrin AM,

Bridon DP,

WPI; 2001-112059/12.

	12		7	٣	11	71		Core repeat of cel
	13		7.	3	13	-		Biocompatible poly
	14		7.	3	14	AAR36707		Adhesion formation
	15		۲.	e	14	AAR53144		RGD peptide deriva
	16		ζ.	e	15	AAR65950		Tripeptide inhibit
	17		۲.	m	12	AAR44666		Platelet aggregati
	18		٠.	.n.	7, 1	AAR53239		Heparin derivative
	20	o (c	27.3	n m		AAR53243		ACE inhibiting nen
	21			m	12	AAR51441		IGF-1 analoque N-t
	22		7	m	15	AAR61092		ACE-inhibiting tri
	23		۲.	m	15	AAR61095		ACE-inhibiting tri
	24		7.	ო	16	AAR70472		Cancer metastasis
	25		۲.	m	16	AAR71717		Potential cross-11
	26		· .	m	16	AAR64689		HPF3 peptide deriv
	27		٠,	m r	9 :	AAR62425		Accelerator peptid
	200		٠,	י ר	1 [	AAMIIU94		Platelet targettin
	3.0		٠,	יו רי	17	AAR90100		reputate iragment o
	31				, c	AAW31143		Platelet-targeting
	32		:	'n	18	AAW25173		RGD-peptide capabl
	33		~	m	18	AAW28457		PECAM-1 cyclic inh
	34		۲.	m	18	AAW28437		PECAM-1 inhibitor
	35		7	m	19	AAW48589		Integrin receptor
	36		7.	m ·	13	AAW56241		Anti-inflammatory
	37		٠.	m r	200	AAW56226		Anti-inflammatory
	200		٠,	<b>"</b>	٦ <u>-</u>	AAW5618/		Anti-inflammatory
	60		٠,	n r	J -	AAMSOLSO		Loop reaton need 4
	40		٠,	n ~	7 6	AAW52447		Loop region used i
	4.2			י ני	20	AAY43493		er for dual
	43			nm	20	AAY43494		for dual
	44			m	20	AAY39827		n peptide
	45			m	22	AAB92359		scellaneous pe
						ALIGNMENT	NTS	
AAB	RESULT 1 AAB91687							
QI.	AAB91687		standard;	Peptide	de;	2 AA.		
X X	AAB91687							
×								
TQ;	22-JUN-	-3001	(first	t entry)	, X,			
DE	Opioid	peptide	de SEQ	ΩI	NO:863	_;		
×								•
X X X X	Protection; blood compo hydroxyl; t	ion; ompon l; th	ction; endogenous therape component; modification kyl; thiol; hormone; gro	enous th modifica hormone;	hera atic ; gr	therapeutic peptide; cation; succinimidyl e; growth factor; ne	peptidase; ; maleimido urotransmit	conjugation; group; amino; ter.
SO	Homo sapi	sapiens etic.						
×								
PN X	WO200069900-A2	-0066	A2.					
2	23-NOV-2000	2000.						
PF	17-MAY-	- 2000;		2000WO-US135	576.			
X X	7 - MAY		066	-013	40		•	
PR R	10-SEP- 15-OCT-	-1999; -1999;	.sn66	s-0153 s-0159	406. 783.			
PA	(CONJ-)		CONJUCHEM	INC.				

```
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-60 amino acids. (I) are useful for modifying therapeutic peptides as an one usitable as drug candidates. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half infe) and specificity as bonding to large molecules decreases. ABB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidy1; maleimido group; amino; hydroxy1; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                      27.3%; Score 6; DB 22; Length 2;
100.0%; Pred. No. 0;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
                                             Disclosure; Page 477; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB91688 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Opioid peptide SEQ ID NO:864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                         2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 G 10
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB91688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AAB91688
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

Disclosure; Page 477; 733pp; English.

```
The present inventors a mountain described and appeared region (III) and a reactive group (II) (e.g. succininally) and maleimido groups) attached to a less therapeutically active amino acid region (III) and a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3.50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth in vivo for the treatment of various disorders. Endogenous therapeutic factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic administration due to rapid degradation by peptidases in the body. Complifies are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Complifies the action of peptidases to increase length of activity (half confirm of peptidases to increase length of activity (half intercellular uptake and interference with physiological processes. Ash890829 to Ash89241 represent peptides which can be used in the constant invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                  invention describes a modified therapeutic peptide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milner PG, Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                 27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 487; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91721 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Opioid peptide SEQ ID NO:897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 G 10
                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB91721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB91721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth
a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                      Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibaudeau K;
                                                                                                                                                                                                                                                                                                                           DB 22; Length 2;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holmes DL,
                                                                                                                                                                                                                                                                                                                     27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 490; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB91731 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Opioid peptide SEQ ID NO:907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2000; 2000WO-US13576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bridon DP, Ezrin AM,
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                     2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                             10 G 10
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            9 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB91731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB91731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidiase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thibaudeau K;
                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                            Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holmes DL,
                                                                                                                                                                                                                                                       27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
.ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 492; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB91740 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Opioid peptide SEQ ID NO:916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112059/12.
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                     2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB91740;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                                                                                                                                                                                                                                    Б
                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB91740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                  QQ
```

```
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/Nydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or caduces the action of peptidases to increase length of activity (half clife) and specificity as bonding to large molecules decreases.
                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thibaudeau K;
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                             DB 22; Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Holmes DL,
                                                                                                                                                                         27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 630; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                                                                                        AAB92149 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide SEQ ID NO:1325.
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-112059/12.
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                          2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2000
                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                           2 9 2
                                                                                                                                                                                                                                                                                                                                                                                          AAB92149;
                                                                                                                                                                                                                                                                                                                              ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ношо
                                                                                                                                                                                                                                                                                                                            RESULT
AAB92149
 555555X8
                                                                                                                                                                                                                                                                         pp
                                                                                                                                                                                                                                                                                                                                                            δ
```

```
The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalantly bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides of 3-50 amino acids. (I) are useful for modifying therapeutic peptides set of, hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules adecreases in the action of the present invention.

CABBO0829 to AAB92441 represent invention.
                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thibaudeau K;
                                                                                                                                      Indels
                                                                                                           Length 2;
                                                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
                                                                                                    27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Miscellaneous peptide SEQ ID NO:1532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 706; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milner PG,
                                                                                                                                                                                                                                                                                         AAB92356 standard; Peptide; 2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2000; 2000WO-US13576.
                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001 (first entry)
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CONJ-) CONJUCHEM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-112059/12.
                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserv
                                                   2 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                       10 G 10
                                                                                                                                                                                                       2 g 2
                                                                                                                                                                                                                                                                                                                          AAB92356;
                                                     Sequence
                                                                                                                                                                                                                                                                          AAB92356
                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                        SSXS
                                                                                                                                                                       ŏ
                                                                                                                                                                                                       g
```

2 AA;

Sequence

S

us-09-485-571-31.rag

```
Sequence encoded by the human low density lipoprotein (LDL) receptor
                                                                  Sterol regulatory element; sterol mediated repression
                       13-JAN-1991 (first entry)
                                                                                                                                                                                                        WPI; 1988-292863/41.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 1
                                                                                                                                                                                                                  P-PSDB; AAN80195.
                                                                                                                                                                                                                                                                                                                                                                                           3 AA;
                                                                                   Homo sapiens
                                                                                                                                                      30-MAR-3.987;
                                                                                                                                     30-MAR-1.988;
                                                                                                   WO8807579-A.
                                                                                                                    06-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 G 10
                                                 promoter.
        AAP81081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP91660;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP91660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                              Rheumatoid arthritis therapy; stomach disease; periodontal membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptides of the invention are collagenase inhibitors useful in the treatment of disease states involving excessive collagen destruction, e.g. rheumatoid arthritis and diseases of the stomach, eye, middle ear, periodontal membranes and skin. AAP30453 gives 86% inhibition of collagenase, c.f. 39% for D-penicillamine in the procedure of Sellers et al., Biochem. J., 167, 353-360, 1977.
                                                                                                                                                                                                              /label= R-G
/note= "R=H,2-6C alkanoyl,6-8C cycloalkylcarbonyl,
2-6C alkoxycarbonyl; pref.
cyclopentylcarbonyl"
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptide(s) useful as collagenase inhibitors - e.g. in treatment of rheumatoid arthritis, etc.
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
               Length 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3;
                                ;
0
               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
o. 0;
              27.3%; Score 6; DB 2
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 6; DB 4
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                   4
/label= D,L-V-(3SH)-NH2
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                             Sequence of collagenase inhibitor.
                                                                                                         AAP30453 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP81081 standard; protein; 3 AA.
                                                                                                                                                                                                                                                                                                                                               (AMHP ) AMERICAN HOME PROD CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; column 4; 3pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1983-17252K/07 (17252K).
                                                                                                                                                                                                                                                                                                             81US-0309367
                                                                                                                                                                                                                                                                                                                              81US-0309367
                                                                                                                                             (first entry)
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                               Key
Modified-site
                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                             07-OCT-1981;
                                                                                                                                                                                                                                                                                                                              07-OCT-1981;
                                                                                                                                            14-JUN-1992
                                                                                                                                                                                                                                                                           US4371465-A.
                                                                                                                                                                                                                                                                                                                                                                Mcgregor WH;
                                                                                                                                                                                                                                                                                            01-FEB-1983
                                               10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 G 10
                                                               2 9 2
                                                                                                                           AAP30453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 g
                                                                                          æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP81081
ID AAP8
                                                                                                  AAP30453
                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                ô
                                                                a
                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A novel purified segment of DNA which comprises a functionally translocatable sterol regulatory element (SRE) confers sterol mediated suppression of structural gene transcription to a selected heterolgous structural gene when located upstream from and proximal to a transcription initiation site of such a gene, providing the segment is free of the structural gene ordinarily under the transcriptional control of the SRE is claimed. Also claimed, a purified segment of DNA comprising a functional translocatable positive LDL receptor gene promoter control element. The example reflects experiments conducted to display generally the positive capability of the 5'-regions of human LDL receptor. First base in AAN80195 is designated -240 in Fig 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic peptide corresp. to residues 12-14 of naturally occurring epidermal growth factor (EGF).
                                                                                                                                                                                                                                                                                                                                             Sterol megulatory elements and positive promoters - used to control expression of heterologous structural genes and screening plasma cholesterol lowering drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epidermal growth factor; angiogenesis; synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3;
                                                                                                                                                                                        Sudhof TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; DB 9; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB .
                                                                                                                                                                                        Russell DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP91660 standard; protein; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example: Fig 1; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label-OTHER
88WO-US01095
                                                             87US-0033302
                                                                                                                          (TEXA ) UNIV OF TEXAS SYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1990 (first entry)
                                                                                                                                                                                        Brown MS, Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
```

```
Peptide core is repeated 2-20 times to form a cell-adhesive protein of mol. wt. 1,500-5,000. The protein is an (ant)agonist of cell-adhesive proteins such as fibronectin. It has high antimetastatic activity against cancer and can be used in immunomodulation, wound healing, platelet aggregation inhibition and alleviatigon of neuro-disorders. See also AAR00722.
         acidic aminoacid, effective against virus with protein-terminated DNA or RNA.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion; anti-metastatic agent; immunomodulation; core repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                      Peptide is effective against inhibiting propogation of DNA or RNA bonded, protein containing viruses eg. Poliovirus, Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptide with repeated sequences of cell adhesion protein used as anti-metastatic agent for cancer and agonist or antagonist of cell-adhesion proteins
                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                             Indels
                                                                                                                                                    DB 11; Length 3; 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3;
                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11;
                                                                                                                                                 27.3%; Score 6; DB 1
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tokura S;
                                                                                                                                                                                                                                                                                                                                                                  Core repeat of cell-adhesive protein.
                                                                                                                                                                                                                                                                                      AAR00718 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; page 14; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azuma I,
                                                ; 4pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89EP-0111468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88JP-0156133
                                                                                                                                                                                                                                                                                                                                          29-MAY-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                             Ouery Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-001305/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saiki I, Nishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                             3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AZUM/) AZUMA
                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                     EP347931-A.
                                                                                                                                                                                                 10 G 10
                                                                                                                                                                                                                        2 9 2
                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                  AAR00718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  б
                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
AAR23219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                            AAR00718
          ŏ
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                               The inventors claim synthetic peptides which correspond to sequences occurring in EGF, but excluding EGF. The peptides are angiogenic and have corresp. applications, eg for the healing of wounds and burns. Their relative shortness means that they pose fewer synthesis problems than the entire EGF molecule. They can be admin. singly or association with each other or in association with an angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                       Synthetic peptide active in stimulating angiogenesis - has sequences corresponding to amino acid sequences occuring in epidermal growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiviral agent contg. tri.peptide (unit) - of basic aminoacid, then alanine, glycine or sarcosine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3;
                        /label=OTHER
/note="(aceto amido methyl) NH2-Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 6; DB 10; Pred. No. 0; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiviral; M2; poliovirus; polio; heatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; SCOL.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR04607 standard; peptide; 3 AA.
                                                                                                                                                               (CSIR ) COMMONWEALTH SCIENT ORG.
                                                                                                                                                                                                                                                                                          Claim 3; page 10; 11pp; English.
/note="H-Gly"
                                                                                                                88WO-AU00300.
                                                                                                                                       87AU-0003629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88JP-0228843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NIHA ) NIPPON MINING KK.
                                                                                                                                                                                                               WPI; 1989-068852/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-129060/17.
            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                       3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antiviral agent.
                                                                                                            10-AUG-1988;
                                                                                                                                       10-AUG-1987;
                                                            WO8901489-A.
                                                                                     23-FEB-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP02078631-A.
                                                                                                                                                                                       McAuslan BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                               stimulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR04607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR04607
```

Q ò

ö

```
Prevention of adhesion formation, partic. post-surgically - comprises administering a RGD-contg. peptide for a time sufficient to permit tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C9H19CO-Arg, C13H27CO-Arg, C15H31CO-Arg, CH3-[(CH(CH3)-(CH2)3]3-CH(CH3)-CH2-CO-Arg or CH3-[(CH(CH3)-(CH2)3]2-CH(CH3)-CH2-CO-Arg"
                                                                                                                                                                                                                                                                                                                                                                                 The secuence is that of an RGD-contg. peptide which is used in a method for prevention of adhesion formation for a time sufficient to permit tissue repair. The method is used for minimising or preventing adhesion formation, partie. In the peritoneum following surgery, but also for e.g. cardiovascular, orthopedic, thoracic, ophthalmic, CNS and other uses. In addn., the peptide inhibits platelet aggregation and does not induce inflammation or trauma
 Tissue repair; peritoneum; surgery; post-surgically; inhibition; platelet aggregation; cardiovascular; orthopedic; thoracic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drug; organ transplantation; rejection; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Asp-OH or Asp-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                          (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR53144 standard; peptide; 3 AA.
                                                                                                                                                                                                                                                                                                                                                       Example; Page 18; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at the site of administration.
                                                                                                                                                92WO-US09494
                                                                                                                                                                             91US-0789231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGD peptide derivative #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Conservative
                                                                                                                                                                                                                                       Rodgers
                                                                                                                                                                                                                                                                WPI; 1993-167381/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            systemic lupus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP05255105-A
                                                                                                                                                06-NOV-1992;
                                                                                                                                                                             07-NOV-1991;
                                                                                                                                                                                                                                     Dizerega GS,
                               ophthalmic;
                                                                                      WO9308818-A.
                                                                                                                     13-MAY-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-0CT-1993.
                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR53144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            – p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmacological activity of an active peptide by preparing an accountion of a liquid polymer modified version of the peptide by covalently binding the peptide to a biocompatible prepolymer under a conditions. The prepolymer is a triol or higher polyol made up of at least 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all last 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all last 75% oxyethylene monomers, has mol.wt. 7000 - 30,000 and has all last proups capped with aliphatic or cycloaliphatic isocyanates, pref. isophorone disocyanate or methylene bis(cyclonexyl disocyanate). The covalent bond is between an NCO group on the prepolymer and an amino, SH, OH or COOH group on the peptide. The modified peptides have increased potency, decreased immunogenicity and longer circulation half-life than the free peptides. Suitable peptides include alkaline phosphatase, haemoglobin, RGD suitable and GHK peptides. The modified peptides mad GHK peptides and confirm and ingenesis, and for for promotion of atherosclerosis or tumour cell mestasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Bioactive peptide improvement by isocyanate-capped poly:ol conjugation - giving prods. which are more potent, have decreased imunogenicity and longer circulation half life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                 Metastatic tumour; wound healing; burn healing; angiogenesis; promoter;atherosclerosis; isocyanate; polyol; prepolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the enhancement of the biological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 3; . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                     Biocompatible polymer-conjugated bioactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adhesion formation prevention RGD-contg. peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%; Score 6; DB 1
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; column 18; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR36707 standard; peptide; 3 AA.
AAR23219 standard; Peptide; 3 AA
                                                                                                                                                                                                                                                                                                                         (GRAC ) GRACE W R & CO-CONN.
                                                                                                                                                                                                                                                 90US-0510260
                                                                                                                                                                                                                                                                            90US-0510260
                                                                                                                                                                                                                                                                                            88US-0266445
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Conservative
                                                                                                                                                                                                                                                                                                                                                     Braatz JA, Heifetz AH;
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-088348/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AA;
                                                                                                                                                                                                                                                 24-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1993
                                                                                                                                                                                                                                                                                            02-NOV-1988;
                                                         18-NOV-1992
                                                                                                                                                                                                                                                                            24-APR-1990;
                                                                                                                                                                                       US5091176-A.
                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 G 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR36707;
                           AAR23219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXXXXXXX
```

ò

ö

Gaps

Search completed: February 12, 2002, 12:30:34 Job time: 367 sec

ö

Gaps

; 0

27.3%; Score 6; DB 14; Length 3; 100.0%; Pred. No. 0; tive 0; Mismatches 0; Indels

Ouery Match 27.3 Best Local Similarity 100. Matches 1; Conservative

10 G 10 | 2 g 2

Qy Db

```
February 12, 2002, 12:38:36 ; Search time 232.64 Seconds (without alignments) 11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                          473505
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_bacteria:*
sp_human:*
sp_human:*
sp_novertebrate:*
sp_novertebrate:*
sp_organelle:*
sp_organelle:*
sp_phage:*
sp_plage:*
sp_plage:*
sp_plage:*
sp_plage:*
sp_plage:*
sp_vorganelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                  US-09-485-571-19
89
                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_17:*
                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9huh9 pseudomonas	Q9eta8 corynebacte	O9ynbl sugarcane s	070681 sugarcane s	027557 methanobact	Q9p9m2 pyrobaculum		Q9ryi5 deinococcus	Q9f5c0 agrobacteri	Q9hyt9 pseudomonas	Q91474 pseudomonas	Q9yz25 lymphocytic	Q9z571 streptomyce	Q9cdb2 mycobacteri	053580 mycobacteri	Q9qar7 bovine coro	Q9qar0 bovine coro	Oggad4 bovine coro	091wr8 oryza sativ
ΩI	6нпн60	Q9ETA8	Q9YNB1	070681	027557	Q9P9M2	Q9R6F9	Q9RYI5	Q9F5C0	Q9HYT9	091474	Q9YZ25	092571	Q9CDB2	053580	Q9QAR7	Q9QAR0	090AQ4	O9LWR8
DB	7	7	12	12	Н	-1	7	7	7	7	7	12	7	7	7	12	12	12	10
% Query Match Length DB	648	173	297	588	1408	785	212	236	424	664	619	2209	447	635	637	207	207	207	259
% Query Match	50.6	49.4	49.4	49.4	49.4	48.3	47.2	47.2	47.2	47.2	47.2	47.2	46.1	46.1	46.1	44.9	44.9	44.9	44.9
Score	45	44	44	44	44	43	42	42	42	42	42	42	41	41	41	40	40	40	40
Result No.	1	7	е	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

st ceeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeeee		1;
synechocyst streptomyce pasteurella homo saplen pseudomonas homo saplen homo saplen homo saplen pyrococcus mycobacteris arabidas alboenothera byrococcus pyrococcus pyrococcus pyrococcus pyrococcus pyrococcus pyrococcus pyrococcus pyrococcus petunia sp. solanum tub edta-degrad treponema plactococcus methylobacia methylobacia	eae; rener P., Lagrou M., Yuan Y., Lim R.M.,	Gaps
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	eae; rener Lian Yuan Lin A	4 ;
P73476 s; Q9kxr7 s; Q9kxr7 s; Q9c100 p; Q9c100 p; Q9c100 p; Q9c100 p; Q9c30	adaceae; Warrener J., Lagr S., Yuan K., Lim R M.V.; Ol, an	.;
200000000000000000000000000000000000000	MENTS  648 AA.  uence update)  otation update)  ivision; Pseudomonadaceae  ivision; Pseudomonadaceae  ivision; Pseudomonadaceae  ivision; Pseudoman S., Yu  Westbrock-Wadman S., Yu  Westbrock-Wadman S., Yu  ", Was A., Larbig K., Lim S., Wu Z., Paulsen I T.,  ", Lory S., Olson M.V.;  onas aeruginosa PAO1, an  ; Oxidoreductase.  8ACF7887D4F CRC64;	Length 648 ; Indels
	te)  ref)  ref)  ref)  ref)  ref)  ref)  ref)  ref)  ref)	engt In
	PRT; 648 AA.  16, Created) 16, Last sequence update) 17, Last annotation update) 17, Last annotation update) 18. Erwin A.L., Mizoguchi S.D. 2. L., Hufnagle W.O., Kowalik Tolentino E., Westbrock-Wadm, Folger K.R., Kas A., Larbi ", Folger K.R., Kas A., Larbi ", Wong G.KS., Wu Z., Paulsi ancock R.E.W., Lory S., Olso e of Pseudomonas aeruginosa il LPyr_redox. dored_FMN. Lredox. dored_FMN. FMN: 1. SEI. Flavoprotein; Oxidoreductase 0 MW; ADID78ACF7887D4F CRC6	" " "
	on; upd on; upd on; upd on; tbrc tbrc aeru	~
	ALIGNMENTS  PRT; 648 AA.  Created) Last sequence up Last annotation last annotation; Last annotation; Last annotation; Last annotation; Last sequence up Last s	. ch
7 2 5	ALIGNMENTS ALIGNMENTS ated) t sequence t sequence t annotati unagle W. no E., Wes no E., Wes G. KS., We eudomonas Y). dox. MN.	Score 45; Pred. No.
P73476 Q9KXR7 Q9CLA0 Q9DUC6 0910C8 015451 015451 0912U5 Q9CD8 Q9CB4 Q9SRA Q9SRA Q9SRA Q9SRA Q9SRA Q9SRA Q9GGGG Q95RB Q9CGG Q95RB Q9CGG Q9CGG Q9CGG	PRT;  Created) Last seq Last seq Last ann mma subd rwin A.L , Hufnao. Higer KR ng G.KR ck R.E.W Pseudom RITY)	ore ed.
	Cre Lias Ervicenti Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Coolge Cool	4
000000000000000000000000000000000000000	(Y; 16, C 116, L 11, L 18. 17, L 19, G 11, G 11, G 11, G 11, G 12, G 13, G 14, World 14, World 16, G 17, G 17, G 18, G	50.6%; 50.0%; ive
334 368 368 368 368 370 370 370 370 370 370 370 370 370 370	NARY; rel. TASE. osa. rel. L., P. N. D. N.	50. 50. tive
ਂ ਜ਼ਰ	PRELIMINARY (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. IDOREDUCTASE aeruginosa. rcteobacteri 287; NA.A. NA. DA N.A. DEINKman F. Q. Pham X. Q. Pham X. Q. DA Oulter S. N. Spencer D. H. Saler M.H.	50. Jarity 50. Conservative
4444444 $0.00000000000000000000000000000000000$	RELIM TTERMS ONEDW ONEDW ONEDW ONEDW N.A. N.A. N.A. N.A. N.A. N.A. N.A. N.A	arit
<b>च च च च च च च च च च च च च च च च च च च </b>	PRELIMINARY  DO11 (TEMBLEEL)  OO1 (TEMBLEEL)  OO1 (TEMBLEEL)  OO1 (TEMBLEEL)  OO1 (TEMBLEEL)  OO1 (TEMBLEEL)  ABB aeruginosa.  Proteobacteri  ABB,  AB,  ABB,  AB,  ABB,  AB,  ABB,  AB,  ABB,  AB,  ABB,  A	h Similarity 11; Conser
444444466666 00000000000000000000000000	CE E E E E E E E E E E E E E E E E E E	ch 1 Si 11;
	ALIGNMENTS  ESULT  9 HU99  C OSHUH9)  C OSHUH9)  T OL-MAR-2001 (TrEMBLrel. 16, Created)  T OL-MAR-2001 (TrEMBLrel. 16, Last sequence update)  T OL-MAR-2001 (TrEMBLrel. 17, Last annotation update)  T OL-MAR-2001 (TrEMBLrel. 17, Last annotation update)  T OL-MAR-2001 (TrEMBLrel. 17, Last annotation update)  E PROBABLE OXIDOREDUCTASE.  S Pseudomonas aeruginosa.  S Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceer  C STRAIN-PAO1;  NOTIL TAXID-207;  (1)  SEQUENCE FROM N.A.  S STOREN - N.A.  S STARAIN-PAO1;  A MEDLING-20437; Pubbed-10984043;  A STARAIN-PAO1;  A STARAIN-PAO1;  A MEDLING-20437; Pubbed-10984043;  A STARAIN-PAO1;  A STARAIN-P	/ Match Local nes 1
20000000000000000000000000000000000000	LT 099 099 0011 011 011 011 011 01	Query M Best Lo Matches
	SESULT  OOS OOS OOS OOS OOS OOS OOS OOS OOS OO	Ou Ma
•		

DB 12; Length 297;

δλ

```
Query Match
Best Local Similarity
'-hag 7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DELTA H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coat protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN)
                                                                                                                                                                                                                                                                                                                                          070681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             027557
                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                027557
                                                                                                                                                                                                              QC
                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Hema M., Srenivasulu J., Joseph J., Gopinath K., Savithri H.S.;
"Molecular characterization and interviral relationships of a flexuous finamentous virus causing mosaic disease of sugarcane (Saccharum Officinarum L.) in India.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL: Y17788, CAA76842.1;
-InterPro; IPR001592; Poty_coat.
Pfam: PF00767; Poty_coat.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A., Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T., Dan H., Prescott J.F.;
Dan H., Prescott J.F.;
"DNA sequence and comparison of virulence plasmids from Rhodococcus infect. Immun. 68:6840-6847(2000).

EMBL; APO01204; BAB16667.1; -
EMBL; APO11204; BAB1667.1; -
Hypothetical protein; Plasmid.
SEQUENCE 173 AA: 18851 MW; F18A637BCA404053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC33701; PLASMID-PREAT701 (P33701);
Takal S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ATCC33701, AND 103; PLASMID-PREAT701 (P33701), AND VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugarcane streak mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                               Corynebacterium equii (Rhodococcus equi).
Plasmid PREAT701 (p33701), and Plasmid virulence.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=43767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2; Length 173;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 AA; 32843 MW; FE8B424F422A8D15 CRC64;
                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 18.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
9
                                                                                                                                                                               173 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                            487 RGGELQVVDAWQVLRGEVRVGR 508
1 RGGRL----AYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.48;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GGRISYASLRYTDETGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=53954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=11083803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potyvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                          O9ETA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9YNB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09YNB1
                                                                                                                     RESULT
Q9ETA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
O9YNB1
LD 099
AC 099
DT 001
DT 001
DE 001
CC 000
CC
                                            qq
                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98037514; pubmed=9371463; Smith D.R., Deucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Smith D.R., Deucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CELL SURFACE GLYCOPROTEIN (S-LAYER PROTEIN) RELATED PROTEIN (S-LAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall J.S., Adams B., Parsons T.J., French R., Lane L., Jensen S.G.; Mol. Phylogenet. Evol. 0:0-0(1998).

EMBL: U75456, AAC16271.1;
InterPro: IPR001205; RNA_pol_p3D.
InterPro: IPR001592; Poty_coat.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 588;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3876EEF59189EA32 CRC64;
                                                                                                                                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                     588 AA.
    Score 44; DB Pred. No. 24; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                             COAT PROTEIN (FRAGMENT).
Sugarcane streak mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66335 MW;
49.4%;
ilarity 43.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.48;
                                                                                                   | ||||: ::|::| |:
191 GELAYKWVQFSVRSGK 206
                                                                             3 GRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |||: ::|::| |:
482 GELAYKWVQFSVRSGK 497
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
588 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Potyvirus.
NCBI_TaxID=53954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=145262;
```

```
2 GGRLAYRLLRFA 13
                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=MAFF301001;
                                                                                                                                               STRAIN=MAFF301001;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=MAFF301001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                 SEQUENCE FROM N.A.
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RYIS
Q9RYIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRA0327
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
   Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                ö
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                Score 44; DB 1; Length 1408;
Pred. No. 1.3e+02;
; Mismatches 6; Indels
                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoproteales; Thermoproteaceae;
Pyrobaculum.
NCBI_TaxID=2277;
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00116; DNA POLYWERASE B; 1.
DNA replication; DNA-binding; DNA-directed DNA polymerase.
SEQUENCE 785 AA; 89748 MW; 10FB8B66A8F3730D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 48.3%; Score 43; DB 1; Length 785; 50.0%; Pred. No. 1e+02; ive 4; Mismatches 4; Indels
                        1408 AA; 152736 MW; .294EC7742ABB29F2 CRC64;
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                       785 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 AA
                                                                                                                                                       Created)
                                                                                                                                       PRT;
                                                                                                                                                                                                                                              STRAIN-GEO 3;
MEDLINE-20100754; Pubmed-10633098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
J. Bacteriol. 179:7135-7155(1997). While, AE000911; AB885988.1; -. Complete proteome. SEQUENCE 14068 AA; 152736 MW; ·2
                                                Ouery Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                         | :| || :| !|
| 318 GAKLGYRTFKFTLKPGR 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium radiobacter.
Plasmid pri-SAKURA.
                                                                                2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                           | |: : |||:| |:|
373 GNRVEWMLLRYAYRLG 388
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GGRLAYRLLRFAIRVG 17
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                             FAMILY B DNA POLYMERASE.
                                                                                                                                                                                             Pyrobaculum islandicum.
                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIORF100 PROTEIN.
TIORF100.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                      09P9M2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9R6F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09R6F9
                                                                                                                                                                                      POLB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q9P9M2
 NE DR SO
                                                                                ò
                                                                                              g
                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA (IV): Characteristics of tra region."; Nucleic Acids Symp. Ser. 39:187-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                  trbJ
                                                                                                                                                             sequence of a plant tumor-inducing Ti plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MAPF301001;
Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
"Genome structure of pri-SAKURA (V): Complete nucleotide sequence of
plasmid pri-SAKURA's vir region in Agrobacterium tumefaciens.";
Nucleic Acids Symp. Ser. 39:265-266(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-StrakURA(I): Strategy for DNA sequencing of Japanese cherry-II plasmid."; Nucleic Acids Symp. Ser. 37:159-160(1998).
                                                                                                                                                                                                                                                                                STRAIN=NAFF301001;
BDDLINE-SB9193120;
Suzuki E., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
Suzuki E., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
"Novel structural difference between nopaline- and octopine- type tegene:construction of genetic and physical map and sequencing of trb/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA.";
Biochim. Biophys. Acta 1396:1-7(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohta N. Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K., "Genome structure of pTi-SAKURA (III): Characteristics of T-DNA."; Nucleic Acids Symp. Ser. 39:185-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=R1;
MEDLINE=20036896; Pubmed=10567266;
White O., Eisen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus NCBL_TexID-1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
SEQUENCE FROM N.A.
STRAIN=NAFE301001;
MEDLINE=20184752; PubMed=10721727;
Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
Katoh A., Yoshida K.;
"Complete nucleotide sequence of a plant tumor-inducing Ti plas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA; 22823 MW; 9533E5438CAC0396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TEMBLrel. 17, Last annotation update)
HYPOTHETICAL 27.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.2%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEIC ACIDS SYMP. Ser. 39:
EMBL; AB016260; BAA87725.1;
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.2
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinoceccus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 GGKMEWRLLRFS 127
```

Gaps

; 0

Indels

Length 424;

5;

Score 42; DB 2 Pred. No. 75; 0; Mismatches

47.2%;

```
424 AA; 47098 MW; 24AF2FB688FC8A87 CRC64;
                                                                                                         Conservative
               Pfam; PF00991; ParA; 1.
                                                                                                                                 2 GGRLAYRLLRFAI 14
                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                  Pseudomonas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PAO1;
                           Plasmid.
SEQUENCE
                                                                                                                                                                                                                            Q9HYT9
                                                                                                                                                                                                                                                                                                          PA3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            091474;
                                                                                                                                                                                                 RESULT 10
Q9HYT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
291474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536
               SQ SQ
                                                                                                                                  ŏ
                                                                                                                                                           g
                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                    ;
0
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.; "Analysis of unique variable region of a plant root inducing plasmid, pRil124, by the construction of its physical map and library."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome structure of Ri plasmid (1): Sequencing analysis of T-DNA and its flanking regions of PRi1724 in Japanese Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.; "Genome structure of Ri plasmid (1):Construction of linking library and physical map of pRil724 in Japanese Agrobacterium."; Nucleic Acids Symp. Ser. 39:189-190(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
Yoshida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŚEÓUENCE FROM N.A.
STRAIN=MARF03-01724;
Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete nucleotide sequence of a Ri (root inducing) plasmid indicates its chimerical structure between Ti and Sym plasmids."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                   ;
0
                                                                               "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001863; AAF12511.1; -.
                                                                                                                                                                                                                       2; Length 236;
                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                             InterPro; IPR000051; SAM_bind.
Hypothetical protein; Complete proteome,
SEQUENCE 236 AA; 27048 MW; 58AA84E95A5DC54C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    424 AA.
                                                                                                                                                                                                                   47.2%; Score 42; DB 62.5%; Pred. No. 39;
                                                                                                                                                                                                                                Pred. No. 39;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Symp. Ser. 42:67-68(1999).
EMBL; AP002086; BAB16251.1; -.
InterPro; IPR000707; ParA.
                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MAFF03-01724;
MEDLINE-20241294; PubMed-10780382;
                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17)
                                                                                                                                                                                                              Query Match
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium rhizogenes. Plasmid pRi1724.
                                                                                                                                                                                                                                                                     2 GGRLAYRLLRFAIRVG 17
                                                                                                                                                                                                                                                                                       73 GGDLARQLLRWAARDG 88
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=MAFF03-01724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-MAFF03-01724;
                                                                                                                                                                                                                                                                                                                                                                                                                                RIORF132 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae;
                                                                                                                                     DRA0327
                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rhizogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                              RIORF132.
                                                                                                                                                                                                                                                                                                                                                             Q9F5C0
Q9F5C0;
                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                           Op
```

```
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Older De Company Pubmed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 2; Length 664;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome, SEQUENCE 664 AA; 73136 MW; 19EBBEF309BDIF4E CRC64;
                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN PA3305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                           664 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PAO1;
MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004753; AAG06693.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, HYPOTHETICAL PROTEIN PA1270.
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.2
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
329 GGRLDYDFLRFLI 341
                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||:| |||| |
|GRMADRLLRLA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRLAYRLLRFA 13
                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
NCBI_TaxID=287;
```

Gaps

ö

5; Indels

Length 447;

ð g

```
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; As to fordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL; AL035569; CAB37584.1; SEQUENCE 447 AA, 46718 MW; 01D72ACIDC201A5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Length 635;
Pred. No. 1.7e+02;
2; Mismatches 3; Indels
                                    Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 AA; 69534 MW; C5B15CAD365A46BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583917; CAC29608.1; -.
Complete proteome.
SEQUENCE 635 AA; 69534 MW: CRRISCARVESTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 AA
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   053580 PRELIMINARY; PRT; 053580; 01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-TN;
MEDLINE=21128732; PubMed=11234002;
                                                                                                            STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTATIVE ACYL-COA SYNTHETASE. FADD32 OR ML0100.
                                                                                                                                                                                                                                                                                                     46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.18;
61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 61...
8; Conservative
                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            30
                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLAYRLLRFAIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                   16 RGSRLAVRGSRFAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 RCDKLAYRFLDFS
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
                                                                                        SEQUENCE FROM N.A.
     SEQUENCE: FROM N.A.
                       STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   о9срв2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9CDB2
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    053580
ID 05
AC 05
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09CDB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                            ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               two strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                    Gaps
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Shmith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAOl, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lymphocytic choriomeningitis virus (strain WE).
Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence comparison of the large genomic RNA segments of two of lymphocytic choriomeningitis virus differing in pathogenic potential for guinea pigs.";

EMBL; AF004519; AAD03396.1;

SEQUENCE 2209 AA; 254432 MW; 40104EFA50EDCCCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2209;
                                                                                                                                                                                                               Score 42; DB 2; Length 679;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.2%; Score 42; DB 12; Length 22.
66.7%; Pred. No. 4.7e+02;
...ematches 2; Indels
                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
Murphy L., Harris D.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                         Hypothetical protein; Complete proteome.
SEQUENCE 679 AA; 73079 MW; B37B15EEED4E5DC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           2209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447 AA
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WE;
MEDLINE-99073699; Pubmed-9857988;
                                                                                        opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004556; AAG04659.1; -.
                                                                                                                                                                                                             47.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY 1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, PUTATIVE OXIDOREDUCTASE.
                                                                                                                                                                                                                                                                                                       539 GGRTADRLIRLAQRYDR 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.7.
                                                                                                                                                                                                                                                                                   2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                             Query Match 47.2
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC8D9.20C.
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: |||||| ||
662 KVVYRLLRFLIR 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RLAYRLLRFAIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11627
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9Y225;
01-MAY-1999 (
01-MAY-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
L PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   092571;
                                                                                                                                                                                                                                                                                                                                                                                                         09YZ25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  092571
                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
Q9YZ25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
Q9Z571
```

ò g ö

Gaps

ö

AA.

```
MEDLINE-9825987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglaneler K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares J., Deciphering the biology of Mycobacterium tuberculosis from the Formation of St. States S., Squares S., Square
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE POLYKETIDE SYMTHASE.
FADD32 OR RV3801C OR MYCOSC.06C.
MYCODacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000873; Amp-bind.
Pfam: PF00501; AMP-binding; 1.
Complete proteome.
SEQUENCE 637 AA; 69231 MW; 0A3A86CED9AE0EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AL022076; CAA17865.1; -. TubercuList; Rv3801c; -.
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=H37RV;
```

; 0

Gaps ;

Query Match
46.1%; Score 41; DB 2; Length 637;
Best Local Similarity 61.5%; Pred. No. 1.7e+02;
Matches 8; Conservative 2; Mismatches 3; Indels

1 RGGRLAYRLLRFA 13 

qq ò

Search completed: February 12, 2002, 12:38:37 Job time: 750 sec

```
February 12, 2002, 12:39:49; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                         100059
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                      US-09-485-571-19
89
1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_39:*
                                                                                                                                                                        Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                Searched:
                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a	score greater than or equal to the score of the result being printed,	and to delived by analysis of the total score distribution.
Pred. No. is the number of re	score greater than or equal t	and to delived by analysis of

	Description	P32194 sus scrofa	P49934 sus scrofa	P32195 sus scrofa	P32196 sus scrofa	O28756 archaeoglob	P22654 bovine coro	052	P26626 turkey ente		P55729 rhizobium s		P25756 pseudomonas		Q04715 petunia hyb	~	P27927 zea mays (m	ä	8	Q9kv12 vibrio chol	7	_	~	Ģ	P24347 homo sapien	Q02853 mus musculu	P75925 escherichia	P34336 caenorhabdi	P28463 synechocyst	O9huw5 pseudomonas	P32386 saccharomyc	37	P06367 saccharomyc	P39516 saccharomyc
SUMMARIES	ID	PG1_PIG	PG5_PIG	PG2_PIG	PG3_PIG	SFSA_ARCFU	YIOR_CVBF	Y IOR_CVBM	Y I OR_CVTKE	TRUB_MYCTU	Y4ZB_RHISN	ALEU_HORVU	GIDA_PSEPU	DP3A_THEAQ	RM16_PETHY	RM16_BRANA	RM16_MAIZE	RM16_ORYSA	NAT_MYCTU	MIAA_VIBCH	CYS2_MAIZE	Y711_HUMAN	MMLC_STRCO	DPO2_AERPE	MM11_HUMAN	MM11_MOUSE	C561_ECOLI	YK11_CAEEL	HEM1_SYNY3	DSD1_PSEAE	YBT1_YEAST	PPSA_MYCTU	R141_YEAST	R142_YEAST
	DB		-	٦	-	٦	-	-	٦	-	٦	7	٦	7	Н	7	-	Н	-	7	٦	7		-	-	-	~	1	H	H	-4	-	7	7
	Length	149	149	147	149	219	207	207	207	298	326	362	630	1220	155	177	185	185	283	315	360	623	705	784	. 488	492	188	266	427	591	1661	1876	136	137
æ	Query Match	8	7	53.9	0	1	₹	4	44.9	43.8	က	ß	m	43.8	2	2	42.7	42.7	42.7	42.7	42.7	C)	2	2	2	2	$\vdash$	Η.	_	_	Η.	;	٠	41.0
	Score	52	51	48	45	42	40	40	40	39	39	39	39	39	38	38	38	38	38	38	38	38	38	m,	37.5	ζ.	37	37	37	37	37	37	36.5	36.5
	Result No.	-	7	m	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29	30	31	32	33

P27069 kluyveromyc P3768 secherichia P41014 bacillus ca P09221 bacillus ps 000110 ictalurid h 09yfnl aeropyrum p P25778 oryza sativ P45079 haemophilus P48301 mus musculu 027509 methanobact P29521 daucus caro Q01447 fusarium so				; Buteleostomi; ;; Sus.	amily by cDNA				TISSUE-Leukocyte;  X MEDLINE-93327946; PubMed-8335113;  XA KOKYAKAY V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A.,	combine features		i. A.,	Kokryakov V.N., porcine	d usage or n degradation.";	Despaux B.,	bial peptide
RS14_KLULA ALDB_ECOLI ATPF_BACCA ATPF_BACCA ATPF_BACCA ATPF_BACCA ATPF_BACCA OGTO_OGTO ORYC_OGTO ORYC_OGTO TEF4_MOUSE COBB_METTH EF11_DAUCA ER11_DAUCA	ALIGNMENTS	PRT; 149 AA.	Created) Last sequence update) Last annotation update) (PG-1) (NEUTROPHIL PEPTIDE 1	Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;	ubMed-8013647; shrer R.I.; a new member of the protegrin family by			, conce	3; Sanyutich E.A., She	blal peptides that achyplesins.";		5; A.A., Abdalla K.O.M	Musoliamov A.X.,	neutrophils. Sequence determination by the combined usage of electrospray ionization mass spectrometry and Edman degradation. FEBS Lett. 330:339-342(1993).	CKIN 1. 8647100; Roumestand C., Chiche L., Despaux B ranjeu	ce of the antimicrobial
137 1 RS14- 512 1 ALDB 163 1 ATPF- 227 1 VG70- 362 1 ORYC_ 440 1 TEF4 447 1 COBB 449 1 EF11- 485 1 EF11-		STANDARD; PI	27, 34, 36, 36,	oa; Chordata; C) la; Cetartiodaci	. 3. 1. 1. 1.	15-288(1994).	141 SEQUENCE FROM N.A. STRAIN-RED DUROC; MEDLINE-95354835; PubMed-7628604; Zhao C., Ganz T., Lebfrer R.I.; The structure of porcine proteorie games "	7-202(1995).	PubMed=833511:	cocyte antimicrodefensins and	148.	PubMed=837550	e of three cat.	lence decerminal Lzation mass spe 19-342(1993).	STRUCTURE BY NMR OF PROTEGRIN 1. MEDLINE-96235220; Pubmed-8647100; Mumelase A., Mangoni M., Roumesta Grassy G., Calas B., Chavanieu A.	"Synthesis and solution structure protegrin-1."; Eur. J. Biochem. 237:575-583(1996)
86 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		1 PIG	21-1993 CT-1996 UL-1998 EGRIN 1	Sus scrofa (Pig). Eukaryota; Metazoa; Mammaliù; Eutheria; NCBL_TaxID=9823;	SEQUENCE FROM N.A SEQUENCE FROM N.A TISSUE-Bone marror MEDLINE-94283613; Zhao C. Liu L., Tidentification o	oning."; 3S Lett. 346:28	DUENCE FROM N.2 QUENCE FROM N.2 ALINE-95354835, DO C., Ganz T.,	3S Lett. 368:19	SSUE=Leukocyte, SLINE=93327946, Cryakov V.N., E	cotegrins: leuk corticostatic	DUENCE OF 131-1	SSUE-Neutrophil DLINE-93387466; rgorodskaya O.A	ernushevich I.V umova O.V.; rimary structum	trrophits, sequential setrospray ioni 3S Lett. 330:33	RUCTURE BY NMR DLINE=96235220; nelase A., Mang assy G., Calas	nthesis and so otegrin-1."; r. J. Biochem.
W W W W W W W A A A A A A A A A A A A A		SU.	DT 01-00 DT 01-00 DT 01-00 DT 15-01 DE PROTI				RP SEQUE RP SEQUE RC STRAI RX MEDLI RA Zhao	RL FEE	RX MEI	RT "PI RT Of	RN [4]	RX MEI		KT neu KT ele KL FEB		

us-09-485-571-19.rsp

```
Sns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
PG2_PIG
        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                     peptide from porcine leukocytes.";
Chem. Biol. 3:543-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                        MEDLINE-97113279; PubMed-8807886;
Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-149 PROVIDE AMIDE GROUP). 6EFBA98429CD6EC4 CRC64;
                                                         "Solution structure of protegrin-1, a broad-spectrum antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                           First 27-MAY-98.

DBS; 1PG1; 27-MAY-98.

InterPro; IPR001894; Cathelicidin.

Pfam; PF00066; Cathelicidin; 1.

ProDom; PD001838; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS_1; 1.

PROSITE; PS00947; CATHELICIDINS_2; 1.

Antiblotic; Signal; Amidation; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                         (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 1; Length 149;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                          PROTEGRIN 1, PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                        MONOCYTOGENES AND C.ALBICANS, IN VITRO.
SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95354035; Pubmed=7628604; ABDLINE-95354035; Pubmed=7628604; Lahac C., Ganz T., Lehrer R.I.; The structure of porcine protegrin genes."; FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY. SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
[6]
STRUCTURE BY NMR OF PROTEGRIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34, Created)
34, Last segi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16677 MW;
                                                                                                                                                                                                                                  EMBL; X79868; CAA56251.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PG-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 01-NOV-1997 (Rel. 35, PROTEGRIN 5 PRECURSOR
                                                                                                                                                                                                                                                          PIR; S34585; S34585
PIR; S36820; S36820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PG5_PIG
P49934;
                                                                                                                                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
PG5_PIG
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Storici P., Zanetti M.;
"A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
Blochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PROTEGRIN 5.
PRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-149 PROVIDE AMIDE GROUP).
(BY SIMILARITY.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROKTYAROV V.N., Harvig S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Profegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).

-I. FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi,
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 1; Length 149;
Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6CC7262429CD6B64 CRC64:
-!- FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                    EMBL; X84096; CAA58892.1;
HSSP; P32194; 1PG1.
InterPro; IPR01894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS.1; 1.
PROSITE; PS00947; CATHELICIDINS.2; 1.
Antibiotic; Amidation; Multigene family; Signal.
SIGNAL
ANDEP 30 130 POTENTIAL.
CHAIN 131 148 PROTEGRIN 5.
MOD_RES 30 30 PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEGRIN 2 PRECURSOR (PG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Bone marrow;
MEDLINE=94071898; PubMed=8250892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93327946; PubMed=8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΜW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.3%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 RGGRLCYCRPRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 61.17
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
124
145
143
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 131-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PG2_PIG
P32195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
```

```
SFSA_ARCFU
028756;
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFSA_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                        PROTECRIN 2.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Bone marrow;
MEDLINE-94283613; PubMed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                               Score 48; DB 1; Length 147;
                                                                                                                                                                                                                                                                                                                                                                    6; Indels
MONOCYTOGENES AND C.ALBICANS, IN VITRO. SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                    InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Signal; Amidation; Multigene family.
SIGNAL 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROTEGRIN 3 PRECURSOR (PG-3).
                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95354835; PubMed-7628604;
Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Leukocyte;
MEDLINE-93327946; PubMed-8335113;
                                                                                                                                                                                                                                                                                                                Ψ.
                                                                                                                                                                                                                                                                                                                                               53.9%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett. 346:285-288(1994).
                                                                                                                  EMBL; L24745; AAA31061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   16478
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLAYRLLRFAIRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                               130
146
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 131-148.
                                                                                                                                                                                                                                                                                                              147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-RED DUROC;
                                                                                                                                                                                                               30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning.",
                                                                                                                                                                                                                                                                             DISULFID
DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PG3_PIG
P32196;
                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                               PROPEP
                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
PG3_PIG
ò
                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@liberine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed=9389475;

Klenk E.-P., Clayton R.A. Tomb J.-F., White O., Nelson K.E.,

Kletchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Karlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Morkenbush J., Lee N.H., Sutton G.G., Gill S.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                     FEBS Lett. 327.231-236(1993).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshine G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-149 PROVIDE AMIDE GROUP). 6F4BA98429CD6ED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 1; Length 149; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                     MONOCYTOGENES AND C.ALBICANS, IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001894; Cathelicidin.
Prfam; PF00066; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE: PS00947; CATHELICIDINS_2; 1.
Antibio:ic; Signal; Amidation; Multigene family.
SIGNAL
SIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-AUG-2001 (Rel. 40, Last annotation update)
SUGAR FERMENTATION STIMULATION PROTEIN HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEGRIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ψ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X83267; CAA58240.1; -. EMBL; X84095; CAA58891.1; -. PIR; S34587; S34587. HSSP; P12194; 1PG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 RGGGLCYCRRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.6
Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaecglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
107
136
138
148
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFSA OR AF1516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaecglobus
```

207 AA.

PRT;

STANDARD;

YIOR_CVBM

153 RLGFRLARYSLRV 165

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-89087718; PubMed-3207501;
Cruciere C., Laporte J.;
"Sequence and analysis of bovine enteritic coronavirus (F15) genome.
I. Sequence of the gene coding for the nucleocapsid protein; analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine coronavirus (strain F15).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                            the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1; Length 219; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                EAD775628C39F915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 207 AA; 23001 MW; A4E5DE61171BAB50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                         reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ann. Inst. Pasteur Virol. 139:123-138(1988).
                                                                                                                          -! - SIMILARITY: BELONGS TO THE SFSA FAMILY

 Mismatches

                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                      "The complete genome sequence of
                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 219 AA; 25061 MW;
                                                                                                                                                                                                                                                                                                          EMBL; AE000997; AAB89729.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                  47.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M36656; AAA42759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.80,

    Sequence of the gene co
of the predicted protein."

                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:|:||| ||:
58 RGGKLSYRL--FAV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLAYRLLRFAI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S06869; S06869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11129;
                                                         Venter J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIOR_CVBF
P22654:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
 ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Verbeek A., Tijssen P.; "Sequence analysis of the turkey enteric coronavirus nucleocapsid and membrane protein genes: a close genomic relationship with bovine
                                                                                                                                                                                              MEDLINE-87151119; Pubmed-3029965;
Lapps W.E., Hogue B.G., Brian D.A.;
"Sequence analysis of the bovine coronavirus nucleocapsid and matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                               Bovine coronavirus (strain Mebus).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Turkey enteric coronavirus (TCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 207; Pred. No. 5.7; % Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 protein.
207 AA; 23054 MW; BE76DC4D663DD32A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .1 protein.
207 AA; 23005 MW; F69E2D8F2F006F77 CRC64;
                                              01-JUL-1989 (Rel. 11, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLEOCAPSID ORF (IORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
HYPOTHETICAL PROTEIN IN NUCLECCAPSID ORF (IORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72:1659-1666(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91311418; PubMed=1856695;
                                01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M16620; AAA66398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.8%;
                                                                                                                                                                                                                                                               Virology 157:47-57(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || :|| |:::||
153 RLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 RLAYRLLRFAIRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; C26347; QQIHBC.
Hypothetical proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Gen. Virol. 72::
PIR; JQ1174; JQ1174
                                                                                                                                                 NCBI_TaxID=11132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MINNESOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11152;
                                                                                                                                                                                                                                                 protein genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronavirus.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
YIOR_CVBM
P10525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIOR_CVTKE P26626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIOR_CVTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ö

DB 1; Length 207;

44.9%; Score 40;

Query Match

ó;

Gaps

; 0

2; Indels

Length 207;

Score 40; DB 1; Pred. No. 5.7; 4; Mismatches

44.9%;

RLAYRLLRFAIRV 16

4

δ

S

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P05167
                                                                                                                                                    Y4ZB_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                       g
                                                                                                                                                                    셤
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE - PSEUDOURIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'-PHOSPHATE + H(2)O.
SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      s:,
                 Gaps
                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Baddoock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamin N., Holroyd Julver S., Osborne J., Woule S., Hamin N., Holroyd Sulston J.E., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRNA PSEUDOURIDINE SYNTHAASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE SYNTHASE) (PSEUSOURIDINE SYNTHASE) (URACIL
               ö
                 Indels
                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002501; TruB_N.
Pfam; PF01509; TruB_N; 1.
Lyase; tRNA processing; Complete proteome.
SEQUENCE 298 AA; 31819 MW; 9F77797DC13B34C6 CRC64;
               ;
                                                                                                                                                 298 AA.
 Pred. No. 5.7;
               Mismatches
                                                                                                                                                                                                                                                                     TRUB OR RV2793C OR MT2862.1 OR MTV002.58C.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL008967; CAA15588.1; -. EMBL; AE007112; AAK47182.1; -. TIGR; MT2862.1; -.
53.8%;
                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
               7; Conservative
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ruberculist; Rv2793c; -.
                                                             153 RLGFRLARYSLRV 165
                                           4 RLAYRLLRFAIRV 16
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1773;
                                                                                                                                                                                                                                                         HYDROLYASE)
                                                                                                                                                   TRUB_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bishai W.;
                                                                                                                     RESULT 9
TRUB_MYCTU
            Matches
                                                                      a
                                                                                                                                                   ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare (Barley).
Bukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Pooldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                               Plasmid sym pNGR234a.
Bacteriu; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perret X.; "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Transposable element; Transposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 356;
  Length 298
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA recombination; Plasmid.
56 AA; 39775 MW; 9F350ABB7E691635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
THIOL PROTEASE ALEURAIN PRECURSOR (EC 3.4.22.16).
); DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1;
Pred. No. 15;
                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE TRANSPOSASE Y428.
                                                                                                                                                                                                                                 356 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                         Mismatches
  Score 39;
                     Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; A3000108; AAB91960.1; -
InterPro; IPR002559; Transposase_11.
Pfam; PF01609; Transposase_11; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE::97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86016732; PubMed=3901004;
                                                                                                                                                                                                                                                                                                                                                                              Rhizobium sp. (strain NGR234).
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%;
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|| ||| | |: | .
293 IAYALLRIAARLNR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAYRLLRFAIRVGR 18
                                                                                                          ||| ||| ||
127 GGRRAYRLAR 136
                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticeae; Hordeum
                                                                                  2 GGRLAYRLLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding;
SEQUENCE 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALEU_HORVU
ID ALEU_HORVU
                                                                                                                                                                                                                                 Y4ZB_RHISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
```

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PapAIN.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_HIS; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
PROFENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                     mitted (WAR-1987) to the EMBL/GenBank/DDBJ databases.
CATALTIC ACTIVITY: HYDROLYSIS OF PROTEINS; ACTS ALSO AS AN
AMINOPEPTIDASE ON PEPTIDE SUBSTRATES WITH FREE N-TERMINI.
SUBCELLULAR LOCATION: VACUOLE-LIKE SUBCELLULAR COMPARTMENT.
INDUCTION: ALEURAIN IS SYNTHESIZED BY THE ALEURONE CELLS
STIMULATED BY GIBBERELLIC OR ABSCISIC ACID.
STMILLARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. ..) (POTENTIAL).
N'LINKED (GLCNAC. ..) (POTENTIAL).
Rogers J.C., Dean D., Heck G.R.; "Aleurain: a barley thiol protease closely related to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A70CCD4A843A1686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIOL PROTEASE ALEURAIN
                                                                           Proc. Natl. Acad. Sci. U.S.A. 82:6512-6516(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 40, Last annotation update)
BITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. NO. 10;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X05167; CAA28804.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                 Rogers J.C.;
Submitted (MAR-1987) to
-!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | |||:| |:
56 RHALRFARFAVRYGK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 RLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
' has 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P07711; 1CJL.
MEROPS; C01.041; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCOSE INHIBITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A25492; KHBH
                                                   cathepsin H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIDA PSEPU
P25756;
                                                                                                                            REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
GIDA_PSEPU
ID GISAP
AC P25756
DT 01-MAX
DT 20-MAG
DE GLUCOS
GN GIDA.
OS PSEUDO
OC BACTER
ON NCBLT
RN [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
RRARRER RRARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
```

ŏ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                           Ogasawara N., Yoshikawa H.;
"Genes and their organization in the replication origin region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N PYROPHOSPHATE + DNA(N).
SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, THE CORE DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA, PSI, AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERAGE ALSO EXHIBITS 3' TO 5' EXONOCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99246387;
MEDLINE=9246387;
Huang V.P., Ito J.; Pubmed=10229580;
"DNA polymerase C of the thermophilic bacterium Thermus aquaticus: classification and phylogenetic analysis of the family C DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus/Deinococcus group; Thermus group; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 39; DB 1; Length 630;
40.0%; Pred. No. 26;
Live 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Evol. 48:756-769(1999).
-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL., 0.101223; BWPSAR, 1011229; BYR002218; GIDA. 1014erPro; IPR002218; GIDA. 1014erDro; IPR001378; GIDA; 1. 1015erDro; PS001378; GIDA; 1. 1015erDro; PS01280; GIDA_1; 1. 1015erDro; PS01281; GIDA_2; PS01281; GIDA_2; GIDA_2; GIDA_2; GIDA_2; GIDA_2; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE III ALPHA SUBUNIT (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1220 AA.
                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: BELONGS TO THE GIDA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GGRAGDPPSIALAHRMRELPLRVGR 196
                                                                       MEDLINE=92204018; PubMed=1552862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGR-----LAYRLLRFAIRVGR 18
                                                                                                                                                                                   bacterial chromosome.";
Mol. Microbiol. 6:629-634(1992).
-!- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X62540; CAA44419.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 10; Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Thermi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DP3A_THEAQ
Q9XDH5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DP3A_THEAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
```

Pred. No. 9.8;

53.3%;

Best Local Similarity

Wed Feb 13 07:51:51 2002

```
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Editing of rps3/rpl16 transcripts creates a premature truncation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion.

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Epermatophyta: Magnoliophyta; eudicotyledons: core eudicots: Asteridae; euasterids I; Solanales: Solanaceae: Petunia.

NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Curr. Genet. 23:472-476(1993).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93306753; Pubmed-8319305;
Sutton C.A., Conklin P.L., Pruitt K.D., Calfee A.J., Cobb A.G.,
Hanson M.R.;
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 1220;
Pred. No. 50;
4; Mismatches 6; Indels
                                                                                                                      EMBL; AF062920; AAD44403.1; -.
InterPor; IPR002309; tRNA-synt_2.
InterPor; IPR003141; PHP_N.
IPR03141; PHP_N.
IPPRam; PF01336; tRNA_anti; 1.
Pfam; PF01336; tRNA_anti; 1.
SMART; SM00481; POLIIIAc; 1.
Transferase; DNA-directed DNA polymerase; DNA replication.
SEQUENCE 1220 AA; 137389 WW; 64EC8BOCE1F44A2B CRC64;
                                                       Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; FOURTH, Mitochondrion.
Ribosomal protein; Mitochondrion.
1859 MW; 79735698EE41B56A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-1993 (Rel. 27, Created)
01-007-1993 (Rel. 27, Last sequence update)
01-007-1993 (Rel. 27, Last annotation update)
MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mendel; 2155; PEThy;rpl16;1.
InterPro; IPR000114; Ribosomal_L16.
Pfam; PF00252; Ribosomal_L16; 1.
PRNSTS; PR00066; RIBOSOMALL16.
PROSITE; PS00586; RIBOSOMAL_L16_1: 1.
PROSITE; PS00701; RIBOSOMAL_L16_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the rpli6 open reading frame."; Curr. Genet, 23:472-476(1993).
                                                                                                                                                                                                                                                                                                                  43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X67028; CAA47422.1; -.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 41.2%,
                                                                                                                                                                                                                                                                                                                                                                                                                1 :: || : || : || 288 GDKMVYRIPRFPLPEGR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Petunia hybrida (Petunia).
                                                                                                                                                                                                                                                                                                                                                                                         2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RM16_PETHY
Q04715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRPL16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcphyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ye F., Bernhardt J., Abel W.O.; "Genes for ribosomal proteins S3, L16, L5 and S14 are clustered in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the mitochondrial genome of Brassica napus L.";
Curr. Genet. 24:323-329(1993).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: BELONGS TO THE LIGP FAMILY OF RIBOSOMAL PROTEINS.
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19801 MW; DE74EE769DCCEC07 CRC64;
   .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                               RMI6_BRANA STANDARD; PRT; 177 AA. P49389; Q96014; 01-FEB-1996 (Rel. 33, Created) 10-FEB-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 12, 2002, 12:39:49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mendel, 7482; BRAna, rpl16;1.
InterPro; IPR000114; Ribosomal_L16.
Pfam; PR00252; Ribosomal_L16; 1.
PRINTS; PR00060; RIBOSOMALL16.
PROSITE: PS00586; RIBOSOMALL16_1; 1.
PROSITE: PS00701; RIBOSOMALL16_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=:94073988; PubMed=8252643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.78;
53.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63653; CAA45189.1; -.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                  15
                                                                                                            | |||:|| : | |
RAGRLSYRAIEAARR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLAYRLLRFAIR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape).
                                                                  1 RGGRLAYRLLRFAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |||:|| : | |
71 RAGRLSYRAIEAARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S36914; S36914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Job time: 802 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Leaf;
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                              qq
                                                                                                                                                                                                                                                                                                          SO WERN WAY OF COLOR OF THE WAY OF THE COLOR OF THE COLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
4.5
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2000
```

- protein search, using sw model OM protein

February 12, 2002, 12:34:36; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec Run on:

1 RGGRLAYRLLRFAIRVGR 18 US-09-485-571-19 89 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result No.	Score	Query Match	Length	DB		Description
П	52	58.4	149	7	S57607	protegrin 1 precur
7		57.3	14	~	857609	Ŋ
ю	48	53.9	147	~	0060NC	~
4	45	20.6		~	A53895	protegrin 3 precur
S	45	50.6		7	C83023	oxic
9	44	49.4	1408	7	н69068	cell surface glyco
7	42	47.2	219	7	C69439	fermen
80	42	47.2	236	7	D75587	hypothetical prote
6	42	47.2	664	7	D83231	
10	42	47.2	619	7	A83488	hypothetical prote
11	41	46.1	447	7	T35824	ъ
12	41	46.1	637	7	E70887	probable fadD32 pr
13	40	44.9	207	<del>, ,</del>	одінвс	hypothetical prote
14	40	44.9		Н	JQ1174	
15	40	44.9		-	806869	-
16	40	44.9	334	7	S77413	_
17	40	44.9	169	7	B83307	17
18	39	43.8	198	7	D75082	phosphate abc tran
19	39	•	298	~	H70884	probable tRNA modi
20	39	•	361	-	кнвн	aleurain (EC 3.4.2
21	39	•	372	7	T24392	
22	39	٠	630	-	BWPSAP	gidA protein - Pse
23	39	43.8	861	~	S77086	
24	38	42.7	144	7	S43766	0
25	38	42.7	147	7	F75013	hypothetical prote
56	38	42.7	155	7	S32194	
	38	42.7	165	7	B71138	hypothetical prote
28	38	42.7	177	7	S36914	ribosomal protein
58	38	42.7	185	-	R5ZM6M	ribosomal protein

probable ribosomal probable phosphogl	cobyric acid synth hypothetical prote	tRNA delta(2)-1sop probable nhoA prot	cysteine proteinas probable nuclear p	nucleoporin homolo hypothetical prote	probable integral	poly(A) polymerase	hypothetical prote	probable large gly	inositol 1,4,5-tri
T03233 F71329	A86763 H70523	B82334 D70605	S59598 T39846	T43197 T23131	T35165 E72515	S75598	T34061	T36105	T31431
7 7	77	~ ~	~ ~	77 77	00	7	~	~	7
185	261 302	315	360 403	434	705	942	1394	1772	2783
42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7	42.7
38	38	8 8	80 80	80 80	80 80	80	8:	8:	<b>8</b> 8
0.1	33	4 N	9 /	338	0.	10	9	44	ιn

## ALIGNMENTS

```
protegrin 1 precursor - pig
N;Alternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (30-1995 #text_change 16-Jul-1999
C;Accession: S66284; S45712; S56820; S34585; S37607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1955
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835
A;Residues: [1-149 < 2HA>
A;Residues: [1-149 < 2HA>
A;Residues: [1-149 < 2HA>
A;Residues: [1-149 < 2HA>
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: [1-149 < 2HA>
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: [1-149 < 2HA>
A;Title: Dimerce: GB:X/9868; NID:9603035; PIDN:CAA56251.1; PID:9603036
A;Accession: S45712
A;Molecule type: mRNA
A;Residues: [1-149 < 2HA>
A;Cross-references: GB:X/9868; NID:93387466
A;Reference number: S36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: protein
A; Residues: 131-148 cMIR>
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort
A; Reference number: S34585; MUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Introns: 66/3; 102/3; 126/3
C; Superfamily: cathelin; cystatin homology
C; Superfamily: cathelin; cystatin homology
C; Superfamily: cathelin; cystatin predicted <SIG>
C; Superfamily: signal sequence #status predicted <SIG>
C; 1-29/Domain: systatin homology <CYS>
F; 20-1129/Domain: propeptide #status predicted <PRO>
F; 31-3148/Product: protegrin 1 #status experimental <WAT>
F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form from follow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.4%; Score 52; DB 2; Length 149; 61.1%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 131-148 <KOK>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 11; Conserv
```

ö

Gaps ; 0

6; Indels

1; Mismatches

11; Conservative

Gaps

.; 0

οy

```
C; Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;131-146/Product: protegrin 2 #status experimental <MAT>
F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-149 < Lab.
A; Residues: 1-149 < Lab.
A; Residues: 1-149 < Lab.
A; Cross-references: EMBL: X84095; NID:9887644; PIDN:CAA58891.1; PID:9887645
R; Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID:94283613
A; Reference number: S45712; MUID:94283613
A; Reference number: S4895
A; Residues: 1-149 < Lab.
A; Residues: 1-140 < Lab.
A; Residues: 140 < Lab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;30-130/Domain: propeptide #status predicted <PRO>F;131-148/Product: protegrin 3 #status experimental <NAT>F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protegrin 3 precursor - pig
NyAlternate names: neutrophil peptide 2
C.Species: Sus scrofa demestica (domestic pig)
C.Species: Sus scrofa demestica (domestic pig)
C.Species: Ol-Dec-1995 #sequence_revision Ol-Dec-1995 #text_change 16-Jul-1999
C.Accession: S66288; AS1895; S34587; S36821; S57608
F.Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A.Filtle: The structure of porcine protegrin genes.
A.Reference number: S66283; MUID:95354835
                                                                                                                                                                                                                                                                Ouery Match 53.9%; Score 48; DB 2; Length 147; Best Local Similarity 64.7%; Pred. No. 0.66; Matches 11; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 45; DB 2; Length 149; 55.6%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 RGGRLCYCRRFFCICVG 147
                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLAYRLLRFAIRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Sim
Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                           A; McLecule type: mRNA
A; Residues: 1-147 <STO>
A; Acrossiou. Size.
A; Acrossiou.
A; Residues: 1-147 <STO
A; Crossiou.
A; Residues: 1-147 <STO
A; Crossiou.
A; Residues: 1-147 <STO
A; Crossiou.
A; Residues: 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence hype: protein
A; Reference number: S36820; MUID: 93387466
A; Residues: 131-146 <MIR>
A; Residues: 131-146 <MIR>
A; Residues: 131-146 <MIR>
A; Rosidues: 131-146 <MIR>
A; Rosidues: 131-146 <MIR>
A; Reference number: S34585; MUID: 93327946
A; Reference number: S34585; MUID: 93327946
A; Recession: S34586
A; Molecule type: protein
A; Residues: 131-146 <KOK>
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  William 2 precursor - pig
William 2 precursor - pig
William 2 precursor - pig
William 2 precursor ineutrophil peptide 3
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: Sus scrofa domestica (domestic pig)
CiSpecies: 19-May-1994 #sequence_revision 19-May-1994 #text_change 16-Jul-1999
CiSpecies: NOWOWO, S36822; S34586
Ristorici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1363-1368, 1993
AiTitle A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a Affectence number: JNO900; MUID:94071898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 2; Length 149; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.3%;
61.1%;
                                                         RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 61.1 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                      g
```

ò qq 0

Gaps

ö

*

```
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; "hou, L.: Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arc A;Reference number: A69250; MulD:98049343
A;Reference number: A69250; MulD:98049343
A;Reference type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-219 <a href="https://doi.org/10.1007/bit.blay.nucleic">kl.KE></a>
A;Residues: 1-219 <a href="https://doi.org/10.1007/bit.blay.nucleic">kl.KE></a>
A;Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89729.1; PID:g26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12511.1; PID:g64
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: D83231
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 559-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic FA;Reference number: A82950; MuID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molccule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06693.1; GSPDB:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C.Accession: D75587
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, I.K.; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, I.K.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.; Tatle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R: A; Reference number: A75250; MUID:20036896
A.; Reference number: A75250; MUID:20036896
A.; Residues: preliminary
A; Residues: 1-236 CWHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein PA3305 [imported] - Pseudomonas aeruginosa (strain PA01) C; Species: Pseudomonas aeruginosa C; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2
Pred. No. 9.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB 2
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.28;
64.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.28;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.2
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.2
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGRLAYRLLRFAIRVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 RGGXLSYRL--FAV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLAYRLLRFAI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: DRA0327
A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6.
169068
cell surface glycoprotein (s-layer protein) related protein - Methanobacterium thermoaut c.Species: Methanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum
C.Species: Methanobacterium thermoautotrophicum thermoautotrophicum thermoautotrophicum thermoautotrophicum Delta H.; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qui, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Reference number: A69000; MUID:98037514
A; Accession: H69068
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                 C;Accession: C83023
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. L.Y, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337
A;Accession: C83023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-648 <STO>
A; Cross-references: GB: AE004911; GB: AE004091; NID: 99951264; PIDN: AAG08371.1; GSPDB: GN001
A; Experimental source: strain PAO1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: Î-1408 <WTH>
A;Cross-references: GB:AE000911; GB:AE000666; NID:q2622623; PIDN:AAB85988.1; PID:q262263
A;Experimental source: strain Delta H
                                                                                                                                                           probable oxidoreductase PA4986 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sugar fermentation stimulation protein (sfsA) homolog - Archaeoglobus fulgidus C;Specides; Archaeoglobus fulgidus C;Specides (5-Dec-1997) #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000 C;Accession: C69439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: PA4986
C;Superfamily: Wethylophilus methylotrophus W3Al trimethylamine dehydrogenase
                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2;
Pred. No. 26;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2;
Pred. No. 8.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRL----AYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.6%;
Best Local Similarity 50.0%;
Matches 11; Conservative
         131 RGGGLCYCRRFFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| || :| :| ||
1318 GAKLGYRTFKFTLKPGR 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: MTH1513
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C69439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

**د** ن

2

```
Accession: B70887

B.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordo; C. Accession: B70887

B.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordo; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroydl Nature 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A.Ritle: Deciphering the biology of Mycobacterium tuberculosis from the complete gene A.Reference number: A70500; MUID:98295987

A.Status: preliminary; nucleic acid sequence not shown; translation not shown

A.Residues: 1-637 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL022076; GB:AL123456; NID:93256026; PIDN:CAA17865.1; PID:929
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
QQIHBC
hypothetical protein (gene N internal ORF) - bovine coronavirus (strain Mebus)
N:Alternate names: IORF protein
C:Species: bovine coronavirus
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
C:Accession: C26347
R:Lapps, W.: Hogue, B.G.; Brian, D.A.
Virology 157, 47-57, 1987
A:Title: Sequence analysis of the bovine coronavirus nucleocapsid and matrix protein
A:Reference number: A94357; MUID:87151119
A:Rocession: C26347
A:Molecule type: genomic RNA
A:Residues: 1-207 <Lapp.
A:Cross-references: GB:Mi6620; NID:9323354; PIDN:AAA66398.1; PID:9807593
C:Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein (gene N internal ORF) - turkey coronavirus
hypothetical protein (gene N internal ORF) - turkey coronavirus
N'Alternate names: IORF protein
C'Species: turkey coronavirus
C'Species: turkey coronavirus
C'Species: turkey coronavirus
C'Accession: 10-104
R'Secession: 10-104
R'Secession: 10-104
R'Secession: 10-1059-1666, 1991
A'Title: Sequence analysis of the turkey enteric coronavirus nucleocapsid and membran
A'Reference number: JQ1172; MUID:91311418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                         C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Gene: fadD32
C/Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
F/81-614/Domain: acetate--CoA ligase homology <ACL>
                                                                                               probable fadD32 protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1
Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.18;
61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.9%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :|| |:||
153 RLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLAYRLLRFA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RLAYRLLRFAIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                RESULT 10
A83488
hypothetical protein PA1270 [imported] - Pseudomonas aeruginosa (strain PAO1)
C; Species: Pseudomonas aeruginosa
C; Species: Date: 15-Sep-2000
B; Accession: A83488
A; Ribero A; Ribero A; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
Cory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathon A; Reference number: A82950; MuID:20437337
A; Accession: A83488
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-679 <STO>
A;Coss.references: GB:AE004556; GB:AE004091; NID:g9947194; PIDN:AAG04659.1; GSPDB:GN001
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C;Accession: T35824
R.Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, February 1999
A;Reference number: Z21589
A;Reference number: Z21589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-447 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AL035569; PIDN:CAB37584.1; GSPDB:GN0070; SCOEDB:SC8D9.20c
                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                            Length 664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 2; Length 447;
Pred. No. 29;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 679;
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
2:
                                                                                                                                         .,
'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                 Score 42; DB 2
Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2
Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SCBD9, 20c
C; Superfamily: hypothetical protein b0837
A; Experimental source: strain PAO1 C; Genetics:
A; Gene: PA3305
                                                                                                                               47.28;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.2%;
58.8%;
                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                |||:| |||| |
| 536 GGRMADRLLRLA 547
                                                                                                                                                                                                                                2 GGRLAYRLLRFA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: PA1270
                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
```

ó

Gaps

; 0

1 RGGRLAYRLLRFAIR 15 

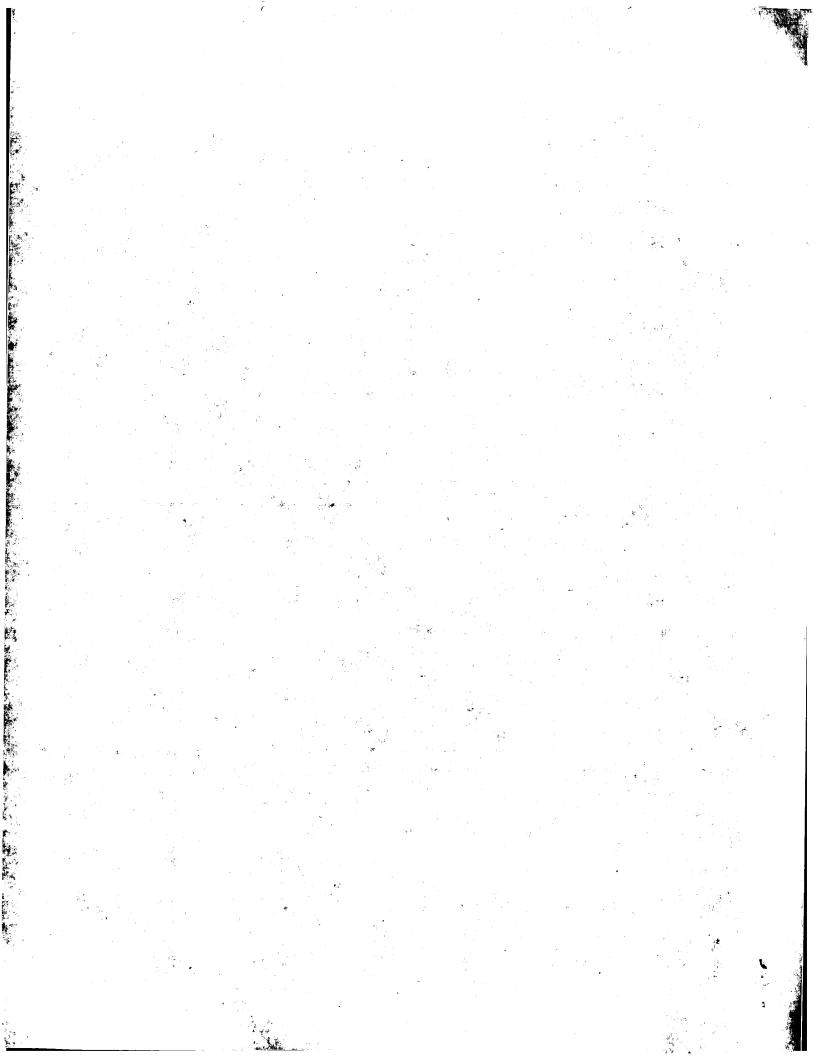
ŏ QQ

16

·

```
RESULT 15
S06869
hypothetical protein (gene N internal ORF) - bowine coronavirus (strain F15)
N;Alternate names: IORF protein
C;Species: bowine coronavirus
C;Species: bowine coronavirus
C;Species: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Jul-1999
C;Accession: S06869
R;Cruciere, C.: Laporte, J.
Ann. Inst. Pasteur Virol. 139, 123-138, 1988
A;Title: Sequence and analysis of bovine enteritic coronavirus (F15) genome. I. - Sequent A;Reference number: S06399; MUID:89087718
A;Recession: S06869
A;Molecule type: genomic RNA
A;Residues: 1-207 <CRD
A;Rote: the source 1s designated as bovine enteritic coronavirus
C;Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C;Superfamily: coronavirus gene N internal ORF
A; Accession: JQ1174
A; Molecule type: genomic RNA
A; Residues: 1-207 < Vers
A; Experimental source: strain Minnesota
C; Comment: The gene encoding this protein is located within the nucleocapsid (N) gene.
C; Superfamily: coronavirus gene N internal ORF
                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

44.9%; Score 40; DB 1; Length 207;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                          Score 40; DB 1; Length 207;
Pred. No. 21;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February 12, 2002, 12:34:37 Job time: 555 sec
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             || :|| |:::||
153 RLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || :|| |:::||
153 RLGFRLARYSLRV 165
                                                                                                                                                                                                                                                                                                                                                           4 RLAYRLLRFAIRV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RLAYRLLRFAIRV 16
                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```



123, App 1, Appl 1, Appl 11, Appl 11, Appl 13, Appl 37, Appl 37, Appl 10, Appl 10, Appl 10, Appl 10, Appl 26, Appl 26, Appl 27, Appl 27, Appl 26, Appl 27, Appl 27, Appl 28, Appl 28, Appl 20, A

Sequence 2 Sequence 1 Sequence 3 Sequence 3 Sequence 3 Sequence 2 Sequence 2

US-08-499-523-37 US-08-752-852A-123 US-08-752-853-12 US-08-752-853-1 US-08-94-294-1 US-09-128-345-16 US-09-128-345-16 US-09-128-345-16 US-09-128-345-33 US-09-128-345-10 US-09-128-345-10 US-09-128-345-2 US-09-128-345-2 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-09-128-345-10 US-08-128-345-10 US-08-128-345-10 US-08-128-345-10 US-08-128-345-10 US-08-128-345-10 US-08-128-345-10 US-08-128-345-10

Sequence

ALIGNMENTS

Sequence 1 Sequence 1 Sequence 1

```
Sequence 230, Application US/08752852A
Patent No. 5994306
CENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Silvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: COTUZZI, LAURA A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: unknown TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-230
COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-752-85:2A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ν
 STATE:
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 230, App
Sequence 63, Appl
Sequence 67, Appl
                                                                                                                                         (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                   February 12, 2002, 12:32:22; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-63
US-09-128-345-63
US-08-499-523-54
US-09-128-345-54
US-09-128-345-54
US-09-128-345-59
US-08-499-523-58
US-08-499-523-58
US-08-499-53-58
US-09-128-345-58
US-09-128-345-58
US-09-128-345-58
US-08-499-523-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-752-852A-128
US-09-128-345-57
US-09-128-345-62
US-08-095-769A-1
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-182-483A-2
US-08-182-483A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-499-523-33
                                                                                                                                                                                                                                                                                                             212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                          RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                 US-09-485-571-19
89
                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                        Perfect score:
                                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB
Maximum DB
                                                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
```

the Americas

```
; LOCATION: group(6, 8, 13, 15); OTHER INFORMATION: /note= "x is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.9%; Score 56; DB 1; Length 18; 61.1%; Pred. No. 0.0033; -ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURSHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 90-4030
INFORMATION OF SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                              TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: WORKLSON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: PENNIE & EDMONDS LLP
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG. SYLVA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
                                   KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-63; Sequence 63, Application US/09128345; Sequence 63, Application US/09128345; Detent No. 6159936; GENERAL INFORMATION:
                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: PSTATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρp
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
Score 58; DB 2; Length 18;
Pred. No. 0.0015;
......... 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAME/KEY: Modified-site
CCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.9%; Score 56; DB 1; Length 18; 61.1%; Pred. No. 0.0033; 1ve 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION UNBER: 29,959
REFERENCE/DOCKET NUBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORRYAKOV, VLADIMIR N.
TILLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       Sequence 63, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence 67, Application US/08499523
; Sequence 67, Application US/08499523
; Patent No. 5804558
; GENREAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
; APPLICANT: HARWIG, SYLVIA S.L.
                      65.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                          1 RGGRLAYRLLRFAIRVGR 18
               Query Match 65.2°
Best Local Similarity 66.7°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITA.
STATE: DC
COUNTRY: USA
TO: 20006-1812
TO: TOO ADABLE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                               RESULT 2
US-08-499-523-63
                                                                                                      ò
                                                                                                                                            QQ
```

g

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                   8, 13, 15)
/note= "X is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: group(6, 15)
OTHEE INFORMATION: /note= "X is a hydrophobic, a
OTHEE INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.8%; Score 55; DB 1; Length 18; 66.7%; Pred. No. 0.0048; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: UGA

ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: TBM PC COMPATIBLE
OMPUTER: TBM PC COMPATIBLE
OMPUTER: TBM PC COMPATIBLE
OFFRANTING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN RC-BOS/MS-DOS
SOFFWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
ATTON NUMBER: US/08/499,523
FILING DATE: US/08/499
FILING DATE: US/08/499
FILING DATE: US/08/499
FILING DATE: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                     Score 56; DB 4;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEHRER, ROBERT I.
PAPPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-499-523-54
Sequence 54, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     62.9%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond 8..13
                                                    NAME/KEY: Modified-site
| LOCATION: group(6, 8, 13
| OTHER INFORMATION: /note
| GOTHER INFORMATION: small
| US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  Query Match 62.9
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 Penr
CITY: Washington
STATE: DC
TOPOLCGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roPoloGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-499-523-54
                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 56; DB 4; Length 18;
Pred. No. 0.0033;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAIL.

COUNTRY: USA
2IP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NATA:
HILING DATE: 03-AUG-1998
FILING DATE: 03-AUG-1998
                                                                         ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, Laura, A.
REGISTRATION NUMBER: 30,72
REFERENCE/DOCKET NUMBER: 867-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFA: (212) 869-9741
TELEFA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
GRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
CLASSIFICATION: 514
NAME: CCTUZZI, LBUTG, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 67, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: FORRYAGOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9000
TELEFAX: (212) 869-9741
TELEX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 anino acids
TYPE: anino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: Modified-site
LOCATION: group(6, 8, 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 62.9
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
                              FILING DATE: 03 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

δ Ω

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: group(6, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.8%; Score 55; DB 4; Length 18; 66.7%; Pred. No. 0.0048; Live 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura, A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-128-345-59
Sequence 59, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, STLVIA S.L.
APPLICANT: HARMIG, STLVIA S.L.
APPLICANT: HARMIG, STLVIA S.L.
APPLICANT: CORRESPONDERS: 76
CORRESPONDENCE: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                 NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  PROTEGRINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLXYCRRRFCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55, DB 1; Length 18;
Pred. No. 0.0048;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: U.C.
COMPUTER: U.C.
COMPUTER: TLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: TLOPPY disk
COMPUTER: Date: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPPOLOGY: linear
RAMPF/KEY: Disulfide-bond
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, SYLVAR S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                       Sequence 59, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-09-128-345-54
; Sequence 54, Application US/09128345
; Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.8%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                     1 RGGRLXYCRRFCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Disulfide-bond LOCATION: 6..15
1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site LOCATION: group(8, 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLCYXRRFFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                  STREET: Zooo
                                                                                                                               US-08-499-523-59
```

q

ö

Gaps

Gaps ö

```
LOCATION: group(6, 15);

OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-52:-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58, Application US/08499523
Fatent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
CORRESPONDENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCES: 76
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN STATEM.

SOFTWARE PATENTIN BATA:

APPLICATION NUMBER: US/08/499,523

FILING ADTE: O'-JUL-1995

CLASSIFICATION: 514

ATTONREY/AGENT INFORMATION:

NAME: MURASHIGE, RATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 1;
Pred. No. 0.007;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.78;
61.18;
                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site LOCATION: group(6, 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLXYCRRRFCVXVGR 18
                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.19
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
      INFORMATICN FOR SEQ ID NO:
                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: V
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "X is a hydrophobic, a small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-499-523-53
Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application US/08499523
Sequence 53, Application Sequence 53, Applicant Lehrer, Robert I.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LARNIG, SYLVIA S.L.
APPLICANT: RORRYAKO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORENSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
• APPLICATION NUMBER: US/09/128,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 4;
Pred. No. 0.0048;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/ACENT INFORMATION:
NAME: WORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
                                                                                                                                                                                                                                                    8067-0054-999
                                         оз 128,345
03-AUG-1998
N. F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFCATION: 514
                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INNORMATION:
NAME: COCUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (712) 790-9090
TELEFAX: (212) 869-9741
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site LOCATION: group(8, 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLCYXRRFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: JOOP-128-345-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Zuv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
```

g õ

```
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                              Sequence 53, Application US/09128345; Patent No. 615936; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HONDININ: PROTEGRINS; UNMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-128-345-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                            ö
                                                                                                                          ;
      small, or a large polar amino acid"
                                                                                    Length 18;
                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                Score 54; DB 1;
Pred. No. 0.007;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 2;
Pred. No. 0.007;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30,742
FR: 8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
FILING AND NUMBER:
FILING AND NUMBER:
                                                                                                                                                                                                                                                                                        Sequence 233, Application US/08752852A; Patent No. 5994306
GEBREAL INFORMATION:
APPLICANT: Chang, Conway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEFAX: 212-869-9741
                                                                            Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: unknown
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-752-852A-233
; OTHER INFORMATION: US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                  RESULT 12
US-08-752-852A-233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                        QQ
                                                                                                                                                          á
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: group(6, 15); OTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-09-128-345-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54; DB 4; Length 18;
Pred. No. 0.007;
1; Mismatches 6; Indels
                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, STIVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                           (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: group(6, 15)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.7
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
```

ó

Gaps

; 0

ò g 13

RESULT 7

11; Conservative

Best Local Similarity

Matches

```
FEATURE:
                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: group(8,13); CTHER INFORMATION: /note= "X is a hydrophobic, a cother information: small, or a large polar amino acid" US-09-128-345-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 4; Length 18;
Pred. No. 0.007;
1; Mismatches 6; Indels
                 COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION 1047A:
ATTORNEY/AGENT INVERMATION:
NAME: COLUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3067-0054-999
TELECAMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRANDEDNESS: single
TOPOLOGEY: linear
NAME/KEY: Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: RORRYAKOV, VLADIMIR N.
ITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSEITCATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Disulfide-bond LOCATION: 6..15 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLAYRLLRFAIRVGR 18
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-499-523-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                    LOCATION: group(6, 15);
COTHER INFORMATION: /note= "X is a hydrophobic, a
COTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-57
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 1;
Pred. No. 0.01;
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959
REPERENGE/COCKET NUMBER: 2000-0540.24
TELECHMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
SEQUENCE CHARACTERISTICS:
LENGTH: 18 anino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 12, 2002, 12:32:22 Job time: 450 sec
                                                                                                                                                                                                                                                                                                                                                                                                                          59.6%;
61.1%;
                                                                                                                                                                                                                                                Disulfide-bond 8.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGGRLXYCRPRFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
```

```
February 12, 2002, 12:30:30; Search time 242.57 Seconds (without alignments) 5.497 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                              522463
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                           1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                              US-09-485-571-19
89
                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_1101:*
                                                                                                                                                                                                       Perfect score:
Sequence:
                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB :
Maximum DB :
                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                               Run on:
```

**SIDSB/gcgdata/geneseqp/AA1980.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1981.DAT:*

**SIDSB/gcgdata/geneseqp/AA1980.DAT:*

**SIDSB/gcgdata/geneseqp/AA1980.DAT:*

**SIDSB/gcgdata/geneseqp/geneseqp/AA1980.DAT:*

**SIDSB/gcgdata/geneseqp/geneseqp/AA1990.DAT:*

**SIDSB/gcgdata/geneseqp/geneseqp/AA1990.DAT:*

**SIDSB/gcgdata/geneseqp/geneseqp/AA1990.DAT:*

**SIDSB/gcgdata/geneseqp/geneseqp/AA1991.DAT:*

**SIDSB/gcgdata/geneseqf/geneseqp/AA1991.DAT:*

**SIDSB/gcgdata/geneseqf 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

on.	Description	Protegrin derivati	Cationic, antimicr	Cationic, antimicr	Antimicrobial prot	Cationic, antimicr	Cationic, antimicr	Protegrin derivati	Peptide which may	Cationic, antimicr	Peptide which may	Antimicrobial prot
SUMMAKIES	10	AAW99406	AAW18151	AAW18152	AAW36429	AAW09084	AAW09085	AAW99403	AAY93616	AAW18153	AAY93669	AAW36432
		20	18	18	18	18	18	20	21	18	21	18
	* Duery Match Length DB	18	18	18	18	18	18	18	18	18	18	18
•	* Query Match	100.0	66.3	66.3	65.2	65.2	65.2	65.2	65.2	64.0	64.0	60.7
	Score	89	29	59	58	58	58	58	28	57	57	24
	Result No.	7	7	m	4	ഗ	9	7	80	σ	10	11

Protegrin derivati Cationic, antimicr Cationic, antimicr Cationic, antimicr Procegrin p6-1. S Protegrin p6-1. S Protegrin p6-1. S Protegrin p6-1. S Antimicrobial prot Antimicrobial prot Antimicrobial prot Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Protegrin peptide p Protegrin peptide p Protegrin peptide p Protegrin peptide p Antimicrobial prot Cationic, antimicr Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide Protegrin peptide	-sheet; secondary structure; .tumour agent; antiviral; assive transport; cytoplasm; .M;	1
20 AAM99408 18 AAW18147 18 AAW18148 16 AAR78151 16 AAR78751 18 AAW36322 18 AAW36322 18 AAW36323 18 AAW36353 18 AAW36353 19 AAW36559 21 AAW36559 22 AAW36559 21 AAY91757 22 AAW36559 13 AAY91757 22 AAB91843 22 AAB91843 23 AAB91843 24 AAW36329 18 AAW36329 21 AAY911030 21 AAY911030 21 AAY93174 21 AAY93612	e; 18 AA.  ide SM2187.  e antibiotic; beta-seriboszyme; antitutic; cell membrane; partier.  jer.  57.  97.  peptides lacking ditive agents into cel.	
559.6 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 560.7 56	lard; pept (first ent lvative pe prin; pept	
2	T 1 AMW99406 s AAW99406; D8-JUN-199 Protegrin Linear; pr Linear; pr Linear; pr Cliss phide AW9907728- AW9907728- CS-AUG-199 D6-AUG-199 CSYNT-) SY Calas B, API; 1999- Derivative	
	A A B B B B B B B B B B B B B B B B B B	

```
ó
                                                                                                              This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The newell derivatives are linear and lack the agents to an organism, e.g. therappeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammallan cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a basic anino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid or proline; A17 may be absent or a basic, neutral/polar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin PC-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 89; DB 20; 100.0%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW18151 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 64; 106pp; English.
Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0499523
95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9637508-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW18151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW18151
            \overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{A}}{\vee}\overset{\mathsf{
```

```
hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of act least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysteine bridge. This peptide is in snake form where all the cysteine residues are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gramnegative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neissenia gonorrhoace. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain xxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin PC-56.
                                                                                                                                                                                                                                                                                                                                                                                                                         66.3%; Score 59; DB 18; Length 18; 66.7%; Pred. No. 0.0032; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW18152 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0451832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||: |||: |||
| rggrlawarrrfavavgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9637508-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW18152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW18152
```

us-09-485-571-19.rag

```
cc where Al = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A5, A1 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino a disulphide bond to give a cesterified forms, all of which may contain a disulphide bond to give a cystene brigher. This peptide is in smake form where all the cysteline brights are replaced by a hydrophobic, small or large polar amino acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-resistance to sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis; Treponema pallidum and Naisseria gonorrhoae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain anti-biotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; hrotozoa; virus; reservation; retrovirus; hrophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogon; multi-drug resistance; pendicillin resistant Staphylococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59; DB 18; Length 18;
Pred. No. 0.0032;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin peptide (229).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36429 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US18544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW36429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW36429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
        ò
```

```
Gaps
                                                                                                                                                                                        The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-postitive and gram-negative bacteria, yeast, fungl, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including madical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, conneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections,
                                                                                                                                                                                                                                                                                                                                                                                          urinary tract infections, systemic candidiasis and oral mucositis, this biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus penumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/Kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                            New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. \mathrm{H}^2\mathrm{W})
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic, antimicrobial, virus-neutralising protegrin IB-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 58; DB 18; Length 18;
Pred. No. 0.0046;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6..15
/note= "results in bullet form peptide"
                                Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                            Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW09084 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US07594.
                                Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
(REGC ) UNIV CALIFORNIA.
                                                             WPI; 1997-297871/27.
                              Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simil
Matches 12; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAY~1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1996
                              SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW09084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW09084
ολ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

/note= "results in bullet form peptide"

/note= "Amidated"

"Acylated"

/note= 6..15

Disulfide-bond Modified-site

```
The second sequence is a specifically claimed example of a peptide, and the second interests of a specifically claimed example of a peptide, A1-2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where A1 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, neutral/polar or small amino acid; A10 and A11 = a basic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of a least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cysteine bridge. Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbe are useful an animals. The protegrins confer resistance to microbe and infactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food, The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antiblotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                             Lehrer RI;
                                                                                                                                                 (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 65; 106pp; English.
                                                           95US-0451832.
          95US-0499523
                                                                                                                                                                                                                                                                        Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AA;
07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
```

Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food

Kokryakov VN, Lehrer RI;

WPI; 1997-033984/03.

(UYCA-) UNIV CALIFORNIA LOS ANGELES.

95US-0451832. 95US-0499523

26-MAY-1995; 07-JUL-1995;

96WO-US07594.

24-MAY-1996;

WO9637508-A1

28-NOV-1996.

preservatives and in eye care solutions

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                       ó
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin IB-289.
           Score 58; DB 18; Length 18;
Pred. No. 0.0046;
1; Mismatches 5; Indels
                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW09085 standard; peptide; 18 AA.
           65.2%;
66.7%;
                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                    |||||| | |||| ||||
| rggrlcyarrrfavcvqr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1997 (first entry)
                                             Local Similarity 66.7
les 12; Conservative
Query Match
Best Local Si
Matches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW09085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW09085
XX
AC AAW0
XX
DT 11-A
XX
XX
Cati
XW
Cati
XW
Cand
KW
C
```

QQ ò

Location/Qualifiers 1

Key Modified-site

Synthetic.

```
The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

Al-A2-A3-A4-A5-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

where A1 = a basic amino acid; A2 and A14 = a small amino acid; A4 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of a retarlified forms, all of which may contain a disulphide bond to give a cysteline bridge. Peptides of this formula are designated bond to give a cysteline bridge. Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anti-imgal agents in comparation of gram-negative bacteria. The protegrins confer resistance to microbal or viral infection in plants by preventing the growth of a virus or microbe are particularly useful for the treatment of sexually transmitted trachments, Treponema pallidum and Neisseria gonoriboeae. They can also be used in eye care solutions and as preservatives for food. The presence of serum) than certain antibiotics and are non-toxic to the alls of the presence of serum) than certain antibiotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.2%; Score 58; DB 18; Length 18; 66.7%; Pred. No. 0.0046; Live 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protegrin derivative peptide SM1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99403 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 65; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.2
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW99403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
XXXXX
```

4

```
(SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
                                                         Temsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW18153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
AAW18153
   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to consult the concrete active agents including crossing the blood-brain barrier.
               Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 20; Length 18;
Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                            Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                            Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 28; 37pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93616 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.2%;
llarity 61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0015073.
                                                                                                                                                                                                                          98WO-FR01757
                                                                                                                                                                                                                                                              97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-FR02939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                        Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-190034/16.
             Linear; protegrin;
disulphide bridge;
anti-inflammatory;
                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticancer agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200032237-A1
                                                                                                                                               WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                          06-AUG-1998;
                                                                                                                                                                                                                                                                12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1999;
                                                                                                                                                                                       18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-2000
                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                          Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93616
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE TO THE TENT OF THE TENT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, machanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mimmalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                       New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin PC-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 21; Length 18;
Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                                                                                                                             Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW18153 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0499523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
   Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-033984/03.
                                                                 WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
```

comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, methanisms the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide

specification describes a pharmaceutical composition, which

Disclosure; Page 8; 34pp; French.

```
;
0
                                                                                                                                                                                                                                                    Gaps
                   The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                     cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                   Score 57; DB 18; Length 18;
Pred. No. 0.0067;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                      Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                AA.
      Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                             AAY93669 standard; peptide; 18
                                                                                                                                                                                                                                     64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-FR02939
                                                                                                                                                                                                                                                                                                                                                                                                                                                98FR-0015073
                                                                                                                                                                                                                                                                      1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                           Query Match
Best Local Similarity
^^hes 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                    Anticancer agent;
                                                                                                                                                                                                                                                                                                                                                                                                       WO200032237-A1.
                                                                                                                                                                                                                                                                                                                                          25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000
                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                           AAY93669;
                                                                                                                                                                                                                                                                                                                                                                             cancer.
                                                                                                                                                                                                                                                                                                       AAY93669
                                                                                                                                                                                                                                                                                                RESULT
ò
                                                                                                                                                                                                                                                                          Q
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; reterovirus; HV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses
                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                    which may be linked to the anticancer agents of the invention
                                                                                                                                                                                                                                      Score 57; DB 21; Length 18; Pred. No. 0.0067;
                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steinberg DA;
                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial protegrin peptide (232).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                    AAW36432 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                    64.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0752852.
95US-0562346.
                                                                                                                                                                                                                                                                                  1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                Chen J, Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                              Local Similarity 66.7 ies 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-297871/27.
                                                                                                                                                                                                18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa.
                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                             AAW36432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang CC,
                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                          AAW36432
                                                                                                                                                                                                                                                                                                                                             RESULT
οy
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                      The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcres associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biooidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant correspondents (Enterococcus pneumoniae and methicillin resistant Staphylococcus cureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 18; Length 18;
Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protegrin derivative peptide SM2189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                            Claim 23; Page 111; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99408 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9..10
/label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Nva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999
(e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calas B,
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99408;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
This peptide represents a linear derivative of the protegrin family of antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The new derivatives are linear and lack the disulphide bridge. The new derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents the chart of the proteins and conlinear active agents the chart of the productions of the passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
   - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                ö
Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cationic, antimicrobial, virus-neutralising protegrin PC-49.
                                                                                                                                                                                                                                                                                                                                Score 54; DB 20; Length 18;
Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note- "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note- "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amidated"
                                              Claim 7: Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18147 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                              60.78;
61.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0451832.
                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                              1 raarlqyrxxrfqxrvqr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                Ouery Match 60.7
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18147;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW18147
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                              q
```

us-09-485-571-19.rag

Lehrer RI;

Kokryakov VN,

Harwig SSL,

(UYCA-) UNIV CALIFORNIA LOS ANGELES.

95US-0451832

26-MAY-1995;

```
where Al = basic amino acid; A5 and A3 = a small amino acid; A4 = a basic or small amino acid; A7 and A14 = a small amino acid; A6 and A18 = a small amino acid; A7 and A14 = a small amino acid; A7 and A14 = a small amino acid; A9, A7 and A14 = a hydrophobic amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A18 may be absent or a basic, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, hydrophobic or small amino acid. This has a charge of at least +3 and its N-terminal acid; and A18 may be absent or a basic, cesterified forms, all of which may contain a disulphide bond to give a reset is anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbe are useful as anti-bacterial, anti-viral and anti-fungal agents in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                               The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cationic, antimicrobial, virus-neutralising protegrin PC-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.6%; Score 53; DB 18; Length 18; 61.1%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW18148 standard; peptide; 18 AA.
               Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Acylated".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0499523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim:
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW18148;
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
The present supraetice is a special communication of the process of the combinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a

Basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino

acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino

acid; A10 and A11 = a basic, hydrophobic, neutral/polar,

hydrophobic or small amino acid; and A18 may be absent or a basic,

neutral/polar, hydrophobic or small amino acid. This has a charge of

cleast +3 and its N-terminal acylated and/or C-terminal amidated or

sterified forms, all of which may contain a disulphide bond to give a

cysteine bridge. Peptides of this formula are designated protegrins and

sterified forms, all of which may contain a disulphide bond to give a

cysteine bridge. Peptides of this formula are designated protegrins and

are settled an implants by preventing the growth of a virus or microbe

are particularly useful for the treatment of sexually transmitted

Alsoare ransed An wirenormanieme of sexually transmitted

Alsoare ransed An wirenormanieme of sexually ransmitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                               present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                             antimicrobial, virus-neutralising protegrin peptide(s) the treatment of microbial infection, as food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cationic, antimicrobial, virus-neutralising protegrin PC-52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 18; Length 18;
Pred. No. 0.031;
2; Mismatches 5; Indels
                                                                                                                                                                                                  preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW18149 standard; peptide; 18 AA.
                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.6%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLAYRLLRFAIRVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                               antimicrobial,
                                                                                                                                                                                                                                       Claim 6; Page 64; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                      WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                           Cationic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW18149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW18149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-A4-C4y-A3-A10-A11-A12-Cys-A14-Cys-A16-A17-A18)

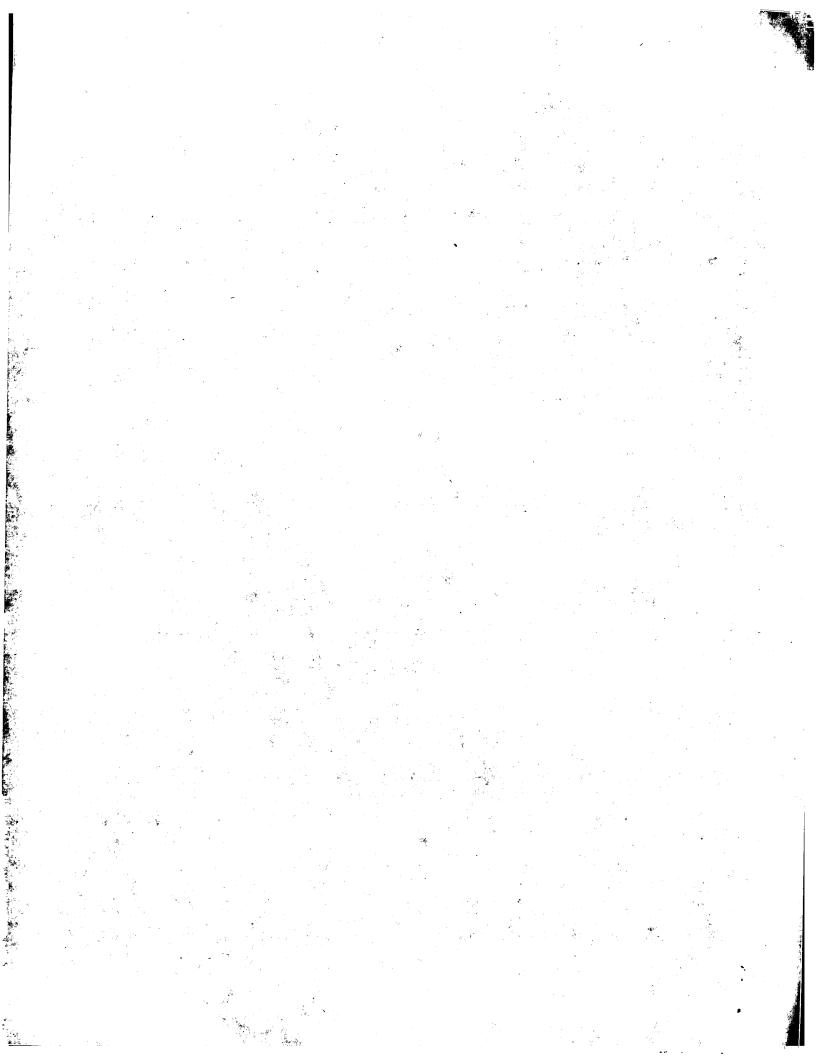
where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar, bydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and instituted or small and and and acidited protection and anti-bacterial, anti-viral and anti-fungal agents in viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are aperticularly useful for the treatment of sexually transmitted alsease caused by microcramisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The the protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antiblodical conditions (e.g. in the presence of serum) than certain antiblodical conditions (e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
/note= "results in kite form peptide"
18
                                                                                                                                                                                                                                                                                                                                                                                             Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                          (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                       /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 64; 106pp; English.
                                                                                                                                                                                                                    96WO-US07594.
                                                                                                                                                                                                                                                                  95US-0499523
95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 AA;
                                           Modified-site
                                                                                                                   WO9637508-A1
                                                                                                                                                                                                                                                                  07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                    24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                             Harwig SSL,
                                                                                                                                                                   28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

Gaps ö Score 53; DB 18; Length 18; Pred. No. 0.031; 5; Indels 2; Mismatches Query Match 59.6%; Best Local Similarity 61.1%; Matches 11; Conservative

ö

1 RGGRLAYRLLRFAIRVGR 18 ò g

Search completed: February 12, 2002, 12:30:30 Job time: 363 sec



```
February 12, 2002, 12:38:35; Search time 232.64 Seconds (without alignments) 11:317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                          473505
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                 473505 segs, 146272329 residues
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                           US-09-485-571-18
89
1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                  Run on:
```

1: Sp_archea:*
2: Sp_barchea:*
3: Sp_tungi:*
4: Sp_human:*
5: Sp_nammal:*
6: Sp_nammal:*
7: Sp_mhc:*
8: Sp_phage:*
10: Sp_phage:*
11: Sp_rodent:*
11: Sp_rodent:*
12: Sp_virus:*
13: Sp_virus:*
14: Sp_unclassified:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_17:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	09vit9 drosophila 09utr5 schizosacch 09utr5 schizosacch 09mcj9 streptococc 064384 bos taurus 064284 streptococc 064284 streptococc 064284 bos taurus 064294 streptococc 064139 bos taurus 064294 streptococc 041718 zea diplope
SUMMARIES	09VIT9 09NFV5 09NFV5 09VIRS 09SXJB0 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS96 09DS983 064294 064294 028139 041718
DB	2000 100 100 100 100 100 100 100 100 100
% Query Match Length DB	1425 1198 1198 518 521 137 1137 1137 1193 515 515 515 515 515 515 515
% Query Match	0.000 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Score	######################################
Result No.	10849398784337110088784337110088784311110088784311110088784311100887843111008878431100887843110088784311008878

	Q9myy8 sus scrota Q92200 emericella O52998 escherichia Q10465 homo sapien
010000000000000000000000000000000000000	46.1 499 6 Q9MYYB 46.1 618 3 Q92200 46.1 800 2 O52998 46.1 7962 4 Q10465
444444444444444444444444444444444444444	41 41 41
01102222222222222222222222222222222222	4 4 4 4 4 4 5 4 5 4 5 4 5

## ALIGNMENTS

us-09-485-571-18.rspt

| || | |:|| ||| | 595 ETGEFRYTEETFSVEV 610

RESULT

1 EGGELSYSEEFFSVSV 16

ò g

```
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.;
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
R. Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Nilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
R. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan G., Zhao Q., Zheng I.,
A. Deng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
Excience 287:2185-2195(2000).
REMBL; AE003663; AAF53826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lagueux M., Perrodou E., Levashina E.A., Capovilla M., Hoffmann J.A.;
"Constitutive expression of a novel complement-like protein in Toll
and Jak gain-of-function mutants of Drosophila.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
FlyBase; FBGn0041180; TepIV.
InterPro; IPR001599; AAM.N.
InterPro; IPR001599; Alpha_2_macroglobin.
Pfam; PF00207; A2M; 1.
Pfam; PF00207; A2M; 3.
Pfam; PF00207; A2M; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEP4 PROTEIN PRECURSOR.
TEP1V OR TEP4 OR CAID363.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1425;
                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 POTENTIAL.
168491 MW; C7FB0FEE5C90AA2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00477; ALPHA_2_MACROGLOBULIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               53.9%; Score 48; DB 5; 62.5%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                             FlyBase; FBgn0041180; TepIV.
InterPro; IPR002890; A2M_N.
InterPro; IPR001599; Alpha_2_macroglobln.
InterPro; IPR002114; PTS_HPr_ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.3. Best Local Similarity 62.5 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | || |:|| || |
524 ETGEFRYTEETFSVEV 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EGGELSYSEEEFSVSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 1496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9NFV5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NFV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ă
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DT1;
MEDLINE-9916057; PubMed=10049822;
Tremblay D.M., Moineau S.;
"Complete genomic sequence of the lytic bacteriophage DT1 of Streptococcus thermophilus.";
Virology 255:63-76(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=972H-;
McDougall R.C., Rajandream M.A., Barrell B.G., Simmonds M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Length 1158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AL132828; CAB60236.1; -
InterPro; IPR000519; RhoGEF.
InterPro; IPR000591; DEP.
InterPro; IPR001801; CNH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EF; 1.
130878 MW; 6FFE8244710D33B1 CRC64;
                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE RHO1 GDP-GTP EXCHANGE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12, Last sequence update)
12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00780; CNH; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus thermophilus bacteriophage DT1.
                                                            PRT; 1158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47; DB
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001849; PH.
InterPro; IPR003880; Phosphopant_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
PUTATIVE TAIL COMPONENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.8%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1122 EGGELLYSTEPIPFSSGE 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00610; DEP; 1.
Pfam; PF00621; RhoGEF; 1.
                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00036; CNH; 1.
SMART; SM00049; DEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RhoGEF;
                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=90410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1158
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                 Q9UTR5
Q9UTR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XJB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9XJB0
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                       Q9UTR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XJB0
                                                                              ACCOORDING TO THE PACE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

ö

ö

Gaps

ö

Indels

2

1; Mismatches

Conservative

Query Match Best Local Similarity Matches 10; Conserv

53.9%; Score 48; DB 5; Length 1496; 62.5%; Pred. No. 48;

```
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4930488L21RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 075231
075231:
                                                                                                                                                                                                                                                                                                                                                                                                                  090596;
                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                              995599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
075231
                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                           965060
                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC AC
  ò
                                                                                                                                                                                                                                                        ò
                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conger myriaster (Conger eel).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Congroldei;
Congridae; Conger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       two Streptococcus mediating bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus thermophilus bacteriophage 7201.
Viruses; dsDNA viruses, no RNA stage; Talled phages; Siphoviridae.
NCBI_TaxID=112023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 9; Length 521;
Pred. No. 29;
                                                                                                                                     9; Length 518;
            Tremblay D.M., Moineau S.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF085222; AAD21893.1; -.
SEQUENCE 518 AA; 58300 MW; 34D230523784CB3B CRC64;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Ogawa T., Ishil C.;
"Galectin from skin of Conger myriaster.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF145054; AAF44526.1; SEQUENCE 521 AA; S6576 WW. AF513FA740013C7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-20088830; PubMed-10620678;
Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,
                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AA
                                                                                                                               51.7%; Score 46; DB
53.3%; Pred. No. 29;
:lve 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of four loci isolated from thermophilus phage genomes responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett. 182:271-277(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0955V7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLEEL 13, Last 01-JUN-2001 (TrEMBLEEL 17, Last CONGER EEL GALECTIN (CONGERIN I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 53.34
"Thea 8; Conservative
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                      478 ELTYLSEPFSIGIGE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:| | ||:||
481 ELTYLSEPFSIGIGE 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ELSYSEEFFSVSVGE 18
                                                                                                                                                                                                               4 ELSYSEEFFSVSVGE 18
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Sinderen D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7943;
STRAIN-DT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCON I.
                                                                                                                                                                                                                                                                                                                                                     Q9MCJ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09PSV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORF34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q9PSV7
                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                    Q9MCJ9
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
ô
                                                                                                                                                                                                                                                                                                                                                         ID ACCOOK OF THE STANDARD OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
STRAIN-C57BL/G5; TISSUE-TESTIS;

XA RADINE-2108560; PubMed-11217851;

XB Arakay J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakaya T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Stauki R., Tomita M., Wagner L., Washio T.,

Rochiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

R Dromstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M.,

R Dromstein M.J., Bult C., Fletcher C., Fullia M., Mombaerts P.,

R Dromstein M.J., Bult C., Radiguez I., Sakamoto N.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wanshar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

R Wanshar-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                 Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 11; Length 117;
Pred. No. 10;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK015647; BAB29915.1; -.
MGD; MGI:1923059; 4930488L21R1k.
SEQUENCE 117 AA; 12868 MW; 665940B7EF891419 CRC64;
                                                                                                                                                                                        689EB34F7E39B4F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                 Score 45; DB 13;
Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA
                                                                                                                                                                                                                                                                                                                                                    Mismatches
EMBL; AE010276; BAA36385.1; -.
HSSP; P26788; 1C1L.
InterPro; IPR001079; Gal-bind_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                            Pfam; PF00337; Gal-bind_lectin; 1.
SMART; SM00276; GLECT; 1.
SROSITE; PS00309; GALAPTIN; 1.
SEQUENCE: 137 AA, 15448 MW; 6891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%;
53.3%;
                                                                                                                                                                                                                                                                                 50.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 17, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                          2 GGBLSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GGFINNSPQRFSVNVGE 37
                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGELSYSEEFFSVSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4930488E21RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 GGRLSHSHQEFSTKL
```

```
Q9VJD1;
                                                                                                                                                                                                                                                       Q9VJD1
                                                                                                                                                                                                                                                                                                                                                                   CG6453
                                                                                                                                                                                                                     10
                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                      Q9VJD1
                                                                                                                                                                                                                                                       δy
                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RDEC-1;
MEDLINE-21153569; PubMed-11254564;
Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E., Kaper J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., Deng Y.K., Lai L.C., McNamara B.P., Donnenberg M.S., Raper J.B.; "The complete sequence of the locus of enterocyte effacement (LEE) from enteropathogente Escherichia coli E2348/69."; Mol. Microbiol. 28:1-4(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterocyte
                                                                                                Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boedeker "..., I.S., Elliott S.J., Johnson L.A., Thate T.E., Kape. "Complete Nucleotide Sequence and Analysis of the Locus of Enter Infect. Immun. 69:2107-2115(2001).

SEQUENCE 446. A.M. A.M. S. SEQUENCE AND SEQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                              SEQUENCE FROM N.A.
Cordes M., Wollam C., Carter T.;
"The sequence of Homo sapiens PAC clone DJ0905J08.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL, AC005189; AAC25527.1;
                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 183 AA; 20911 MW; 17E7040069D3E842 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48/15.1; -.
48804 MW; DD782F98D00F6632 CRC64;
                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 44; DB 90.0%; Pred. No. 18; Live 0; Mismatches
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequenc
01-JUN-2001 (TrEMBLrel. 17, Last annotat
WUGSC:H_DJ0905J08.3 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P00518; IPHK.
InterPro; IPR000119; Euk_pkinase.
Pfam: PF00069; pkinase, I.
PROSITE; PSS011; PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98254123; PubMed=9593291;
                                                                      Homo sapiens (Human),
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 17, C
(TrEMBLrel. 17, L
(TrEMBLrel. 17, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                        Waterston R.;
Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
' 9; Conserv?
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSYSEEFFDV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-RDEC-1;
                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AJ15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9AJ15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTT
DTT
DTT
DTT
DTT
SQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
RA Addms W.D., Celniker S.E., Holt R.B., Evans C.A., Gocayne J.D.,
RA Addms W.D., Celniker S.E., Holt R.B., Evans C.A., Gocayne J.D.,
RA Addms W.D., Celniker S.E., Holt R.B., Fanding R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Bardon R.C., Rogers Y.-H.C., Blazej R.G., Chang Q., Chen L.X.,
Barandon R.C., Baker E.G., Helt G., Walson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Da Helt G., Walson C.R., Miklos G.L.G.,
RA Ballew R.M. Basul A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Basaley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Basaley E.M.,
RA Burtis K.C., Budam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Durblo S.D., Delcher A., Deng Z., Mays A.D., Dew I., Dolshakov S.,
RA Dorkova D., Botchan M.R., Bouck J., Brokstein P., Brottiar P.,
RA Dorkova D., Botchan M.R., Bouck J., Brokstein P., Brottiar J.,
RA Durblo S., Dolcher A., Dohnes M., Dugan-Rocha S., Dunkov B.C.,
RA Durblo K.J., Pavagelista C.C., Ferraz C., Ferriar C., Ferria C.,
RA Harris N.L., Harvey D., Halman T.J., Hernandez J.R., Houck J.,
RA Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A.,
A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchun K.A.,
A Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Markei B., McInton T.C., Moried M.P., McDerson D.,
RA Mount S.M., Moy M. Murphy L., Murny D.M., Nelson D.L.,
RA Bazzolo M., Pittand G.S., Pan S., Pollard J., Weller E., Shen H.,
Spier E., Spradling A.C., Simpson M., Stupski M.P., Smith T.,
RA Spier E., Shork S., Wolley K.C., Wu D., Yung S., Zhu S., Shirk R.,
RA Sher B.C., Shork S., Zhan M., Wonger E., Wang S., Yong S., Zhu S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                       Gaps
                                                                                    ;
0
              Length 446;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CG6453 PROTEIN.
                                                                                . 9
          5;
                                                                                                                                                                                                                                                                                                                                                                                                548 AA.
          DB
                                                                            Mismatches
       Score 44;
                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: TO EF-HAND FAMILY. BEBL; AE0003655; AF53621.1; -. HSSP; PO1130; LLDL. FlyBase; FB9n0032643; CG6453.
   49.4%;
                                                                                                                                                                                      2 GGELSYSEEFFSVSVGE 18
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY,
```

us-09-485-571-18.rspt

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=64186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           064283;
01-AUG~1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOSNCKX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              046384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         064283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          046384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
064283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
046384
                                                                                                                                                                                                                                                                                                                                                                             Matches
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98138491; PubMed=9478004;
MEDLINE-70. Cooper C.B., Schnetkamp P.P.;
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.;
"CDNA cloning of the human retinal rod Na-Ca + K exchanger: comparison with a revised bovine sequence.";
Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).
EMBL; AF025480; AAC13320.1;
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BISNCKX.

Bison bison (American bison).

Bison bison (American bison).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bison.

NCBI_TaxiD=9901;
                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                    5; Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Length 300
                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                        4F486B724D64732E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2BE592DA5AB9781E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELECTRON TRANSEER FLAVOPROTEIN SUBUNIT ALPHA.
ETFA OR VNC2151G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 AA.
                                                                                                                                                                                                                                 Score 44; DB:
Pred. No. 66;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                InterPro; IPR000886; ER_target.
InterPro; IPR002172; LDL_recept_A.
FMRT; PR00136; efhand; 1.
FMART; SM00192; LDLs; 1.
FROSITE; PS00018; EF_HAND; UNKNOWN_1.
FROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS50068; LDLRA_2; 1.
Calcium-binding; Glycoprotein.
SEQUENCE 548 AA; 61539 MW; 4F486B7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20504483; PubMed-11016950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31671 MW;
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                    49.4%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1998 (TrEMBLrel. 08, NA-CA+K EXCHANGER (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4%,
-how 8; Conservative
                                                                                                                                                                                                                                                                                                                                                  350 EGEEDQYDDEEPDVGVGE 367
                                                                                                                                                                                                                                                                                                             1 EGGELSYSEEEFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 55.6 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9HND2;
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
046383
                                                                                                                                                                                                                                                                                                                                                                                                                                                       046383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HND2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
Q9HND2
                                                                                                                                                                                                                                                                                                                                                     g
S W D D R B D R W D D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R 
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

```
No W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welli R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
A lam M. Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
T. Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EBHE, ABGOGIU3; ARGO03881;
P. R. Interpro; IPR001308; ETF_alpha.
R. Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 58, SKDA PROTEIN.
Streptococcus thermophilus bacteriophage Sfi21.
Viruses; dSDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lij
SEQUENCE FROM N.A.
Tucker J.E., Winkfein R.J., Cooper C.B., Schnetkamp P.P.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AP025664; AAB8884.1; -.
InterPro; IPR002613; Na_Ca_Ex.
Pfam; FF01699; Na_Ca_Ex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7941A055D5C34B29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AA; 33466 MW; B86AFDB6A5A8E1E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 6;
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 AA; 52337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NA-CA+K EXCHANGER (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.3%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 06, TrEMBLrel. 06, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 GGDVDIADAEFLVSVG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 EGGEVKGDEDEGEIQAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
```

ö

```
ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
MEDLINE-98160788; PubMed-9499809;
Designer F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98160788; PubMed=9499809;
Desidere F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 58, KDA PROTEIN.
Streptococcus thermophilus bacteriophage Sfil9.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         48.3%; Score 43; DB 9; Length 515; -53.3%; Pred. No. 90; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
48.3%; Score 43; DB 9; Length 515;
Best Local Similarity 53.3%; Pred. No. 90;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                   Virology 241:345-356(1998).
EMBL, AF115103; AAC39282.1; -.
Hypothetical protein.
SEQUENCE 515 AA; 58543 MW; 10DB11E438C157B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIROLOGY 241:345-356(1998).
EMBL, AF115102; AAC39296.1; -.
Hypochetical protein.
SEQUENCE 515 AA; 58475 MW; 09DE9B6AC7A4880D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       515 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 48.3
Best Local Similarity .53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 ELTYLSEPFSIGTGE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475 ELTYLSEPFSIGTGE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       064294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
064294
AC 064294,
DT 01-AUG-
DT 01-AUG-
DE HYPOTHIO
OC VITUSECT
OC V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
   RX
RA
RT
RT
RT
DR
SO
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
```

Search completed: February 12, 2002, 12:38:36 Job time: 749 sec -

```
43.8
    900
  34
                                                                                                                              February 12, 2002, 12:39:48; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                              100059
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                           US-09-485-571-18
89
1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_39:*
                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                    Run on:
```

		Description		m	_		_			Q9rrx5 deinococcus	P21817 homo sapien		P11970 populus nig		-		P30266 bacillus fi		_	P00292 cucurbita p	_	Q15475 homo sapien	_		Q16881 homo sapien		P08198 halobacteri				P32194 sus scrofa	P17340 lycopersico		27	P32695 escherichīa
SUMMARIES		ID	LEG1_CONMY	EBSD_ENTFA	TRMU_DEIRA	S17A_HUMAN	PLAS_POPNI	YP6_AGRTU	SYI_AQUAE	SYFB_DEIRA	RYNR_HUMAN	PLAS_HORVU	PLAT_POPNI	KPR2_YEAST	KPR4_YEAST	LPXB_HELPY	CATE_BACFI	YB89_YEAST	FAED_ECOLI	PLAS_CUCPE	SIX1_MOUSE	SIX1_HUMAN	S17A_RABIT	YQHB_BACSU	TRXB_HUMAN	TRXB_BOVIN	CSG_HALHA	XFP_SCHPO	PLAS_MERPE	PLAS_SOLTU	PG1_PIG	PLAS_LYCES	- 1	- 1	YJBN_ECOLI
		BB				-1		-1														-											7		
		Length	135	253	380	414	168	191	926	820	5032	155	168	318	355	360	448	529	812	66	273	284	397	442	497	499	852	825	66	66	149	170	241	286	330
æ	Query	Match	50.6			•	48.3		٠	47.2	٠			•	•		46.1		٠	٠	•	44.9		4	٠	4.	4		٠	٠			43.8	٠	
		Score	45	45	45	44	43	43	43	42	42	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	4	39.5	39	39	39	38	39	39	39
	Result	No.	1	7	e	4	2	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31	32	33

015315 homo sapien P34054 trichoderma P55811 rhizopus ni P09095 bacillus br P21675 homo sapien P16960 sus scrofa P39695 bacillus su Q92346 schizosacch P20422 daucus caro 0991c2 conger myri P32195 sus scrofa P49934 sus scrofa		teleostomi; ; Congroidei;  Conger  Congerin I, in new structure PHYSIOLOGICAL ILY.	5; 0; Gaps 0;
	NTS	AA.  je) jate) into) into) n conger eel, C i.; iv. Hotta H., iv.; iv.; iv. Hotta H., iv.; iv.; iv. Hotta H., iv.; iv.; iv.; iv.; iv.; iv.; iv.; iv.;	DB 1; Length 13 1.9; thes 4; Indels
R51B_HUMAN INAL_TRIHA LEU2_RHINI TYCA_BACBR T2DI_HUMAN RYNR_FIG CME3_BACSU CME3_BACSU PLAS_DAUCA LEG2_COMY PG2_PIG PG5_PIG	ALIGNMENTS	PRT; 135 AA.  ted) sequence update) sequence update) b-BINDING LECTIN 1). el). ta; Craniata; Vertebrati i; Teleostei; Anguillif i; Teleostei; Teleostei; Anguillif i; Teleostei; Teleostei; Teleostei; Teleostei; Teleostei; Teleostei; Teleostei; Teleostei; Teleostei; Teleo	Score 45; DB pred. No. 1.9 4; Mismatches
.8 350 .8 573 .8 750 .8 1088 .8 1875 .8 5035 .3 776 .7 97 .7 135 .7 147 .7 144		1.  CCOINY STANDARD; 19  UG-1992 (Rel. 23, Last sequence-1992 (Rel. 23, Last sequence-1992 (Rel. 23, Last sequence-1992 (Rel. 23, Last sequence-1992 (Rel. 23, Last sequence-1992).  Tyota: Metazoa: Chordeta;	Similarity 52.9%; 9; Conservative LLSYSEEEFSVSVGE 18 ::                 IINNSPORFSVNYGE 36
8 9 9 9 9 9 9 9 9 9 9 9 9 9		ULT 1  1COMMY  1.EG1_COUNT  1.EG2_COUNT  1.EG2_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG3_COUNT  1.EG4_COUNT	GGE GGE
w w w w w w w d d d d d d d d d d d d d		RESULT LEGI_CONM LEGI_CONM LEGI_CONM DT 01-A DT 30-M D	Query Match Best Local Matches Qy 2 GGE Db 20 GGF

us-09-485-571-18.rsp

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
       δŏ
                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                  01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE)
                                                                                                                                                                                          Bensing B.A., Dunny G.M.,

"Cloning and molecular analysis of genes affecting expression of
binding substance, the recipient-encoded receptor(s) mediating mating
binding substance, the recipient-encoded receptor(s) mediating mating
J. Bacteriol. 175:7421-7429(1993).

-!- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
-!- PATHWAY: THIRD STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-!- SIMILARITY: BELONGS TO THE TYPE-I 3-DEHYDROQUINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORMS A SCHIFF-BASE INTERMEDIATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 1; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F8F1436A80906B02 CRC64;
                       253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.6;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    ssis; Lyase.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01487; DHquinase_I; 1.
PROSITE; PS01028; DEHYDROQUINASE_I; 1.
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-R1;
MEDLINE-20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                    IPR001381; DHquinase_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Aromatic amino acid biosynthesis;
                                                                                                                                                                                  MEDLINE=94042918; PubMed=8226689:
                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 AA; 28085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.30,
Thes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L23802; AAC36854.1;
                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcus radiodurans.
                                           (Rel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGGELSYSEEEF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGGEMAFSEENY 97
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                     (TYPE I DHQASE).
                                                                                                                                         NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRMU OR DR1759
                                        01-JUN-1994
                                                                                                                               Enterococcus
                    EBSD_ENTFA
P36923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRMU_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RTK1;
          EBSD_ENTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
TRMU_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
RESULT
                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID
DT
DT
DDT
DDT
DDE
OX
OX
RRN
RR
RX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TESSUE-Placenta, and Liver:
MEDLINE-99003259; PubMed=9786912;
Sanjo H., Kawai T., Ažira S.;
Sanjo H., Kawai T., Ažira S.;
PRAKS, novel serine/threonine kinases related to death-associated protein kinase that trigger apoptosis.";
J. Biol. Chem. 273:29065-29071(1998).
I. FUNCTION: PHOSPHORYLATES THE MYOSIN LIGHT CHAIN (MLC) AS AN EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR
                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + TRNA = S-ADENOSYL-L-HOMOCYSTEINE + TRNA CONTAINING 5-METHYLAMINOMETHYL-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Grosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchun K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methyltransferase; tRNA processing; Complete proteome.
80 AA; 42184 MW; 000160AFCC980A53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA AND IN LOWER
LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
PTM: AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
SERINE/THREONINE KINASE 17A (EC 2.7.1.-) (DAP KINASE-RELATED
APOPTOSIS-INDUCING PROTEIN KINASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 380;
Pred. No. 5.6;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: CYTOPLAMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002017; AAF11314.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 AA; 42184 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.68;
                                                                                                                                                                                                                                                                          radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 EGFELEFAEPQFAVAPGQ 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INITIATION OF APOTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    THIOURIDYLATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR1759:
                                                                                                                                                                                                          Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S17A_HUMAN
Q9UEE5;
```

```
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TURN
   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus nigra (Lombardy poplar)
Bukaryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida I; Malpighiales; Salicaceae; Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Freeman H.C.;
"The crystal structure of poplar apoplastocyanin at 1.8-A resolution.
The geometry of the copper-binding site is created by the polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                      InterPro: IPR002019; Euk_pkinase.
InterPro: IPR002090; Ser_thr_kin_actsite.
Figam; PF00069; pkinase; 1.
SMART; SM0020; S_TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1; Length 414;
Pred. No. 9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-84135769; PubMed=6698995;
Garrett T.P.J., Clingeleffer D.J., Guss J.M., Rogers S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-CV. ITALICA; TISSUE-Leaf; STRAIN-CV. ITALICA; Jenzelewski V., Haehnel W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           K->A: LOSS OF ACTIVITY.
0C140290438C2A1A CRC64;
                                                                                                                                                                                                                                                                                                                                         POLY-PRO.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Proc. Royal Soc. N.S. Wales 112:45-62(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PLASTOCYANIN A, CHLOROPLAST PRECURSOR.
                                                                                                                                                                                                                                                                                                      Phosphorylation; Nuclear protein; Apoptosis. DOMAIN 61 321 PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA.
                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-FAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
MEDLINE-84010876; PubMed-6620385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. ITALICA;
Ambler R.P.;
Unpublished results, cited by:
                                                                                                     EMBL; AB011420; BAA34126.1; -. HSSP; P00518; 1PHK. MIM; 604726; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                  46559
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 90.0
مام 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111111 | 280 LSYSEEEFDV 289
                                                                                                                                                                                                                                                                                                                                                                                                                414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LSYSEEEFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Freeman H.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLAS_POPNI
P00299;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT .5
PLAS_POPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A PACA CONTRACT OF THE CONTRAC
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         -!- FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P7001 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I.
-!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOMPLASTS.
-!- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B.
-!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
Guss J.M., Freeman H.C.;
"Structure of oxidized poplar plastocyanin at 1.6-A resolution.";
J. Mol. Biol. 169:521-563(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00157; PLASICALIMATE, 1.
ProDom, PD001235; Copper_LD1ue; 1.
PR0SITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family; 3D-structure.

CHLOROPLAST.
                                                                                                                     Colman P.M., Freeman H.C., Guss J.M., Murata M., Norris V.A. Ramshaw J.A.M., Venkatappa M.P.; "X-ray crystal structure analysis of plastocyanin at 2.7-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLASTOCYANIN A. PLASTOCYANIN-LIKE.
                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mendel; 12195; POPni;PetE;1.
InterPro; IPR001235; Copper_blue.
InterPro; IPR000923; Copper_blue1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00127; copper-bind; 1. PRINTS; PR00156; COPPERBLUE. PRINTS; PR00157; PLASTOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z50185; CAA90564.1; -. PIR; A00309; CUPX.
                                                                                                                                                                                                                    Nature 372:319-324(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB, 2PCY 15-JAN 86.
PDB, 4PCY 15-JAN 86.
PDB, 4PCY 15-JAN 91.
PDB, 5PCY 15-JAN 91.
PDB, 5PCY 15-JAN 91.
PDB, 1PLC 31-GAN 91.
PDB, 1PLC 31-GAN 94.
PDB, 1PND, 31-JAN 94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
168
168
106
153
156
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
84
90
93
100
110
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
70
106
153
156
161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendel; 12195;
                                                                                                                                                                                           resolūtion.
```

17020 MW; 901B21A7573DBF82 CRC64;

```
RESULT
δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-84207942: PubMed-6327292; Gielen J., de Beuckeleer M., Seurinck J., Deboeck F., de Greve H., Lemmers M., van Montagu M., Schell J.; "The complete nucleotide sequence of the TL-DNA of the Agrobacterium EMBO J. 3:835-846(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
ASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE)
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                 Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 1; Length 191;
Pred. No. 5.7;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumor; T-DNA; Plasmid; Hypothetical protein.
191 AA; 21466 MW; 138EBA961E3EEE95 CRC64;
                                                                        ; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                               DB 1;
                                                                                                                                                                                                                                                                                             23-007-1986 (Rel. 02, Created)
23-00T-1986 (Rel. 02, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                  191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      956 AA.
                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                             Score 43;
                                                   Pred. No.
                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
20-AUG-2001 (Rel. 40, Last ann
                                                 44.48;
                             48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X00493; CAA25171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.78;
                                                                                                            EGGELSYSEEFFSVSVGE 18
                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens. Plasmid pTiAch5.
Query Match
Best Local Similarity 44...
Best Local Similarity 64...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.77
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last
ISOLEUCYL-TRNA SYNTHETASE
                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| ::||: | | |
111 DGGRINYSKNEYSSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL PROTEIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGGELSYSEEFFSVS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQAG6T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ILES OR AQ_305.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A04498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crown gall
SEQUENCE
                                                                                                                                                                                                                                                            YP6_AGRTU
P04030:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYI_AQUAE
066651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ILERS)
                                                                                                            Н
                                                                                                                                                                                                                 RESULT 6
YP6_AGRTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYI_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                g
                                                                                                            ò
                                                                                                                                                                                                                                                              HD DE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anterec,
Pram; PF00133; tRNA-Synt__,
PRINTS; PR00984; TRNASYNTHILE.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Metal-binding; Zinc; Complete proteome.
SITE 60 77 0mplete proteome.
SITE 624 628 "KMSKS" REGION.
SITE 624 628 "KMSKS" REGION.
"INTING 627 627 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYEB_DEIRA STANDARD; PRT; 820 AA.
09RRX5;
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6.1.1.20) (PHENYLALANINE--
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                   Nature 392:353-358(1998).

1- CATALYTIC ACTIVITY: ATP + L-ISOLEUCINE + TRNA(ILE) = AMP +
PYROPHOSPHATE + L-ISOLEUCYL-TRNA(ILE).

1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).

1- SUBUNIT: MONOMER (BY SIMILARITY).

1- SUBCELLULAR LOCATION: CYTOPLASMIC.

1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Frechum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     radiodurans R1.";
Science 286:1571-1577(1999).
-1- CATALYTIC ACTIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000683; AAC06614.1; -. InterPro; IPR003300; tRNA-synt_1a. InterPro; IPR001412; tRNA-synt_1. InterPro; IPR002301; tRNA-synt_ile. Pfam; PF00133; tRNA-synt_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRNA LIGASE BETA CHAIN) (PHERS).
PHET OR DR2357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896 EGGEVQIEGEELPVKVG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EGGELSYSEEEFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYFB_DEIRA
```

ó

```
CCD HIS-2434
 VARIANT
  between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92128959; PubMed-1774074; Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S., Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S., Derdemezi J., Britz B.A., Duff C.L., Worton R.G., McLennan D.H.; A substitution of cysteine for arginine 614 in the ryanodine receptor is potentially causative of human malignant hyperthermia."; Genomics 11:751-755(1991).
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MH ARG-248, AND VARIANTS CYS-471; LEU-1786 AND CYS-2059. MEDLINE-2372020; Pubmed-1354642; Gillard E.F., Otau K., Fujii J., Duff C., de Leon S., Khanna V.K., Britt B.A., Worton R.G., McLennan D.H.; Polymorphisms and deduced amino acid substitutions in the coding sequence of the ryanodine receptor (RYRI) gene in individuals with malignant hyperthermia."; Genomics 13:1247-1254(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Skeletal muscle;
MEDLINE-90130482; PubMed-2298749;
Zorzato F., Fujii J., Otsu K., Phillips M., Green N.M., Lai F.A.,
Melssner G., Maclennan D.H.
"Molecular cloning of cDNA encoding human and rabbit forms of the
Ca2+ release channel (ryanodine receptor) of skeletal muscle
sarcoplasmic reticulum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                             SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN FAMILY. SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                1; Length 820;
                                                                                                                                                                                                                                                                                                         7; Indels
           TETRAMER OF TWO ALPHA AND TWO BETA CHAINS
                                                                                                                                                                                                                                          820 AA; 86984 MW; 1BE394EB78F7493E CRC64;
PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE)
                                                                                                                                                                                                                                                                               Score 42; DB 1
Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        5032 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
         SUBUNIT: TETRAMER OF TWO ALPHA AND SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 265:2244-2256(1990).
                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                          EMBL; AE002066; AAF11903.1; -.
                                                                                                                                                                                                                                                                               47.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                        757 GGELLESVEPFDVFTGE 773
                                                                                                                                                                                                                                                                                                                                 2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MH CYS-614.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 820 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR RYDR
                                                                                                                                                                                                                                                                                                                                                                                                                        RYNR_HUMAN
P21817;
                                                                                                                                                                                                                                                                                                                                                                                                           RYNR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYR1
                                                                                                                                                                                                       TIGR
ò
                                                                                                                                                                                                                                                                                                                                                        g
```

```
WEDLINE-94035118; PubMed-8220423; WEDLINE-94035118; PubMed-8220423; Quane K.A., Healy J.W.S., Keating K.E., Manning B.M., Couch F.J., Palmucci L.M., Doriguzzi C., Fagerlund T.H., Berg K., Ording H., Bendixen D., Mortier W., Linz U., Muller C.R., McCarthy T.V.; "Mutations in the ryanddine receptor gene in central core disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT MH ARG-341.
MEDILE-94282042; PubMed-8012359;
MEDILE-94282042; PubMed-8012359;
Quane K.A., Keaping K.E., Manning B.M., Healy J.M.S., Monsieurs K.,
Heffron J.J.A., Lehane M., Heytons L., Krivosic-Horber R., Adnet P.,
Ellis F.R., Monnier N., Lunardi J., McCartbly T.V.;
"Detection of a novel common mutation in the ryanodine receptor gene
in malignant hyperthermia: implications for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95152512; PubMed-7849712;
Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E.,
Censier K., Urwyler A., Klausnitzer M., Muller C.R., Heffron J.J.A.,
McCarthy T.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lynch F.J., Krivosic-Horber R., Reyford H., Monnier N., Quane K., Adnet F., Haudecoeur G., Krivosic I., McCarthy T., Lunardi J.; "Identification of heterozygous and homozygous individuals with the novel FYR1 mutation Cys35Arg in a large kindred."; Anesthesiology 86:620-626(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Detection of a novel RYR1 mutation in four malignant hyperthermia pedigrees.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The substitution of Arg for Gly2433 in the human skeletal muscle ryanodine receptor is associated with malignant hyperthermia."; Hum. Mcl. Genet. 3:2181-2186(1994).
WEDLINE-99(035177: Property of the property of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene in malignant hyperthermia:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S., Frodis W., Britt B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98051290; PubMed-9389851;
MEDLINE-98051290; PubMed-9389851;
Quane F.A., Ording H., Keating K.E., Manning B.M., Heine R.,
Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,
"Detection of a novel mutation at amino acid position 614 in
ryanodine receptor in malignant hyperthermia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection of a novel Tyr to Ser mutation in a pedigree with associated central cores."; Genomics 23:236-239(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT MH SER-522.
MEDLINE-95130087; PubMed-7829078;
Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,
Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT MH ARG-2433.
MEDLINE-95187156; Pubmed-7881417;
Phillips M.S., Khanna V.K., de Leon
McLennan D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Genet. 3:1855-1858(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MH ARG-35.
MEDLINE-97219028; Pubmed-9066328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Anaesth. 79:332-337(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MH TRP-552.
MEDLINE-97284075; PubMed-9138151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heterogeneity studies.";
Hum. Mol. Genet. 3:471-476(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarthy T.V.; "Mutation screening of the RYR1
                                                                                                                                                                                                                                                                                                                                     Genet. 5:46-50(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            malignant hyperthermia.";
Nat. Genet. 5:51-55(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT MH ARG-2433.
```

```
1-1 JUDGILES.

1-1 JUDGILES.

1-1 JUDGILES.

1-2 DISEASE: A DEFICIENCY IN THE RYANODINE RECEPTOR MAY BE THE CAUSE OF MALICHANTY TYPERTHERMIA (MH) AND OF CEMTRAL CORE DISEASE OF MUSCLE (CCD). MH IS AN AUTOSOMAL DOMINANT DISORDER OF SKELETAL MUSCLE (ADD). MH IS AN AUTOSOMAL DOMINANT DISORDER OF SKELETAL MUSCLE AND IS ONE OF THE MAIN CAUSES OF DEATH DUE TO ANESTHESIA. COMMONIX USED INHALATIONAL ANESTHETICS SOCH AS LALOTHANE AND BY DEPOLARIZING MUSCLE RELAXANTS SUCH AS SUCCINYLCHOLINE. THE CLINICAL FEATURES OF THE MYOPATHY ARE HYPERTHERMIA, ACCELERATED MUSCLE METABOLISM, CONTRACTURES. METABOLIC ACTIONSIS, TACHYCARDIA AND DEATH, IF NOT TREATED WITH THE POSTSYNAPTIC MUSCLE RELAXANT, VITRO" CONTRACTURE TEST (IVCT): OBSERVING THE MAGNITUDE OF CONTRACTURE INDUCED IN STRIED OF MUSCLE IISSUE BY CAFFEINE ALONE AND HALOTHANE ALONE. PATIENTS WITH NORMAL RESPONSE ARE MH NORMAL (MHN), THOSE WITH ABRORMAL RESPONSE ALONE OR HALOTHANE ALONE ARE MH EQUIVOCAL (MHE(C) AND MEH(H) RESPONSE ARE MH NORMAL ALONE ARE MH EQUIVOCAL (MHE(C) AND MEH(H) RESPECTIVELY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE-20081079; Pubmed-10612851;
Gencik M., Gencik A., Mortier W., Epplen J.T.;
"Novel mutation in the RYR1 gene (R2454C) in a patient with malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperthermia.";
Hum. Mutat. 15:122-122(2000).
-!- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS MH LEU-2434 AND HIS-2453.
MEDLINE=99158296; PubMed=10051009;
Barone V., Massa O., Intravaia B., Bracco A., Di Martino A.,
Tegazzin V., Cozzolino S., Sorrentino V.;
"Mutation screening of the RYRI gene and identification of two novel
mutations in Italian malignant hyperthermia families.";
J. Med. Genet. 36:115-118(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V., Krivosic Horber R., Censier K., Comi G., Adnet P., Wolz W., Lunardi J., Muller C.R., McCarthy T.V.;
"Novel mutations at a CpG dinucleotide in the ryanodine receptor in malignant hyperthermia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of novel mutations in the ryanodine-receptor gene (RYR1) in malignant hyperthermia: genotype-phenotype correlation."; Am. J. Hum. Genet. 62:599-609(1998).
                                                                                                                                                                                                                                                                                                                       Manning B.M., Quane K.A., Ording H., Urwyler A., Tegazzin V., Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J., Vaughan P., Censier K., Bendixen D., Comi G., Heytens L., Monsieurs K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Screening of the ryanodine receptor gene in 105 malignant hyperthermia families: novel mutations and concordance with the in vitro contracture test."; Hum. Mol. Genet. 8:2055-2062(1999).
                                                               "Detection of a novel mutation in the ryanodine receptor gene i
Irish malignant hyperthermia pedigree: correlation of the IVCT
response with the affected and unaffected haplotypes.";
J. Med. Genet. 34:291-296(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brandt A., Schleithoff L., Jurkat-Rott K., Klingler W., Baur
Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M., Heffron J.J.A., McCarthy T.V.;
                                                                                                                                                                                                                                                VARIANTS MH CYS-2162; HIS-2162; MET-2167 AND MET-2205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99415746; PubMed=10484775;
                                                                                                                                                                                                                                                                                             MEDLINE=98163444; PubMed=9497245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98111378; PubMed=9450902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutat. 11:45-50(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS MH CYS-2458 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS MH.CYS-2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehmann-Horn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +
HARDER STANDER STANDER
```

ş

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
         THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
-!- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN CONSTITUTES THE 'FOOT' STRUCTURE STANNING THE JUNCTIONAL GAP BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE DIHYDROPYRIDINE RECEPTOR.
-!- MISCELLANEOUS: RYANODINE IS AN ALKALOID THAT BINDS TO THE CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY.
-!- SIMILARITY: LOCAL & LOW WITH THE NICOTINIC ACETYLCHOLINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nielsen P., Gausing K.;
"In vitro binding of nuclear proteins to the barley plastocyanin gene
promoter region.".
Eur. J. Blochem. 217:97-104(1993).
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I- FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN P700 AND THE CYTOCHROME B/F COMPLEX IN PHOTOSYSTEM I. SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAROID MEMBRANE SURFACE IN CHLOROPLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of cDNA clones and
                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                  Score 42; DB 1; Length 5032;
Pred. No. 2.8e+02;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08, Last sequence update)
35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 AA.
                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-OV. BOMI;
Nielsen O.S., Gausing K.;
"The precursor of barley plastocyanin: s
gene expression in different tissues.";
FEBS Lett. 225:159-162(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. 217:97-104(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. NK 1558;
MEDLINE=94039081; PubMed=8223592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S00206; S00206.
HSSP; P00289; 2PCF.
Mendel; 8616; HORVu; PetE;1.
InterPro; IPR001235; Copper_blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08, Created)
                                                                                                                                                                                                                                                                                                                                                                                    3731 EGGENGEAEEEVEVSFEE 3748
                                                                                                                                                                                                                                                                                      47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z28347; CAA82201.1; -.
                                                                                                                                                                                                                                                                                                                                                         1 EGGELSYSEEEFSVSVGE 18
                                                                                                                                                                                                                                                                                                   Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, La
PLASTOCYANIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08,
                                                                                                                                                                        (N-ACHR) SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLAS_HORVU
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAS_HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                           qq
     88888888888888888
                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ς;
```

```
InterPro; IPR001235; Copper_blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                    KPR2_YEAST
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERRATUM.
                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                              RESULT 12
KPR2_YEAST
                                                                                                           CHAIN
                                                                                                                                 METAL
                                                                                                                                              METAL
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiated and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                      Populus nigra (Lombardy poplar).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.

NCBI_TaxID=3691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PLASTOCYANIN PARTICIPATES IN ELECTRON TRANSFER BETWEEN POO AND THE CYTOCHROME BAF COMPLEX IN PHOTOSYSTEM I. SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOLD MEMBRANE SURFACE IN CHLOROPLASTS.

SMILARTY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF POPLAR PLASTOCYANINS A AND B. SIMILARIY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    ö
PFEMN: PF00127; Copper-bind; 1.
PRINTS: PR00156; COPPERBLUE.
PRINTS: PR00157; PLASTOCYANIN.
ProDom; PD001235; Copper-blue; 1.
PROSITE: PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane; Transit peptide.
Transit peptide.
1 58 CHIADDDIAGE
                                                                                                                                                                                                            Score 41; DB 1; Length 155;
Pred. No. 9.8;
?; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. ITALICA;
Dinitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
"Complete amino acid sequence of poplar plastocyanin b.";
FEBS Lett. 226:17-22(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. ITALICA
Reichert J. Jenzelewski V., Haehnel W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                          DPPER (BY SIMILARITY).
-> N (IN CV. NK 1558).
DAA7EABE5F6F4F91 CRC64
                                                                                                                    (BY SIMILARITY).
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
02-OCT-ANG-2011 (Rel. 40, Last annotation update)
PLASTOCYANIN B, CHLOROPLAST PRECURSOR.
                                                                                                                                                                                                                                                                                                                                    168 AA
                                                                                      CHLOROPLAST.
PLASTOCYANIN.
                                                                                                                     COPPER
                                                                                                                                          COPPER
                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                             Ψ.,
                                                                                                                                                                                                            46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 250186; CAA90565.1; -. PIR; S00210; S00210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00299; 4PCY.
Mendel; 12196; POPni;PetE;2.
                                                                                                                                                                            15709
                                                                                                                                                                                                                                                        2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                       67 GGVLVFEPNDFSVKAGE 83
                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE OF 70-168
                                                                                                                                                                                                                                                                                                                                PLAT_POPNI
P11970;
                                                                                                                                                                 VARIANT
SEQUENCE
                                                                                               CHAIN
DOMAIN
                                                                                                                     METAL
METAL
                                                                                                                                          METAL
                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                          PLAT_POPN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                                                                                                                                                                                                                                                                                               RESULT
 õ
                                                                                                                                                                                                                                                                             셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C A MILIGAN J. S. Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Avilles E., Berno A., Brennan T., Carpenter J., Chenry J.M., Avilles E., Berno A., Brennan E., Hartzell G., Hunicke-Smith S., Hyman E., Nakahara K., Naman D., Lew H., Lin D., Mossedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EmbL/Genbank/DBM databases.

-!- CANALYPIC A. THEOSE 1-DIPHOSPHATE - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
1-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last anotation update)
RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (EC 2.7.6.1) (PHOSPHORIBOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Phosphoribosylpyrophosphate synthetase (PRS): a new gene family Saccharomyces cerevisiae.";
Yeast 10:1031-1044(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                  PRODOM; PONO1235; Copper_llue; 1.
PROSITE; PS00196; COPPER_BLUE; 1.
Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
Transit peptide; Multigene family.
1 69 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter A.T., Narbad A., Pearson B.M., Beck K.-F., Logghe M., Contreras R., Schweizer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter A.T., Narbad A., Pearson B.M., Beck K.-F., Logghe M.,
Contreras R., Schweizer M.;
Yeast 11:191-191(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerharct H., Switzer R.L., Smith J.M., Hove-Jensen B.;
Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                           F20DA6EA2038AEEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                          PLASTOCYANIN B.
PLASTOCYANIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYROPHOSPHATE SYNTHETASE 2).
PRPS2 OR PRS2 OR PRS OR YER099C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                        COPPER.
                                                                                                                                                                                                                                                                                                                         COPPER
                                                                                                                                                                                                                                                                                                                                                                                 COPPER
                                                                                                                                                                                                                                                                                                  COPPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
InterPro; IPR000923; Copper_bluel.
Pfam; PF00127; Copper-bind; 1.
PRINTS; PR00156; COPPERBLUE.
PRINTS; PR00157; PLASTOCYANIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SKQ2N;
MEDLINE=95084630; PubMed=7992503;
                                                                                                                                                                                                                                                                                                                                                                                                              ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDGSLAFVPSEFSVPAGE 94
                                                                                                                                                                                                                                                                                                                                                                                                              16981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bropagan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
PATHWAY: THIS ENZYME IS UTILIZED BY BOTH THE DE NOVO & THE SALVAGE STHRANDAY: BY WHICH ENDOGENOUSLY FORMED OR EXOGENOUSLY ADDED PYRINDINE, PURINE, OR PYRIDINE BASES ARE CONVERTED TO THE CORRESPONDING ALBONUCLEDSIDE MONOPHOSPHATES.

SIMILARITY: BELONGS TO THE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contreras R., Fiers W., Logghe M., Molemans F.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-FIBOSE 5-PHOSPHATE = AMP +
5-PHOSPHO-ALPHA-D-RIBOSE 1-DIPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 2.7.6.1)
                                                                                                                                                                                                                                                                                                                                                                                            Pfan, PF00156; Pribosyltran; 1.
PROSITE; PS00114; PRPP_SYNTHETASE; 1.
Nucleotide biosynthesis; Transferase; Kinase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGNESIUM (POTENTIAL).
AGNESIUM (POTENTIAL).
8B970E98084F5D71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGNESIUM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 4
PHOSPHORIBOSYL PYROPHOSPHATE SYMTHETASE 4)
PRPS4 OR PRS4 OR YBL068W OR YBL0619.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.1%; Score 41;
50.0%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAGNESIUM
MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGNESIUM
                                                                                                                                                                                                                                                                                    EMBL; X7414; CAA52436.1; -...
EMBL: U18839; AAB64654.1; -...
FIR: S37225; S37225.
SCD: S0000901; PRS2.
InterPro; IPR000842; PRPP_synthetase.
InterPro; IRR000866; Pribosyltran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34765 MW;
                                                                                                                                                                                                                                                                       EMBL; X75075; CAA52969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 GVYQYSNKETSVTIGE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C;
                                                                                          FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPR4_YEAST
P38063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
KPR4_YEAST
 STITE DEPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: UDP-2,3-BIS(3-HYDROXYTETRADECANOYL)GLUCOSAMINE + 2,3-BIS(3-HYDROXYTETRADECANOYL)-BETA-D-GLUCOSAMINYL 1-PHOSPHATE - UDP + 2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-1,6-BETA-D-2,3-BIS(3-HYDROXYTETRADECANOYL)-BETA-D-GLUCOSAMINYL 1-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=26695 / ATCC 700392;

STRAIN=26695 / ATCC 700392;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.";
Nature 388:539-547(1997).
-!- FUNCTION: CONDENSATION OF UDP-2,3-DIACYLGLUCOSAMINE AND
2,3-DIACYLGLUCOSAMINE-1-PHOSPHATE TO FORM LIPID A DISACCHARIDE,
A PRECURSOR OF LIPID A, A PHOSPHORYLATED GLYCOLIPID THAT ANCHORS
THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE CELL
THE LIPOPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                     DB 1; Length 355;
                                                                                                                                                      Kinase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                        MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
MAGNESIUM (POTENTIAL).
41EBD027E5399E46 CRC64;
                                                                                                                                                                                       MAGNESIUM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIPID-A-DISACCHARIDE SYNTHASE (EC 2.4.1.182).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 AA.
                                                                                                                                                                                                                                                                                                                46.1%; Score 41; DB
50.0%; Pred. No. 24;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: LIPID A BIOSYNTHESIS. SIMILARITY: BELONGS TO THE LPXB FAMILY.
                                                                                                           Pfam; PF00156; Pribosyltran; 1.
PROSTIE; PS00114; PRPP_SYNTHETASE; 1.
Nucleotide biosynthesis; Transferase;
Multigene family.
                                                                    InterPro; IPR000842; PRPP_synthetase.
InterPro; IPR000836; Pribosyltran.
                                                                                                                                                                                                                                                                 ΜW.
               EMBL; 235829; CAA84888.1;
PIR; S45804; S45804.
                                                                                                                                                                                                                                                             39059
                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        3 GELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             69 GVYQYSNKETSVTIGE
                                                      S0000164; PRS4
                                                                                                                                                                                                                                                           355 AA;
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPXB OR HP0867
                                     PIR; S45804;
SGD; S0000164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPXB_HELPY
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 8
                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                      METAL
                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPXB_HELPY
                                                                                                                                                                                                                                                                                                                                                     Matches
qq
                                                                                                                                                                                                                                                                                                                                                                                        δ
```

```
OUTE P.G., Krulwich T.A.;

OUTE P.G., Krulwich T.A.;

Submitted (CCT-1991) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES

- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

- SUBCELLULAR LOCATION: CYTOPLASHIC (PROBABLE).

- SIMILARITY: BELONGS TO THE CATALASE FAMILY. HPIT SUBFAMILY.

- SIMILARITY: BELONGS TO THE CATALASE FAMILY. HPIT SUBFAMILY.

- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.

- CATALYTIC ACTIVITY IS STATEMENT IS INSTITUTED.

- CATALYTIC ACTIVITY IS STATEMENT IS IN NO WAY MODIFIED AND ADDITION OF A STATEMENT IS IN THE CATALASE FAMILY.

- CATALYTIC ACTIVITY IS STATEMENT IS IN NO WAY MODIFIED AND ADDITION OF A STATEMENT IS IN NO WAY MODIFIED AND ADDITION OF A STATEMENT IS IN NO WAY MODIFIED AND ADDITION OF A STATEMENT IS A STATEMENT IN STATEMENT IN STATEMENT IS A STATEMENT IS A STATEMENT IN
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R PIR; S27490; S27490.

R HSSP; P21179; 11PH

IN ThterPro.; IPRO02226; Catalase.

B PAINTS; PR00057; CATALASE.

DR PRINTS; PR00067; CATALASE.

DR PROSTIE; PS00437; CATALASE.

DR PROSTIE; PS00438; CATALASE.

DR PROSTIE; PS00438; CATALASE.

DR PROSTIE; PS00438; CATALASE.

TR PROSTIE; PS00438; CATALASE.

A PROSTIE; PS00438; CATALASE.

A PROSTIE; PS00438; CATALASE.

B PROSTIE; PS00438; CATALASE.

A PROSTIE; PS00438; CATALASE.

B PRIMILARITY.

BY SIMILARITY.

TARBER LIGAND (BY SIMILA)
                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%; Score 41; DB 1; Length 448; Ilarity 57.1%; Pred. No. 30; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 360;
Pred. No. 24;
2; Mismatches 4; Indels
                                                                                             InterPro; IPR003835; LpxB.
Pfam; PF02684; LpxB; 1.
Transferase; Glycosyltransferase; Lipid A biosynthesis;
Lipid synthesis; Complete proteome.
SEQUENCE 360 AA; 41517 MW; 420421646FCE067D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51673 MW; 4D14048CB7023FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus firmus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ATALASE (EC 1.11.1.6) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 AA
  or send an email to license@isb-sib.ch).
                                                  EMBL; AE000596; AAD07909.1; -
                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.
75
75
148
448
448
448 AA; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     1 EGGELSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                     35 EGKEVLYSPREFSI 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1399;
                                                                             TIGR; HP0867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATE_BACFI
P30266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
CATE_BACFI
                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNERGEN
```

ó;

Gaps

ö

2; Mismatches

```
| ||:|||: ||
LKVSEDEFSLKAGE 46
5 LSYSEEEFSVSVGE 18
                 33
ò
              Dp
```

Search completed: February 12, 2002, 12:39:49 Job time: 802 sec

Ĺ

```
GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2002, 12:34:36; Search time 126.85 Seconds (without alignments)

10.809 Million cell updates/sec
```

Title:
Perfect score: 89
Sequence: 1 EGGELSYSEEFSVSVGE 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Couery No. Score Match Length DB ID Description

1 47 52.8 1158 2 750454 Probable rhol GDP2 45 50.6 135 2 821102 Phypothetical protection of the composition of the composition

catalase (EC 1.11.	ArgE/DapE/Acyl fam	probable regulator	outer membrane ush	elastic titin - hu	plastocyanin - fie	hypothetical prote	hypothetical prote	homeotic protein s	hypothetical prote	conserved hypothet	GumC protein - Xan	conserved hypothet	thioredoxin reduct	cell surface glyco	myosin Myok - Dict
S27490	E75324	S46116	MMECOF	138346	CUVM	T02322	B84718	S60751	A69186	E69958	S67819	G72358	266677	A28459	JG0183
7	7	7	٦	7	٦	7	7	7	7	7	7	~	٦	7	7
449	459	529	812	7962	66	136	236	273	280	442	449	486	499	852	828
46.1	46.1	46.1	46.1	46.1	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9
41	41	41	41	41	40	40	40	40	40	4.0	4.0	40	7,0	۲0	0.5
30	31	32	33	34	35	36	37	38	36	40	41	42	. 43	44	45

## ALIGNMENTS

	RESULT 1 T50454
	probable rhoi GDP-GTP exchange protein [imported] - fission yeast (Schizosaccharomy
	C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
	C;Accession: T50454 R:McDougall, R.C.: Rajandream, M.A.: Barrell, B.G.: Simmonds, M.: Churcher, C.M.
	submitted to the EMBL Data Library, November 1999
	A;Kererence number: 225030 A;Accession: T50454
	A; Status: preliminary; translated from GB/EMBL/DDBJ
	A:Molecule Cype: UNA A:Residues: 1-1158 <mcd></mcd>
	A;Cross-references: EMBL:AL132828; PIDN:CAB60236.1; GSPDB:GN00066; SPDB:SPAC1006.06
	A Experimental source: strain 972h(-); cosmid c1006
	A;Gene: SPDB:SPAC1006.06
	A; Map position: 1
	A;Introns: 835/1; 9/5/3 C;Superfamily: CDC24 homology
	52.8%; Score 47;
	Best Local Similarity 55.6%; Pred. No. 20; Marches 10. Concernative 1. Microsphere 7. Indele 0. Gane 0.
	t, mismaccines ', micers o, caps
	Qy 1 EGGELSYSEEFSVSVGE 18
	Db 1122 EGGELLYSTEDIPESSGE 1139
	RESULT 2
	\$21102
	Lectin - ea (Conger myriaster)
	C.Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 26-Aug-1999
	C; Accession: S21102
	R; Muramoto, K.; Kamiya, H.
	BIOCDIM. BIOPHYS. ACTA ILIV, 129-1150, 1992.  North December 2014 Commence of a locating from control of a mirriagion of a
	A; riche, in amino did sequence of a rectif from conget eer, conget myridacer, sor.
_	A.Accession: S21102
	A;Status: preliminary
	A;Molecule (1ype: protein b.pacidinas 1-13 Amib.
-	C:Superfamily: beta delactoside-binding lectin
	Query Match 50.6%; Score 45; DB 2; Length 135;
	98; Pred. No. 4.1;
	5) CONSELVACIAVE 4) MISHIGICINES 4) THUGELS 0) Gaps

45-

residues 70-168

```
J. Mol. Baiol. 192, 361-387, 1986
A;Title: Crystal structure analyses of reduced (Cu(I)) poplar plastocyanin at six phi A;Title: Crystal structure analyses of reduced (Cu(I)) poplar plastocyanin at six phi A;Reference number: A58637; MUID:84010876
A;Contents: annotation; X-ray crystallography, 1.80 angstroms
R;Guss, J.M.; Preeman, H.C.
J. Mol. Biol. 169, 521-563, 1983
A;Title: Structure of oxidized poplar plastocyanin at 1.6 Angstroms resolution.
A;Reference number: A58639; MUID:84010876
A;Contents: annotation; X-ray crystallography, 1.60 angstroms
R;Colman, P.M.; Freeman, H.C.; Guss, J.M.; Murata, M.; Norris, V.A.; Ramshaw, J.A.M.
A;Title: X-ray crystal structure analysis of plastocyanin at 2.7 angstrom resolution
A;Reference number: A93194
A;Contents: annotation; X-ray crystallography, 2.7 angstroms
C;Connent: Plastocyanin is found loosely bound to the inner thylakoid membrane surfact; C;Connent: petE
A;Gene: pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OQAGGT

Nypothetical protein 6 - Agrobacterium tumefaciens plasmids

C;Species: Agrobacterium tumefaciens

C;Species: Agrobacterium tumefaciens

C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 16-Jul-1999

C;Accession: A04498; S28691

E;Gielen, J; De Buckeleer, M.; Seurinck, J; Deboeck, F.; De Greve, H.; Lemmers, M. R.; Desoeck, T.; De Greve, H.; Lemmers, M. A;Title: The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefac.

A;Reference number: A91001; MUID:84207942

A;Accession: A04498

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unpublished results, cited by Freeman, H.C., J. Proc. Royal Soc. N.S. Wales 112, A; Reference number: A94471
                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-168 CKBL;
A; Cross-references: EMBL: 250185; NID:9929812; PIDN:CAA90564.1; PID:9929813
A; Experimental source: var. italica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricuss, J.M.; Freeman, H.C. submitted to the Brookhaven Protein Data Bank, September 1986
A.Reference number: A50737; PDB:5FCZ
A.Contents: annotation; X-ray-crystallography, 1.80 angstroms, residues R.Guss, J.M.; Harrowell, P.R.; Murata, M.; Norris, V.A.; Freeman, H.C. J. Mol. Biol. 192, 361-387, 1986
                         C; Accession: $58209; A00309
K; Reichert, J.; Jenzelewski, V.; Haehnel, W.
Submitted to the EMBL Data Library, July 1995
A; Description: Kinetic studies of recombinant poplar plastocyanins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Molecule type: protein
A.Residues: 70-127, 22B',131-168 <AMB>
R.Guss, J.M.; Freeman, H.C.
submitted to the Brookhaven Protein Data Bank, March 1992
A.Reference number: A51342; PDB:1PLC
A.Contents: annotation; X-ray crystallography, 1.33 angstroms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 1
Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.48
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | |:: |||:| ||
77 DDGSLAFVPSEFSISPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A00309
                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Ambler, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                     RESULT 3
hypothetical protein (ebsc 5' region) - Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Species: Enterococcus faecalis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 20-Oct-2000
C;Accession: 104939
R;Bensing, B.A.; Dunny, G.M.
J. Bacteriol. 175, 7421-7429, 1993
A;Title: Cloning and molecular analysis of genes affecting expression of binding substan
A;Reference number: A49939; MUID:94042918
A;Reference number: A49939; MUID:94042918
A;Reference number: A49939
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <BEN>
A;Cenetics:
C;Genetics:
A;Cenetics:
A;Start codon: GTG
C;Superfamily: 3-dehydroquinate dehydratase; 3-dehydroquinate dehydratase homology
F;19-239/Domain: 3-dehydroquinate dehydratase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.J.;
C.; Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE002017; GB:AE000513; NID:g6459527; PIDN:AAF11314.1; PID:g645953
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trans (5-methylaminomethyl-2-thiouridylate)-methyltransferase - Deinococcus radiodurans (5)Species: Dec.1999 #sequence_revision 03-Dec-1999 #text_change 17-mar-2000 (5)Accession: H75357 (8)Mhite, 0.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. (7)Mith, H.O.; Venter, J.C.; Fraser, C.M. (7)Mith, H.O.; Venter, J.S.; Smith, H.O.; Venter, J.S.; Smith, H.O.; Venter, J.S.; Smith, H.O.; Venter, J.S.; Shith, H.O.; Venter, J.S.; J.S.; Shith, H.O.; Venter, J.S.; J.S.; Shith, H.O.; Venter, J.S.; Shith, H.O.; Venter, J.S.; Shith, H.O.; Venter, J.S.; J.S.; Shith, H.O.; Venter, J.S.; J.S.; Shith, H.O.; Venter, J.S.; J.S.; J.S.; Shith, H.O.; Venter, J.S.; J.S.; Shith, H.O.; Venter, J.S.; Shith, H.O.; J.S.; J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plastocyanin a precursor (validated) - Lombardy poplar
C;Species: Populus nigra var. italica (Lombardy poplar)
C;Date: 31-May-1980 #sequence_revision 31-Oct-1997 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 45; DB
58.3%; Pred. No. 8.1;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 1
C;Superfamily: probable membrane protein YDL033c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB
Pred. No. 14;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || || ::| :|:|: |:
EGFELEFAEPQFAVAPGQ 386
                                               20 GGFINNSPQRFSVNVGE 36
    GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
77, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EGGELSYSEEFF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||:::||| :
86 EGGEMAFSEENY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: DR1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
CUPX
δ
                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dp
```

ö

Gaps

m

Page

4

```
48.3%;
                                                                                                                                                                                                                                                                                            48.3%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGGELSYSEEEFSVSVG 17
                                                                                                                                                                                                                                                                                            Query Match.

Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475 ELTYLSEPFSIGTGE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 ELTYLSEPFSIGTGE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ELSYSEEEFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                  A; Residues: 1-515 <DES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
D84365
electron transfer flavoprotein subunit alpha [imported] - Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001
C; Species: Halobacterium sp. NRC-1
C; Species: NRC-1
S; Ng, W.V.; Kennedy, S.P.; Mahalras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Jung, W.V.; Kennedy, S.P.; Mahalras, T.
Jung, K.H.; Alam, W.; Freatlas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A; Accession: D84365
A; Accession: D84365
A; Accession: D84365
A; Accession: D84365
A; Residues: 1-322
A; CGenetics:
C; Genetics:
A; Genetic
A;Residues: 1-191 cGIE>
A;Cross-references: GB:X00493; GB:J05108; GB:X00282; NID:g39062; PIDN:CAA25171.1; PID:g3
A;Cross-references: GB:X00493; GB:J05108; GB:X00282; NID:g39062; PIDN:CAA25171.1; PID:g3
A;Experimental source: plasmid priAch5
B;Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plant Mol. Biol. 2, 335-350, 1993
A;Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octd
A;Reference number: S28691
A;Accession: S28691
A;Accession: S28691
A;Accession: S28691
A;Accession s28691

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable tail component protein 515 - Streptococcus thermophilus phage 5fi19
C;Species: Streptococcus thermophilus phage 5fi19
C;Species: Streptococcus thermophilus phage 5fi19
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-yul-2000
C;Accession: T09272
R;Desiere, F:: Lucchini, S.; Brussow, H.
R;Desiere, F:: Lucchini, S.; Brussow, H.
A;Title: Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchar A;Reference number: 216607; MUID:98160788
A;Accession: T09272
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 1;
Pred. No. 13;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GGDVDIADAEFLVSVG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.3
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGELSYSEEEFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EGGELSYSEEEFSVS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
NID:92982996; PIDN:AAC06614.1; PID:92983002; GB:AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Desiere, F.; Lucchini, S.; Brussow, H. Virology 241, 345-356, 1998
A;Title: Evolution of Streptococcus thermophilus bacteriophage genomes by modular A;Reference number: 216607; MUID:98160788
A;Reference number: 216607; MUID:98160788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392, 353-358, 1998
Affile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: G70327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: G70327
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: EMBL:AF032121; NID:95524032; PIDN:AAC39282.1; PID:92935675
C;Superfamily: Streptococcus phage Sfil9 probable tail protein 515
C;Reywords: tail protein
A;Cross-references: EMBL:AF032122; NID:95523999; PIDN:AAC39296.1; PID:92935690 C;Superfamily: Streptococcus phage Sfil9 probable tail protein 515 C;Keywords: tail protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-956 <AQF> A;Cross-references: GB:AE000683; NID:g2982996; PIDN:AAC06614.1; PID:g2983002; A;Experimental source: strain VF5 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                        probable tail component protein 515 - Streptococcus thermophilus phage Sfi21 C;Species: Streptococcus thermophilus phage Sfi21 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: 702203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoleucine--tRNA ligase (EC 6.1.1.5) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: isoleucine--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 515
                                                                                                                                         Length 515
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                            5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB;
Pred. No. 37;
2; Mismatches
                                                                                                                                         Score 43; DB Pred. No. 37; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-515 <DES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          896 EGGEVQIEGEELPVKVG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

о Э

Φ

Gaps

ö

Indels

Length 243;

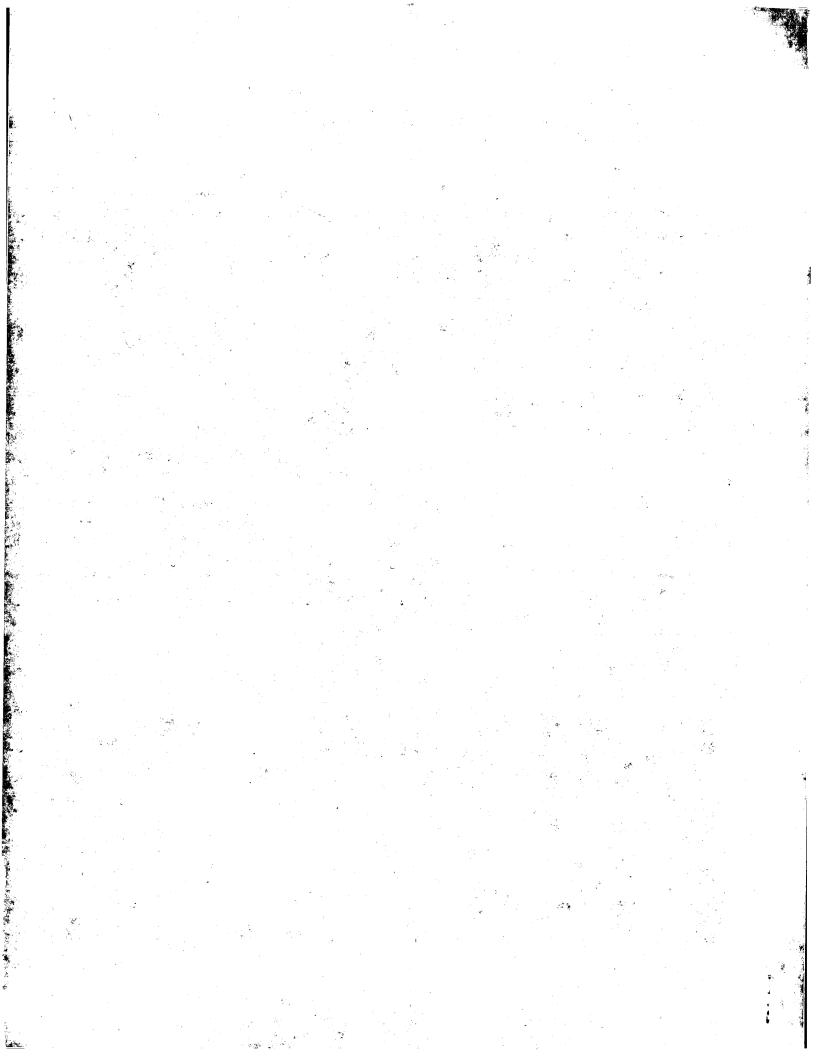
```
DNA-binding protein WRKY3 homolog F3L17.120 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C;Accession: T10685
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999
A;Recerence number: 216652
A;Accession: T10685
A;Molecule type: DNA
A;Residues: 1-324 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL080283; GSPDB:GN00062; ATSP:F3L17.120
A;Experimental source: cultivar Columbia; BAC clone F3L17
                                                                                                                                                                                                                             Score 42; DB 2;
Pred. No. 24;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB;
Pred. No. 33;
4; Mismatches
                                    A;Map position: 1
A;Introns: 8/3; 41/1; 53/3; 140/1; 164/2; 211/1
                                                                                                                                                                                                                             47.2%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.28;
58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:| : :::|: | ||
168 GGDLHFFKKKFNFSAGE 184
                                                                                                                                                                                                                                                                                                                                                                                           2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                    Query Match 47.2
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : || :|: |||:
135 KSAELEFSKENFSVSL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EGGELSYSEEFFSVSV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.2
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | |||:|:||
64 FDENEFSISMGE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: ATSP:F3L17.120
A,Map position: 4
A;Introns: 223/2; 265/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
A; Gene: CESP:C55C2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: F25H2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kabour 12
Kansposable retroelement homolog - perennial teosinte
N.Alterinate names: ZLRS7 protein, long repetitive sequence protein ZLRS 7
C; Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 07-Dec-1999
C; Accession: JG4641; S52246
R; Monfort, A.: Vicient, C.M.; Raz, R.; Puigdomenech, P.; Martinez-Izquierdo, J.A.
DNA Res. 2, 255-261, 1995
A; Title Molecular analysis of a putative transposable retroelement from the Zea genus v
A; Reference number: JC4641; MUID:97021439
A; Reference number: DNA
A; Residues: 1-156 < MON>
A; Residues: 1-156 < MON>
A; Residues: 1-156 < MON>
A; Residues: I-156 < MON>
A; Residues: DNA
B; Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-243 <GOE>
A;Cross-references: EMBL:AF003144; NID:g2088754; PID:g2088759; PIDN:AAB54197.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                  C.Species: Bos printigenius taurus (cattle)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C.Accession: $20969 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C.Accession: $20969 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
R.Reilaender, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.
EMBO J. 11, 1689-1695, 1992
A.Title: Primary structure and functional expression of the Na/Ca,K-exchanger from k A.Reference number: $20969, MUID:92258377
A.Accession: $20969
A.Accession: $209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                          Na+/Ca2+,K+-exchanging protein - bovine
N:Alternate names: Na+/Ca2+,K+ antiporter; Na/Ca,K-exchanger
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein C55C2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.2%; Score 42; DB 2; Length 156; 72.7%; Pred. No. 15; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid C55C2.
A;Reference number: 218311
A;Accession: T15225
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 93;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  805 EGGEVKGDEDEGEIOAGE 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4'
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: |||||||
19 GDSEYSEEEFS 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GELSYSEEEFS 13
                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

Length 324;

.; 3

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-573 <WIL>
A; Cross-references: EMBL: Z79754; PIDN: CAB02094.2; GSPDB: GN00019; CESP: F25H2.6
A; Experimental source: clone F25H2
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dypothetical protein F25H2.6 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: T21355
R; Wilkinson, J
Submitted to the EMBL Data Library, September 1996
A; Reference number: Z19411
A; Reference number: Z19411
A; Reference number: T21355
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Nolecule type: DMA
A; Caenoria (Fig. 1979)
A; Species: Description (Fig. 1979)
A; Species: Description (Fig. 1979)
A; Species: DMA
A; Species: Specie
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
A;Introns: 5/2; 60/3; 100/3; 205/3; 268/3; 320/3; 353/2; 487/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 573;
4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2
Pred. No. 61;
3; Mismatches
```

Search completed: February 12, 2002, 12:34:36 Job time: 554 sec



Appli

Sequence 54, Sequence 57, Sequence 62, Sequence 228, Sequence 228, Sequence 9, A Sequence 57, Sequence 57, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 12, Sequence 2, A Sequence 2, A Sequence 2, Sequence 2, Sequence 2, A Seq

Appl Appl Appl Appl Appl Appl Appli Appli Appli Appli

OM protein

ë ö

Run

Sequence:

Minimum DB Maximum DB

Database

Result Š

Searched:

```
Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY. USA

ZIP: 2006-1812

COMPUTER READBLE FORM:
MEDIUW TYPE: BLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN 1994
CLASSIFICATION: 435
ATTONREY/AGEAN INFORMATION:
NAME: MURASHIGE KATE H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEEX: 90-4030
INFORMATION FOR SEQ ID NO: 25:
SEQUIDENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
US-08-499-523-54
US-08-499-523-57
US-08-499-523-62
US-08-752-852A-227
US-08-752-852A-228
US-08-752-852A-228
US-08-752-853A-228
US-09-128-345-54
US-09-128-345-57
US-09-128-345-57
US-09-128-345-57
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-09-128-345-52
US-08-128-345-52
US-08-128-343-2
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 1;
Pred. No. 0.2;
3; Mismatches
                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                         US-08-182-483A-25; Sequence 25, Application US/08182483A Patent No. 5693486; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGRLCYSRKKWCVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino act.
STRANDEDNESS: single
modOf,OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
    ; TOPOLOGY:
US-08-182-483A-25
     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Appli
Sequence 1, Appli
Sequence 63, Appl
Sequence 67, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 64, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 57, Appl
Sequence 58, Appl
                                                                                               February 12, 2002, 12:32:22; Search time 106.12 Seconds (without alignments) 3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, App]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24,
Sequence 45,
Sequence 45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-182-483A-25
US-08-243-879A-24
US-08-128-345-45
US-08-1128-345-45
US-08-113-828-1
US-08-919-627-1
US-08-919-523-67
US-08-499-523-67
US-08-499-523-67
US-08-128-345-63
US-08-128-345-49
US-08-128-345-49
US-08-182-483A-28
US-08-182-483A-28
US-08-182-483A-28
US-08-199-523-48
US-08-499-523-53
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
US-08-499-523-58
US-08-499-523-65
US-08-499-523-65
US-08-499-523-65
US-08-499-523-65
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-128-345-58
-09-128-345-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-58
US-09-128-345-69
US-09-201-641-4
                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                  1 EGGELSYSEEFFSVSVGE 18
                                                                                                                                                       US-09-485-571-18
89
                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                              Scoring table:
                                                                        ı
```

ö

Gaps

ö

20022333544 2002233354 200233355 20023335 2003335 2003335 20035

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 1; Length 18;
Pred. No. 0.2;
3; Mismatches 4; Indels
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8667-0054-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HARWIG, STLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09128345
Patent No. 6159936
                                                                                                    ATTORNET/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION INUMBER: 29,959
REPERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.7
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 18 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGRLCYSRKKWCVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-499-523-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-128-345-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-128-345-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 18;
                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 45, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYNKOV, VLADIMIR N.
TITLE OF INVENTION: PROFESTINS
NUMBER OF SEQUENCES: 76
                                                                    Sequence 24, Application US/08243879A Patent No. 5708145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20 TELECOMMINICATION INFORMATION: TELEPHONE: (202) 887-1500 TELEX: 90-4030 INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRLCYSRKKWCVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                             RESULT 2
US-08-243-879A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY:
US-08-243-879A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-08-499-523-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
```

```
49.4%; Score 44; DB 2; Length 307; 90.0%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
APPLICANT: GOli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0068-1 DIV
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650-855-0555
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEDM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,627
FILING DATE: AUGUST 28, 1997
PRIOR APPLICATION NUMBER: US 08/713,828
FILING DATE: SEPTEMBER 13, 1996
FILING DATE: SEPTEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09096245 Patent No. 5977320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-645-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 LSYSEEEFDV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.
                                                                                                                                                                        COUNTRY: U.S. ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94304
                                                                                                                                         CITY: Palc
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-919-627-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-096-245-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                               Gaps
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1; Length 307;
Pred. No. 9.8;
0; Mismatches 1; Indels
                         Score 46; DB 4; Length 18; Pred. No. 0.2;
                                                           3; Mismatches , 4; Indels
                                                                                                                                                                                                                                                                                  APPLICANT: Bandman, olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE
TITLE OF INVENTION: KINASE GAMMA SUBUNIT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 1843 04

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM OF SASTEM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,828
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence 1, Application US/08919627; Sequence 1, Application US/08919627; Patent No. 5833981 GENERAL INFORMATION: APPLICANT: Bandman, Olga
                                                                                                                                                                                                                            Sequence 1, Application US/08713828 Patent No. 5683910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-01
TELECHONE: 415-85-055
TELEFAX: 415-85-055
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                       51.7%;
ilarity 56.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.4
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                2 GGELSYSEEEFSVSVG 17
                                                                                                                     2 GGRLCYSRKKWCVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
     Query Match
Best Local Similarity
'. hog 9, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 LSYSEEEFDV 198
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo
STATE: CA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CLONE: (
US-08-713-828-1
                                                                                                                                                                                           RESULT 5
US-08-713-828-1
                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

0; Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                    NAME/KEY: Modified-site

LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

US-08-499-523-63
                                                                                                                                                                                                                Score 43; DB 1; Length 18;
Pred. No. 0.6;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: group(6, 8, 13, 15)
CHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: LEHRER, ROBERT I.

APPLICANT: HARMIG, SILVIA S.L.

APPLICANT: HARMIG, SILVIA S.L.

TITLE OF INVENTION: PROTEGRINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:

STREET: 2000 Pennsylvania Ave. N.W., Ste. 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%; Score 43; DB 1;
50.0%; Pred. No. 0.6;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MURABLIGE, KARE H.
REGISSTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/08499523
Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                48.3%;
                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                          2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                2 GGRLXYXRRFFXVXVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 887-076
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.0 Matches 8; Conservative
            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DO COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACROUAL
ACROCATION
SOCIATION
SOCIATION
SOCIATION
SOCIATION
SOCIATION
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NOMBER: US/08/499,523
                                                                        APPLICALLO...
APPLICALLO...
ATING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0068 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: WIRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%; Score 44; 90.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,245
                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match . 49.4
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  ; LIBRARY:
; CLONE: Consensus
US-09-096-245-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 LSYSEEEFDV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LSYSEEEFSV 14
                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: por IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

8

```
8, 13, 15)
/note= "X is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 4; Length 18;
Pred. No. 0.6;
0; Mismatches 8; Indels
                                                                         COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CRASSIFICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COCTUZZI, Lautra, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 799-909
TELEPAX: (212) 869-9741
TELEPX: (6141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
FENTAL: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESEE: PENNIE & EDMONDS LLP
STREIT: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                    1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 67, Application US/09128345
Patent No. 6159936
GENERALINORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGRLXYXRRFXVXVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ADDRESSEE: PENNIE &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10036-2711
                                                           New York
                STREET: 1155 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                         STATE: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%; Score 43; DB 2; Length 18; 50.0%; Pred. No. 0.6; 1, Mismatches 6; Indels
                                                                                                                                                  APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Ghen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8067-034-999
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENTING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 63, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                         Sequence 230, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COLUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE,DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-90-9090
TELEFAX: 66141
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
21P: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGRLCYARRFFAVCVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
2 GGRLXYXRRRFXVXVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-NOV CLASSIFICATION: 435
                                                                           US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                    CITY: New STATE: NY COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-128-345-63
```

ò 셤

ö

Gaps ö Gaps

ö

```
Score 42; DB 1; Length 18;
Pred. No. 0.88;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME:
NUMBER:
CRESTRATION NUMBER: 29,959
REFERENCE/TOCKET NUMBER: 29,959
REFERENCE/TOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 10 NO:
TELEFEX: 90-4030
INFORMATION FOR SEQ 1D NO: 28:
SEQUENCE CHARACTERISTICS:
CRESTRATION FOR SEQ 1D NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: /note= "This position is Har." US-08-243-879A-28
              ; OTHER INFORMATION: /product= "homoarginine(Har)"
US-08-182-483A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1;
Pred. No. 0.88;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
TILLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                 Sequence 28, Application US/08243879A
Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/08499523; Patent No. 5804558; GENERAL INFORMATION:
                                                                                            47.28;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEHRER, ROBERT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                        Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                  2 GGKVCYGRXRFSVCVG 17
                                                                                                                                                                        2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGKVCYGRXRFSVCVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                         RESULT 14
US-08-243-879A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-4,99-523-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
LOCATION: group(6, 8, 13, 15)
CTHER INFORMATION: /note= "X is a hydrophobic, a
CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-67
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 4; Length 18;
Pred. No. 0.6;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: -
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 13-JAN 1994
FILING DATE: 13-JAN 1994
FILING DATE: --NANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEHRRK, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-909
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEX: 90-44330
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29, Application US/08182483A Patent No. 5693486 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             48.38;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
10
                                                                                                                                                                                   18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGRLXYXRRFXVXVG 17
                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-182-483A-29
                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

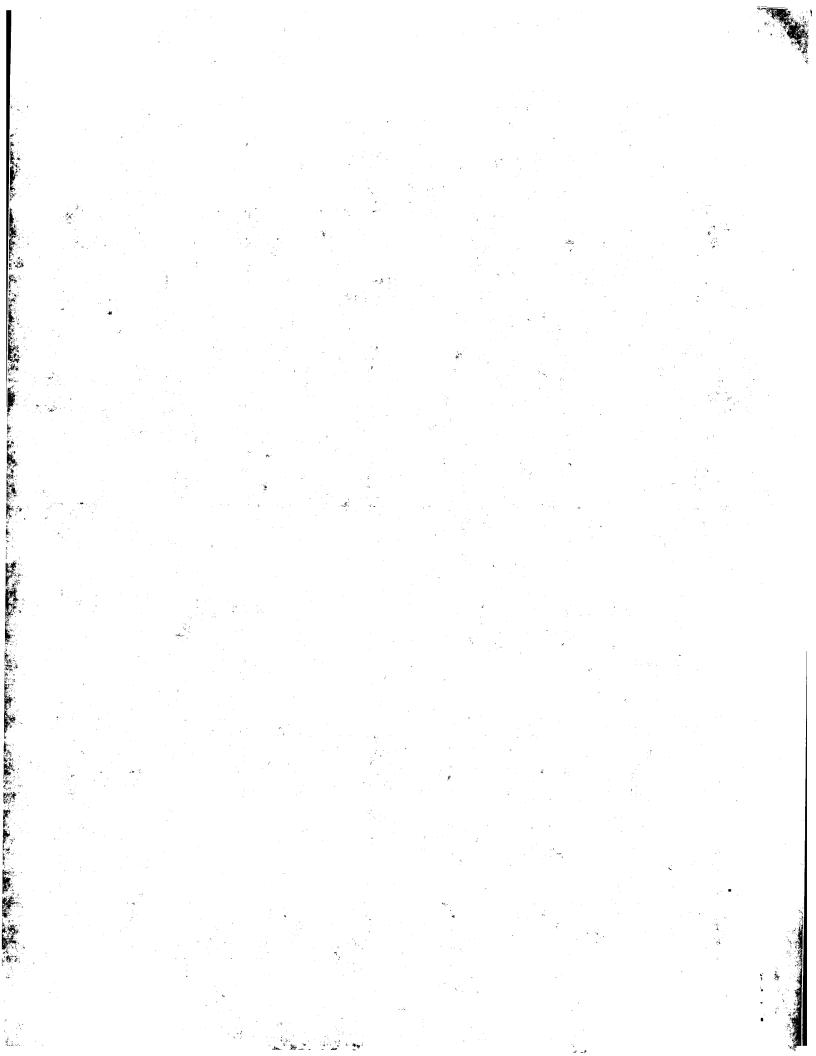
Gaps

ó

```
APPLICANT: HARMIG, SYLVIA S.L.
APLICANT: NOKKTAKOV, VLADIMIR N.
TITLE OF RIVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: JOHN PERSON
CITY: Washington
CITY: Washington
CITY: Washington
CITY: Washington
COMPITE DOG-HBI
COMPUTER REDABLE FORM:
HEDIOM TYPE: DOG-HBI
COMPUTER REDABLE FORM:
HEDIOM TYPE: TOPOS/MS-DOS
SOFTAME: PAREDENIN RELEASE #1.0, Version #1.30
COMPUTER REDABLE FORM:
HEDIOM TYPE: O'-JUL-1995
COMPUTER REDABLE FORM:
HEDIOM TYPE: O'-JUL-1995
COMPUTER REDABLE FORM:
HEDIOM TYPE: O'-JUL-1995
COMPUTER REDABLE FORM:
HEDIOM TYPE: APPLIANCE AND HELSE
COMPUTER REDABLE FORM:
HEDIOM TYPE: STATE H.
ANTORNEY ARE THE TO-JUL-1995
FILING DATE: O'-JUL-1995
FILING D
```

Search completed: February 12, 2002, 12:32:22 Job time: 450 sec

2 GGELSYSEEFFSVSVG 17 ||::| |||||||| 2 GGKVCYGRXRFSVCVG 17



Antimicrobial prot Cationic, antimicr Cationic, antimicr Protegrin peptide Cationic, antimicr Cationic, antimicr Cationic, antimicr

Arabidopsis thalia Arabidopsis thalia

DRAK1 protei protein kina

Novel

Novel

Arabidopsis thalia Arabidopsis thalia

Ryanodine receptor Protegrin derivati

Total number of

Searched:

score:

Perfect

Sequence:

protein

ĕ

Run on:

Scoring table:

sed

08 08

Minimum Maximum Database

```
Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                AAE01921
AAG08139
AAG18601
AAG11601
AAR11510
AAR193411
AAX32322
AAX32322
AAX33322
AAX33323
AAX36426
AAW36428
AAW36428
                                              AAW09085
AAR78777
AAW18151
                                                                                                                                                                                                                                                                                                AAW18153
AAW09081
AAW09082
                                                                                                                  AAG11602
AAG42799
                                                                            AAW18152
                                                                                                           AAG08140
                                                                                                                                       AAE01904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protegrin derivative peptide SM1739.
                                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                          AAW99405 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-FR01757
97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chavanieu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1999
 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW99405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calas E,
                                                                                                                                                                                                                                                                                                                                                                                                AAW99405
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                            Protegrin derivati
Protegrin derivati
Peptide which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protegrin-like pep
Protegrin-like pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protegrin derivati
                                                                          (without alignments)
5.497 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                 Search time 242.57 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                             // Sides/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/ Sides/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/ Sides/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/ Sides/gcgdata/geneseq/geneseqp/AA1999.DAT:*
                  Ltd
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                            522463 seqs, 74073290 residues
                                                                 February 12, 2002, 12:30:29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93616
AAW99412
AAY93177
AAY93179
AAY93615
AAR93615
AAB30450
AAW34892
AAW76803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW99405
AAW99403
                                             protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                            EGGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωī
                                                                                                    US-09-485-571-18
89
                                                                                                                                                                                                                   length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                       A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
18
18
18
18
18
41
307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0
66.3
66.3
57.3
57.3
57.3
51.7
51.7
51.7
51.7
```

Protegrin peptide Soybean beta-carot Marigold beta-hydr Soybean beta-carot Antimicrobial prot Antimicrobial prot Antimicrobial prot Antimicrobial pept Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr Cationic, antimicr

- nsed

of antibiotic peptides lacking disulfide bridges to deliver active agents into cells

WPI; 1599-190034/16.

Derivatives as carriers

Peptide which may Protegrin peptide Amino acid sequenc Novel human phosph Human phosphorylas

Score

Result . 9 ö

Gaps

. 0

Length 18;

Score 59; DB 20; Pred. No. 0.0028;

66.3%; llarity 75.0%; Conservative

Query Match Best Local Similarity Matches 12; Conserv

18 AA;

Sequence

χX

2 ggrlsysrrrfsvsvg 17

ö

Gaps

, 0

Length 18; Indels

17

GGELSYSEEFFSVSVG

Pred. No. 0.00 0; Mismatches

```
This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies for their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                               100.0%; Score 89; DB 20;
100.0%; Pred. No. 2.9e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                              Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                AAW99403 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grassy G,
Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97FR-0010297
                                                                                                                                                                                                                        1 EGGELSYSEEEFSVSVGE 18
                                                                                                                                                                                                                                    1 eggelsyseeefsvsvge 18
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190034/16.
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT: EM SA.
                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                          08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                      AAW99403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calas B,
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                     AAW99403
ID AAW9
                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                           ρp
                                                                                                                                                                                                                                                                                                         ò
```

```
This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family wheih contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 28; 37pp; French.
```

RESULT

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                             Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 21; Length 18; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                 Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                              Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 34pp; French.
            AAY93616 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                      99WO-FR02939.
                                                                                                                                                                                                                                                                                                  98FR-0015073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.3%;
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                              Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || |||| |||||
ggrlsysrrrfsvsvg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                               (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                         WO200032237-A1
                                                                      25-SEP-2000
                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                                     26-NOV-1999;
                                                                                                                                                                                                                                                                                                 30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                             Temsamani J,
                                                                                                                                                                                                                                       08-JUN-2000
                                        AAY93616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
AAY93616
              g
```

us-09-485-571-18.rag

__inked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"

Location/Qualifiers

```
Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example I; Page 13; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                             Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                    (SYNT-) SYNT:EM SA.
                                                                                                                                                                                               40200032236-A1.
                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                  26-NOV-1.999;
                                                                                                                                                                                                                                                                                                                            30-NOV-1998;
                                                                                                                                                                                                                                        08-JUN-2000
                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         Clair P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonuclectides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blod-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                        Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 20; Length 18;
Pred. No. 0.06;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaczorek
                                                                                                                                                   Protegrin derivative peptide SM2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grassy G,
                        AAW99412 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93177 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ggrlsysrrrfststg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calas B, Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-190034/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1998;
                                                                                                         08-JUN-1999
                                                                                                                                                                                                                                                                                                                                           WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999
                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                 AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
AAW99412
ID AAW9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $\circ{\circ}{\circ}$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\circ$\ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

for

useful

Temsamani J;

98FR-0015074. 99WO-FR02938

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1-X16; (b); BXXBXXXXBBXXXXBBXXXXBBXB, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must correct forms of (a)-(c) containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be cerver oforms of (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, carciplessins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main caregories based on their structure: (i) peptides with alpha-halices, carcopins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides (a)-peptides continuing bends due to the presence of with no major structure but containing bends due to the presence of corresidues, e.g. bactericins and PR39. The peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the BBB and is conjugated to a doxorubicin molecule by a succinate con linker. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 21; Length 18;
Pred. No. 0.06;
); Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.3
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gerlsysrrrfststg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by a glycoamide linker
```

Page

ö

Gaps

ö

Indels

9

Mismatches

;

Conservative

10;

Matches

2 GGELSYSEEFFSVSVG 17

ŏ

```
The invention relatices to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous (b); BXXBXXXBBBXXXXXXBX or (c) BXXBXXXBBXB, where: each of XI-XI6 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must can deach X is an aliphatic or aromatic a. The linear peptide may be retro forms of (a)-(c) containing a side chain that includes a basic group; containing at least 5, preferably at least 7 consecutive as from (a)-(c) containing D- and/or L-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c) reptides able to cross the BBB include protegrins, Antennapedia, tachyplesins, transportan, etc. of these several families have cytolytic tachyplesins, transportan, etc. of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. protegrin, tachyplesins, defensins; (ii) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides containing bends due to the presence of the residues, e.g. protegrin, tachyplesins, defensins; (iii) peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on terpresents a synthetic linear peptide designed on peptides and corresponded to a dalargin molecule by a disulphide linker. Conjugates of the linear peptide designed on peptides and pervent or diagnose brain cancer, Alzheimer's or conjugateses, prevent or diagnose brain cancer, Alzheimer's or studying drug behaviour in BBB models.
                                                                                                                                                               neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                                                                                                                                            blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nseful for
                                                                                                                                                                                                                                                                                                                                                     /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of linear peptides as vectors for active ingredients, useful diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of linear peptides,
                                                                                                                    Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temsamani J;
AAY93179 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example II; Page 20; 54pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98FR-0015074.
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-422871/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                             WO200032236-A1
                                                                                                                                                                                                                                                                                                          Key
Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1998;
                                                                               06-DEC-2000
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
```

DB 21; Length 18;

Score 51; DB 21 Pred. No. 0.06;

57.3%; 62.5%;

Query Match Best Local Similarity

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                       Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                            Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                  Colin De Verdiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 21
Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                            AAY93615 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR78773 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                 99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                          98FR-0015073.
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1995 (first entry)
2 ggrlsysrrrfststg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ggrlsysrrrfststg 17
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412166/35
                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                         WO200032237-A1
                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                  25-SEP-2000
                                                                                                                                                                                                                                                                                                                26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                        30-NOV-1998;
                                                                                                                                                                                                                                                                                      08-JUN-2000,
                                                                                                       AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR78773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                AAY93615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR78773
                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XX XX E
```

```
29-MAR-2000; 2000WO-US08561.
                                                                                                                    Dowling CA;
                                                                         99US-0129111
                                                                                                                                      WPI; 2030-679520/66.
                                                                                               (HSUD/) HSU D K.
                                                                                                                    Liu F,
            WO200062076-A1.
                                                                         13-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy
                                19-OCT-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW34892;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                    Hsu DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW34892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                            New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. porcine) leukocytes; or analogues of these peptides in which 1-4 of the peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation or esterification, and can be in linear or cystine-bridged form. D-Amino acid residues can be present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galectin; Galectin-3; cell growth; tumour; metastasis; cirrhotic liver;
hepatocellular carcinoma; liver neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a fragment of an Eel galectin family member.
                                                                                                                                                                                                                                                               Antibiotic peptide-based cpds, designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                              protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a specific example of the protegrin analogues in which Cys(8, 15) have been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
0.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46;
Pred. No.
                                                                                                                                                                                                                         Lehrer RL;
                                                                                                                                                                                                                                                                                                         Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB30450 standard; peptide; 41
                                                                                                                                                         93US-0095769.
94US-0182483.
94US-0243879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%;
56.2%;
                                                                                                                           94WO-US08305.
                                                                                                                                               93US-0093926
                                                                                                                                                                                                                        Kokryakov VN,
           Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ggrlcysrkkwcvsvg 17
                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                            WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                           20-JUL-1994;
                                                                                 W09503325-A.
                                                                                                                                               20-JUL-1993;
                                                                                                                                                                               17-MAY-1994;
                                                                                                                                                                                                                        Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2001
                                                                                                      02-FEB-1995
                                                                                                                                                          26-JUL-1993
                                          antifungal;
                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB30450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB30450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
a
```

```
AAB30440-85 represent peptides derived from galectin family members. Galectin-3 has been associated with assorted processes such as cell growth, tumour transformation, and metastasis. It is composed of two domains: a carbohydrate-binding region on the carboxy terminal which binds saccarides with terminal galactose residues, and an amino terminal domain consisting of tandem repeats of nine amino acids. The expression of galectin-3 is induced in cirrhotic liver and hepatocellular carcinoma, and so is useful as a marker of cirrhotic liver and hepatocellular carcinoma. Galectin-3 is used in diagnostic, prognostic and therapeutics for the treatment and prevention of hepatocellular carcinoma. It is useful for determining whether an individual is suffering from hepatocellular carcinoma or is likely to suffer from hepatocellular carcinoma or any neoplasm of liver origin or cirrhosis of the liver in the future.
Cirrhotic liver and hepatocellular carcinoma marker galectin-3, useful in diagnostic, prognostic and therapeutic methods for treating and preventing hepatocellular carcinoma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylase kinase gamma subunit; replacement therapy; glycogen utilisation disorder; muscle glycogenosis; hypoglycaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "putatively contains the catalytic kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "putatively contains 2 calmodulin binding domains required to activate the protein complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 21; Length 41;
Pred. No. 1.6;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human phosphorylase kinase gamma subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW34892 standard; Protein; 307 AA.
                                                                                                                                                 Example 3; Page 37; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGELSYSEEFFSVSVGE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ggfinnspgrfsvnvge 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AA;
```

ò

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                            The present sequence represents a novel human phosphorylase kinase gamma subunit, characterised as having homology to other phosphorylase kinase subunit, characterised as having homology to other phosphorylase kinase as subunits. Recombinant human phosphorylase gamma subunit is useful for replacement therapy in cases of glycogen utilisation disorders, e.g. muscle glycogenosis, causing muscular weakness and atrophy, or transformed with the DNA encoding the present sequence can also be used to screen for modulators of human phosphorylase kinase gamma subunit cativity, i.e. potential therapeutic agents. The protein can also be used continuity, i.e. potential therapeutic agents. The protein can also be used to suppress mutant forms of the this gene. The protein can be used to raise specific antibodies, useful as immunoassay reagents.

C Fragments of the DNA encoding the present sequence can be used cativation, e.g. to detect or quantify gene expression, to isolate thosphorylase kinase gamma subunit-expressing genes and for mapping the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylase kinase gamma subunit: HPHKG; human; treatment; glycogen; pathophysiological condition; phosphorylase kinase; PHK; hypoglycemia; muscle glycogenosis; atrophy; metabolic abnormality; growth; diagnosis; kidney dysfunction; failure; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                          New nucleic acid encoding human phosphorylase kinase gamma subunit used for replacement, or gene, therapy of glycogen utilisation disorders, also for drug screening and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%; Score 44; DB 18; Length 307; 90.0%; Pred. No. 24; 1; Indels
                                               /note= "important for catalytic activity"
168..170
/note= "important for catalytic activity"
/note= "putative substrate binding site"
154
                           'note= "putative substrate binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human phosphorylase kinase gamma subunit HPHKG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW76803 standard; Protein; 307 AA.
                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 25pp; English.
                                                                                                                                               96US-0713828.
                                                                                                                                                                      96US-0713828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                           (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                    Goli SK;
                                                                                                                                                                                                                                        WPI; 1997-548985/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 AA;
                                                                                                                                                                                                                                                       N-PSDB; AAT93887.
             Binding-site
                                                                                                                                             13-SEP-1996;
                                                                                                                                                                     13-SEP-1996;
                                                                                              US5683910-A.
                                     Active-site
                                                              Active-site
                                                                                                                      04-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1999
                                                                                                                                                                                                                   Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW76803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW76803
XX
AC AAW7
XX
DT 15-7
XX
XX
DY HWA
XX
KW Phos
KW Phos
KW Phos
KW KW Aidn
  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
HPHKG. The polypeptides and nucleic acids encoding them can be used for treating pathophysiological conditions caused by aberrant forms of phosphorylase kinase (PHK) and by deficiencies in PHK activity. They can utilisation and consequent glucose depletion, e.g. muscle glycogen utilisation and consequent glucose depletion, e.g. muscle glycogenosis, involving muscular weakness and atrophy, and hypoglycemia, which may lead dysfunction or failure. The products can also be used for antibody production, detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylase kinase; gamma subunit; glycogen; calcium dependent; catabolism; glucose; mobilisation; glycogen phosphorylase; GP; regulation; phosphorylation; activation; genetic heterogeneity; muscle; liver; hepatic; glycogenosis; deficiency; disease; exercise intolerance; weakness; muscular atrophy; hypoglycaemia; hepatomegaly; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human phosphorylase kinase gamma subunit - used to develop products for treating e.g. conditions associated with diminished glycogen utilisation and consequent glucose depletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a human phosphorylase kinase gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 20; Length 307;
Pred. No. 24;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human phosphorylase kinase (Phk) gamma subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY52303 standard; Protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1A-B; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.48; S
                                                                                                                                                97US-0919627.
                                                                                                                                                                                                  96US-0713828
97US-0919627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0096245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                             Goli SK;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-008645/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 lsyseeefdv 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LSYSEEEFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV62129
Homo sapiens.
                                                                                                                                             28-AUG-1997;
                                            US5833981-A.
                                                                                                                                                                                                                       28-AUG-1997;
                                                                                                                                                                                               13-SEP-1996
                                                                                              10-NOV-1998
                                                                                                                                                                                                                                                                                                                          Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5977320-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY52303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
```

ò

us-09-485-571-18.rag

```
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB65625;
                                                                                                                                                                                                                                                                                      Seguence
                                  Akira S,
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB65625
                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                This sequence legicalises a movel yamme account. Or prospers, place.

This sequence legicalises a movel yamme account. Or prospers of the regulates glycogen phosphorylases (GP), which is responsible for the catabolic breakdown of glycogen to glucose.

Phy Rhosphorylates GP, thereby activating it, leading to mobilisation of glucose reserves for ATP production. Phy consists of 4 different subunits: regulatory alpha and beta subunits, calmodulin (delta subunit) and the catalytic gamma subunit. Since the enzyme is composed of 4 non-identical subunits, Phy deficiency has significant potential for genetic heterogeneity. Muscle glycogenosis caused by Phx deficiency leads to exercise intolerance, weakness and muscular atrophy. Hepatic phy deficiency is also associated with certain hepatic diseases characterised by hypoglycaemia and hepatomegaly. This Phx gamma subunit or enzymatically active fragments thereof may be used to raise pathophysiological conditions caused by aberrant forms of Phx, and deficiencies in Phx activity. Prior art treatment for Phx deficiency related disease involves dietary regimes which do not prevent the
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRAKI; DRAK2; DAP kinase related apoptosis inducing kinase; human; apoptosis; breast cancer; ovarian cancer; lymphoma; autocimmune disease; viral infection; adenovirus; poxvirus; HIV; Alzheimer's disease; Parkinson's disease; arteriosclerosis; alcoholism; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                            sequence represents a novel gamma subunit of phosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 21; Length 307;
Pred. No. 24;
); Mismatches 1; Indels
                                                                                                               A new antibody to human phosphorylase kinase gamma subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY27161 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                    Claim 1; Fig 1; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0108150.
97JP-0367640.
97JP-0367641.
98JP-0108149.
 96US-0713828
97US-0919627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-JP05974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                 (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        course of the disease.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
'... 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DRAK1 protein.
                                                       Goli SK, Bandman O;
                                                                             2000-021958/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 isyseeefdv 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LSYSEEFFSV 14
                                                                                                                                                                                                                                                                                                                                                                             307 AA;
                                                                                       N-PSDB; AAZ38239
13-SEP-1996;
28-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-APR-1998;
26-DEC-1997;
26-DEC-1997;
17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9933961-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY27161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes.
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

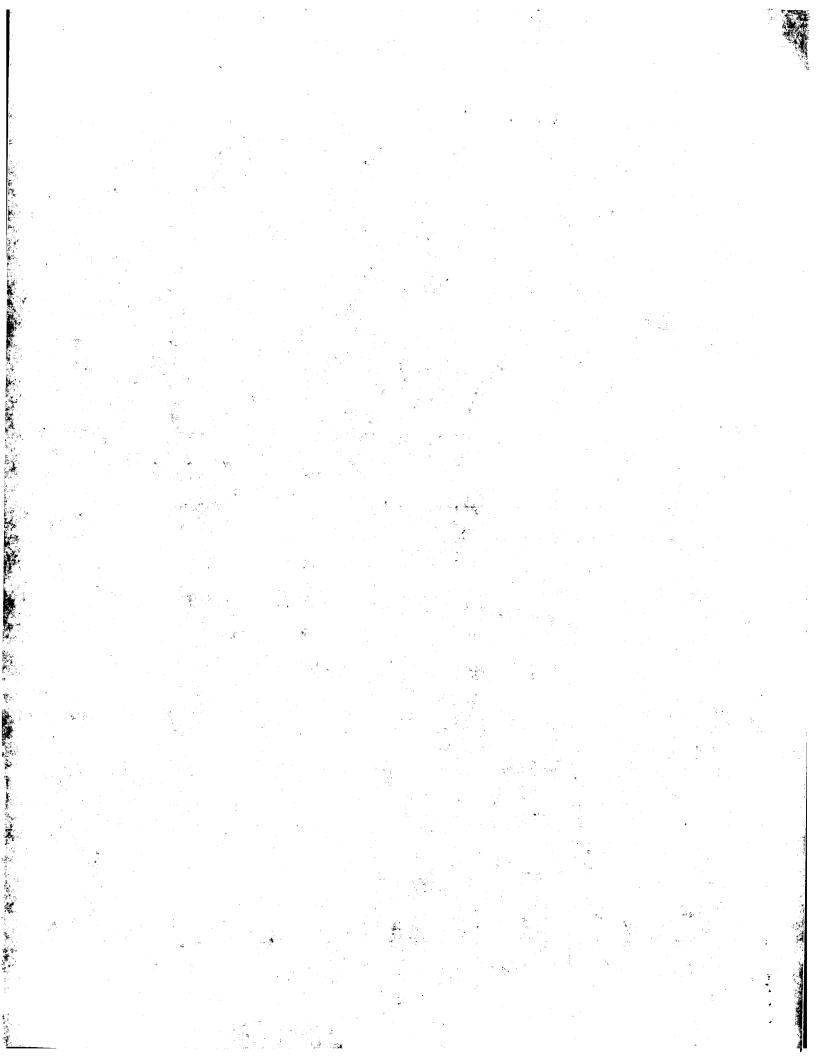
```
apoptosis inducing kinase) having apoptosis inducing activity. The kinases can be expressed recombinantly by transforming host cells with vectors comprising the nucleic acids encoding the kinases. The kinases are useful in the treatment, prevention, diagnosis and investigation of diseases with which apoptosis is associated, such as hormonally regulated cancer (such as breast cancer, ovarian cancer, lymphoma); autolimune diseases; viral infections (such as heroes, adenovirus, poxvirus, HIV); Alzheimer's disease; Parkinson's disease; arteriosciarosis; alocholism; rheumatoid arthritis; and diabetes. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatclogical; antidabetic; antiinfertility; qene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                      New kinase with apoptosis induction activity useful in the treatment of cancer, autoimmune diseases and viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides kinases DRAK1 and DRAK2 (DAP kinase related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 20; Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sudersanam S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 134-137; 180pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein kinase, SEQ ID NO: 151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB65625 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human DRAK1 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%;
(ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-2000; 2000WO-US14842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0136503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-032161/04.
N-PSDB; AAF44651.
                                                                                                                               WPI; 1999-430239/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 lsyseefdv 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LSYSEEEFSV 14
                                                                 Kawai T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SUGE-) SUGEN INC.
                                                                                                                                                                    N-PSDB; AAX89196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200073469-A2.
```

```
Search completed: February 12, 2002, 12:30:30 Job time: 363 sec
           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΩ
                                                                                                  and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and cassays. The kinase polypeptides may be used as antigons in diagnostic assays. The kinase polypeptides may be used as antigons in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase expression and activity, bisases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, conflictive stress related disorders, renal failure, oxidative-stress related disorders, chronic inflammatory pelvic disease, multiple sclerosis, asthma, chronic inflammatory pelvic disease, multiple sclerosis, asthma, conventint, attended the convention of contractions of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                         protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucostitis; gram-negative sepsis; endocarditis; pneumonia; blocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.4%; Score 44; DB 22; Length 414; 90.0%; Pred. No. 34;
                                                                                     The present sequence is a novel protein kinase. The novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
neurodegenerative diseases and/or cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial protegrin peptide (229).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW36429 standard; peptide; 18 AA.
                                            Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US18544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0752852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 lsyseefdv 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LSYSEEEFSV 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1995,
17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW36429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
  δλ
```

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fung, concluding gram-positive and gram-negative bacteria, yeast, fung, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, concluding medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcress associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/Kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                      New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. \rm HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 18; Length 18;
Pred. No. 1.3;
2; Mismatches 6; Indels
        Steinberg DA;
Lehrer RI,
                                                                                                                                                                                                                                                                                                            Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%;
50.0%;
    Gu CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.3
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGELSYSEEFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ggrlcyarrrfavcvg 17
                                                                         WPI; 1997-297871/27.
Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
```

us-09-485-571-18.rag



immun immun

1mmn

Lmmun

Lmmun Lamun immun immun

Lmmun Lmmun Lmmun Lmmun Lmmun

1 mm n

rumun

us-09-485-571-17.rspt

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
"Conservation of an intact vif gene of human immunodeficiency virus type 1 during maternal-fetal transmission.";
J. Virol. 72:1092-1107(1998).

EMBL: AF019547; AAC024161;
InterPro; IPR00475; Viral_infect.
Pfam; PF00559; Vir. 1.
Probom: PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22454 MW; EB2DC350D41A8BA30 CRC64;
                                                                                     human
                                                                                                                                                                         human
                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                                                 human
                                                     human
                                                                                                                                           านแลก
                                                                                                                                                                                             human
                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                               านกลก
                                                                                                                                                                                                                                                                               namur
                                                                                                                                                                                                                                                                                                                 numan
                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                         пвши
                                                                                                                       human
                                                                                                                                                           namar
                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                 human
                                                                       านผลก
                 0080252
0111955
0111955
0056016
0056017
0056018
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
0056031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
Viruses: Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 12;
Pred. No. 5.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                          056040
056041
09WPC9
09E2F6
09E2F5
09E2F3
09E2F3
                                                                                                                                                                                                                                                                                                                                                                                                  Q9E2F1
Q9E2F0
Q9E2E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98105749; PubMed-9445004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17, VIF PROYEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%;
ilarity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||::||||
RGVSIEWRKRKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CM03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          056033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
071966
ID 071
AC 071
DT 01.
 544440

544440

544440

544440

644440

644440

644440

644440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

64440

6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          056033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   056033 human immun 071966 human immun 071971 human immun 071971 human immun 071971 human immun 098024 human immun 011952 human immun 011954 human immun 058070 human immun 050809 human immun 05081 human immun 051166 human immun 071266 human immun
                                                                                                                  Search time 232.64 Seconds (without alignments) 11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          473505 seqs, 146272329 residues
                                                                                                                    February 12, 2002, 12:38:34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      summaries
                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9E2B2
O11952
O11954
O55970
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q73433
Q71266
Q71276
Q73432
Q89450
Q89250
                                                                                                                                                                                                                      1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_fung1:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_mammal:*
sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL_17:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                                           US-09-485-571-17
89
                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_phage: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %
Query
Match I
```

Minimum DB seq Maximum DB seq

Database

Perfect score:

Run on:

Scoring table: Seguence:

ö

071966 PRELIMINARY; PRT; 071966; 01-AUG-1998 (TrEMBLrel. 07, Created)

immun

Q73432 human i Q89450 human i Q80250 human i

Score

Š

Result

STRAIN-HIV-1JC;

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                Chordata; Craniata; Vertebrata; Euteleostomi; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Isolation and Complementation of a Flagellar P-ring Mutant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Gonzalez-Pedrajo B., De La Mora J., Ballado T., Camarena L.,
                                                                                                                                                              A Sato F., Ishida W., Hasegawa T., Mukoyama H.;

"Equine mRNA for chromogranin A.";

Submitted (mAR-1999) to the EMBL/GenBank/DDBJ databases.

R BABD 5570; BAA76748.1;

R InterPro; IPR001819; Chromogranin_AB.

R InterPro; IPR001990; Garain.

R Pfam; PF01271; Granin; 1.

R PRINTS; PR00559; CHROMOGRANIN.

R PROSITE; PS00422; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.

R PROSITE; PS00423; GRANINS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1363;
67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodobacter sphaeroides.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF317649; ARG312086.1;
InterPro; IPR001444; Flag_bb_rod.
InterPro; IPR001899; Gram_pos_anchor.
Pfam; PF00460; flg_bb_rod; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN 1.
SEQUENCE 1363 AA; 133154 MW; AD7BB4856117808C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FLAGELLAR HOOK-ASSOCIATED PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 6
Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.6%; Score 45; DB 57.9%; Pred. No. 67; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     973 RSVSVSYEGQSYTLRMTGG 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q79071;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGVSVSFRRSYSLR--GG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 RSMKLSFRARAYGFRG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGVSVSFRRRSYSLRG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                           TISSUE=ADRENAL MEDULLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodobacter.
NCBI_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dreyfus G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9F5K8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9F5K8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      079071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9F5K8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             079071
                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID DATE OF THE STANDARD OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 12; Length 192;
Pred. No. 8.5;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 45; DB 12; Length 192; 66.7%; Pred. No. 8.5; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                        Mwaengo D.M., Novembre F.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR049494; ARC68843.1; -.
InterPro; IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mwaengo D.M., Novembre F.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ARO(49495; AAC(68852.1; -.
InterPro; IRR00475; Viral_infect.
Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22599 MW; 0D0E1456317A0673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00349; VIRIONINFECT.
PRODOM; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22398 MW; A6E790B042ABC996 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       071971;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN.
                                                                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          furan immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, CHROMOGRANIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GVSVSFRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GVSVSFRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||::|:||||
| 84 GVSIEWRKRSYS 95
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11676;
```

STRAIN-HIV-1NC;

09XS63; E98X60 4

RESULT

g ò

Q9XS63 ID Q9 AC Q9 DT 011 DT 011 DE CH

VIF PROTEIN.

071971

RESULT 071971

g à

1;

```
STRAIN=MNT3.5F.16;
Ahmad N., Yedavalli V.S.R.K.;
ALOW Conservation of Functional Domains of Human Immunodeficiency
Virus Type 1 vif and vpr Genes Correlates with Lack of Vertical
Transmission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97068252: PubMed-8911580;
Tominaga K., Kato S., Negishi M., Takano T.;
Ta high frequency of defective vif genes in peripheral blood mononuclear cells from HIV type l-infected individuals.";
AIDS Res. Hum. Retroviruses 12:1543-1549(1996).
BMBL. D70861: BAA20303.1;
PinterPro; IPR00475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRIONATS; PRO0349; Viral_infect.
SEQUENCE 192 AA; 22595 MW; SB4CF50CCB63E9BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 12; Length 192;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.3%; Score 43; DB 12; Length 192; 53.8%; Pred. No. 18; ative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF275640; AAG32213.1; -.
InterPro: IPR000475; Viral_infect. Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRTONINFFCT. Proposition PD000063; Viral_infect; 1.
NON_TER 192 aA; 22726 MW; BA38FB592232DA07 CRC64;
  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-JUN-2001 (TrEMBLrel. 17, VIF 23 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 4/.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||||::||:|| ||:|
83 QGVSIEWRKRRYSTQVG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGVSVSFRRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.3
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||::|:||
83 QGVSIEWRKRTYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            011954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          011952 011952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
011954
ID 011954
AC 011954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
011952
     DDT REAL WAY AND THE WAY AND THE REAL WAY AND THE REAL WAY AND THE WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Characterization of human immunodeficiency virus type 1 vif gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-VIO5002B1H;
Hassaine G., Agostini I., Candotti D., Bessou G., Caballero M.
Agut H., Autran B., Barthalay Y., The French ALT Study Group,
                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-PATIENT AlO;
MEDLINE-94303241; PubMed-8030283;
Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%; Score 44; DB 12; Length 192; ilarity 47.1%; Pred. No. 12; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 12; Length 192;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     long-term asymptomatic individuals.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL. AFI43128; AAD37895.1;
InterPro, IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRONINFECT.
PPODOEM; PD000063; Viral infect; 1.
SEQUENCE 192 AA; 22506 MW; 5A876245CFA996C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22504 MW; 3163F6B8524974F7 CRC64;
                                                                                                                                                                                                                                                                                         "In vivo genetic variability of the HIV-1 vif gene.";
Virology 203:43-51(1994).
EMBL: Z30679; CAA83159.1; -.
PIGEPPRO: IPRO0045; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROTEIN.
                                               Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9E2B2;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
VIF (VIRAL INFECTIVITY FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||::|:| | : |
83 QGVSIEWRKRRYSTQVG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||::||:|| | : |
83 QGVSIEWRKRRYSTQVG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGVSVSFRRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGVSVSFRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Than 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Kuehn J.E.;
```

09WPB4;

**09WPB4** 

g

ò

Vigne R.;

Q9E2B2

RESULT Q95282 ID Q9 AC Q99 DT 01

æ

õ 셤

ö

Gaps

ö

Gaps

```
Maddock J., Bhatt A., Koch M., Skidmore J.;
"Identification of an essential Caulobacter crescentus gene encoding a member of the Obg family of GTP-binding proteins.";
J. Bacteriol. 179:6426-643[1997].
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21173698; PubMed=11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J., Heidelberg J.F., Alley M.R.K., Ohtea N., Maddock J.R.,
Potocka I., Heidelberg J.F., Alley M.R.K., Ohtea N., Maddock J.R.,
DeBoy R.T., Dodson W.C., Newton A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J. Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
EMBL, AE0019407; AAM51202.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yedavalli V.R., Chappey C., Matala E., Ahmad N.;
"Conservation of an intact vif gene of human immunodeficiency virus
"type I during maternal-fetal transmission.";
J. Virol. 72:1092-1102(1998).
EMBL. AFU19553; AAC03422.1;
InterPro; IPR000475; Viral_infect.
                                                                                                    Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DF81EAC1012A5266 CRC64;
      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GTP-BINDING PROTEIN (GTP-BINDING PROTEIN CGTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 2
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                        STRAIN-NA1000;
MEDLINE-97474268; Pubmed-9335292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CM09;
MEDLINE=98105749; PubMed=9445004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1OBG.
PROSITE; PS00905; GTP1_OBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 354 AA; 37871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00349; VIRIONINFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 06, C
(TrEMBLrel. 06, L
(TrEMBLrel. 17, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GVSVSFRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSVSFREKYIEYGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
VIF PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11676;
                                                                                      CGTA OR CC0315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; CC0315;
                                                                                                                                            Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         056039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   056039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
056039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
          Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C STRAIN-BM07;

X MEDLINE-98105749; PubMed=9445004;

X Pdavalli V.R., Chappey C., Matala E., Ahmad N.;

Y Conservation of an intact vif gene of human immunodeficiency virus

XT "Conservation of an intact vif gene of human immunodeficiency virus

XT Type 1 during maternal-fetal transmission.";

J Virol 7:1092-1102(1989).

BR EMBL; AF0134469; AAC02348.1;

DR FPO0045; Viral_infect.

DR PRINTS; PRO00349; Viral_infect.

DR PRINTS; PRO00349; Viral_infect;

DR PRINTS; PRO00063; Viral_infect;

SEQUENCE 192 AA; 22507 MW; D9A8F709DC2912D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=9706825; PubMed=8911580;
Tominaga K., Kato S., Negishi M., Takano T.;
Tominaga K., Kato S., Negishi M., Takano T.;
A high frequency of defective vif genes in peripheral blood mononuclear cells from HIV type l-infected individuals.";
AIDS Res. Hum. Retroviruses 12:1543-1549(1996).
EMBL; D70864; BAA20305.1; -.
InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 12; Length 192;
Pred. No. 18;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 43; DB 12; Length 192; 53.8%; Pred. No. 18; Live 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22578 MW; 30251A6F286C165E CRC64;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF 23 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VIF PROPIEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1,
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.5,
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||::|||:
83 RGVSIEWRKRGYN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||::|:||
83 QGVSIEWRKRTYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                055970;
```

g

δ

030861; RESULT 12 030861 ID 030861 rAC 030861 030861

Matches

g δŻ

ö

Gaps

ö

Length 354; 6; Indels

```
ö
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-95191036; PubMed-7884906;

Sova P., van Ranst M., Gupta P., Balachandran R., Chao W., Itescu S., MCKInley G., Volsky D.J.;

"Conservation of an intact human immunodeficiency virus type 1 vif gene in vitro and in vivo.";

J. Virol. 69:2557-2564(1995).

EMBL; U42253 AAA83802.1; -.

Interpro; IPRO00475; Viral_infect.

Pfam; PF00559; Viff. 1.

Probom; PD0000635; Viral_infect; 1.

SEQUENCE 185 AA; 21449 MW; D73CFA994D541E2A CRC64;
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                               Score 42; DB 12; Length 141;
Pred. No. 19;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.2%; Score 42; DB 12; Length 185; 53.8%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-MBCC54;
Oclrichs R.B., McPhee D.A., Deacon N.J.;
Submitted (JAN.1998) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF042103; AAD03218.1; -
InterPro: IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22511 MW; E052974F0BC1DA27 CRC64;
ProDom; PD000063; Viral_infect; 1.
NON_TER 141 141
SEQUENCE 141 AA; 16756 MW; 38D693B7A32F094F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2001 (TrEMBLrel. 17, VIRUS INFECTIVITY FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             071266;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-JUN-2001 (TrEMBLrel. 17,
VIF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                               :|||::|:|||
76 QGVSIEWRKRYS 88
                                                                                                                                                                                                                                                              1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGVSVSFRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           073433
073433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            071266
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
073433
AC 073433
AC 073433
DT 01-NOV-
DT 01-JUNOV-
DE VIRUS
DE VIRUS
OC VITUS
OC VITUS
OC NITUS
OC NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
071266
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
        STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
ö
                                 Gaps
                                 ö
 Score 42; DB 12; Length 192; Pred. No. 27; Aismatches 2; Indels
Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
```

1 RGVSVSFRRRSYS 13

:|||::|:||| 83 QGVSIEWRKRGYS

Db

95

Search completed: February 12, 2002, 12:38:35 Job time: 748 sec

```
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                             protein search, using sw model
               Copyright
                                                                •
                                                             OM protein
```

February 12, 2002, 12:39:48; Search time 67.2 Seconds (without alignments) 9.821 Million cell updates/sec

Run on:

RGVSVSFRRRSYSLRGGR 18 US-09-485-571-17 89 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

٦

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	bos taurus	human immun	nicotiana t	helicobacte	helicobacte	buchnera ap	escherichia	escherichia	pseudomonas	homo sapien	human papil	bacteriopha	bacteriopha	ornithorhyn	schistosoma	mycoplasma	t bifunctio	mus musculu	rattus norv	drosophila	bacteriopha	homo sapien	anopheles s	dasyurus vi	antechinomy	antechinus	parantechin	sarcophilus					
	escri	P05059	P04596	P04598	P04597	P18805	P05900	P12503	P49627	Q9zmd3	025074	P57469	P37246	P42641	004804	P10645	P50809	P20345	P07537	P35307	095043	P53663	9x0x60	P26339	P10354	Q9vrb3	037893	P02671	061608	P42135	018745	P42130	018768	P42151
	Ŏ	ā	Δ,	Ā	<u>a</u>	ď	屳	ď	ď	ö	ö	ď	ď	ď	ā	ď	ā,	ď,	ā,	Ġ.	a	<u>D</u> ,	ä	ď	'n.	ä	Ö	₫	ō	Ã	Ö	ď	0	ď
SUMMARIES	ID	CMGA_BOVIN	VIF_HV126	VIF_HV1B5	VIF_HV1EL	VIF_HV1ND	VIF_HV1RH	VIF_HV122	RL13_TOBAC	Y303_HELPJ	Y303_HELPY	Y389_BUCAI	INSI_ECOLI	YHBZ_ECOLI	PFES_PSEAE	CMGA_HUMAN	VE2_HPV36	VG12_BPPH2	VG12_BPPZA	HSP1_ORNAN	RL13_SCHMA	P65_MYCPN	PUR9_THEMA	CMGA_MOUSE	CMGA_RAT	C6V1_DROME	VG12_BPB03	FIBA_HUMAN	NOS_ANOST	HSP1_DASVI	HSP1_ANTLA	HSP1_ANTSW	HSP1_PARBI	HSP1_SARHA
	03	-	Н	-4	-	-	-	٦	7	-		-	-	7	-	-	٦	-	-	-	-	-	-	-	-	-	Н	-	П	П	Н	П	٦	п
	Query Match Length DB	449	188	192	192	192	192	192	202	360	360	334	383	390	446	457	209	854	854	9	184	423	452	463	466	520	860	998	1247	9	61	61	61	61
dР	Query	48.3	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	•	44.9	44.9	44.9	44.9	•	•	٠				•	43.8	•		٠	•	•	42.7	٠.	42.7	42.7	42.7
	Score	43	41	41	41	41	41	41	41	41	41	40	40	40	40	40	40	40	40	39	39	39	38	39	39	39	39	39	39	38	38	38	38	38
	Result No.	н	7	3	4	2	9	7	8	6	10	11	12	13	14	15	16		18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33

	422.7 422.7 7.24 422.7 7.24	62 63 63 132 192	~~~~	HSP1_DASRO HSP1_MURLO HSP1_ANTST VIF_HV1LW	SRO KLO SST 11	P42134 P42140 P42129 Q70623 P03401	dasykaluta murexia lon antechinus human immun
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	192 193 193 193 193 193 193 193 193 193 193	777777	VIE_HVIMN VIE_HVINS VIE_HVINA VIE_HVIX2 R131_BRANA R132_BRANA RL13_ARATH	IN 15 2 2 INA INA	P05898 P12504 P31820 P35964 P41128 P41129	human immun human immun human immun brassica na brassica na arabidopsis
SUL		STANDARD;	ä	ALIGN	ALIGNMENTS RT; 449 AA.		
AC P05059; P79392; DT 13-AUG-1987 (Re DT 01-NOV-1988 (Re	'9392; 17 (Rel. 18 (Rel.	05,	Created) Last seq	Created) Last sequence update)	update)		

20-AUG-2001 (Rel. 40, Last annotation update) CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I) [CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE-Bos taurus (Bovine). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. SEQUENCE FROM N.A.
MEDLINE-92140395; Pubmed-1779968;
Iacangelo A.L., Grimes M., Eiden L.E.;
"The bovine chromogranin A gene: structural basis for hormone replation and generation of biologically active peptides.";
Mol. Endocrinol. 5:1651-1660(1991). CATESTATIN]. 

of SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=86300648; PubMed=3755681;
Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,
Mallet J., Huttner W.B.;
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranin A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure of bovine chromogranic A: a representative (
"The primary structure A: a representative (
"The primary structure A: a representative (
"The primary structure A: a

[3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-86311345; PubMed=3018587;
MEDCINE-86311345; PubMed=3018587;
Igcangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;
Bovine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues.";
Nature 323:82-86(1986).

T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A., "Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from the cDNA sequence."; Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987). Levine M.A.;

SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE,7728583; Pubmed-9074643;
Kang Y. K., Yoo S.H.;
"Identification of the secretory vesicle membrane binding region of chromogranin A.";
Chromogranin A.";
FEES Lett. 404:87-90(1997).

us-09-485-571-17.rsp

```
CHARACTERIZATION OF CATESTATIN.
MEDLINE-97439785; PubMed-9294131;
Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
Gill B.M., Parmer R.J.;
"Novel autocrine feedback control of catecholamine release. A discrete
chromogranin a fragment is a noncompetitive nicotinic cholinergic
                    Yoo S.H., Albanesi J.P.; "a22(+)-induced conformational change and aggregation of chromogranin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99025667; PubMed-98037955,
Tsigelly I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
Khan I., Parmer R.J., O'Connor D.T.,
"Mechanism of action of chromogranin A on catecholamine release:
molecular modeling of the catestatin region reveals a beta-
strand/loop/beta-strand structure secured by hydrophobic interactions
Regul. Pept. 77:43-53(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M., van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.; Antibacterial activity of glycosylated and phosphorylated chromogranin A-derived peptide 173-194 from bovine adrenal medullary chromaffin granules "."
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 266-312.
MEDLINE-8931945; Pubmed-2756155;
Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,
Chang D., Tatemoto K.;
                                                                                                                                MEDLINE=91142185; PubMed=1996343; Salind B., Rader M.-F., Aunis D.; Salindo E., Rill A., Bader M.-F., Aunis D.; Chromostatin, a 20-amino acid peptide derived from chromogranin A, inhibits chromaffin call secretion."; Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION OF CATESTATIN.
MEDLINE-99000113; PubMed-9786174;
Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
"Mechanism of cardiovascular actions of the chromogranin A fragment catestatin in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CABOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
BEDLINE-99459228: Pubmed-10527498;
Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
"Chromogranin A from bovine adrenal medulia: molecular characterization of glycosylations, phosphorylations, and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION OF VASOSTATIN-1.
MEDLINE-20219105; Pubmed-10753865;
Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
Aunis D., Metz-Boutigue M.-H.;
"Antibacterial and antifungal activities of vasostatin-1, the N-
                                                                                                                                                                                                                                                                                                                                                                                                               characterization of bovine pancreastatin.";
                                                                                                                  SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN
                                                                                                                                                                                                                                                                       Galindo E., Rill A., Bader M.-F., Aunis D.;
Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
                                                                           Biol. Chem. 265:14414-14421(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         omaffin granules.";
Biol. Chem. 271:28533-28540(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clin. Invest. 100:1623-1633(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       minal fragment of chromogranin A."
Biol. Chem. 275:10745-10753(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-STRUCTURE MODELING OF CATESTATIN.
    MEDLINE=90354431; PubMed=2387861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Chromaffin granules;
MEDLINE=97067080; PubMed=8910482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 191-212 (CHROMACIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Regul. Pept. 25:207-213(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides 19:1241-1248(1998).
                                                                                                                                                                                                                                                                                                                                                                                                               'Isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antagonist.
                                                                                                                                                                                                                                                      ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminal
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                        -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
                                                                                                                 -i- FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM
CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-
COMPETITIVE NICOTINIC CHOLINEGIC ANTAGONIST.

-i- FUNCTION: VASOSTATIN-I HAS AWTIBACTERIAL ACTIVITY AGAINST GRAM-
POSITIVE BACTERIA M.LUTEUS, B.UBSTHEIS, S.PROGENES, M.FORTUTUM,
S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-
BCOLI, E.CLOACAE, S.TYPHIMMRIUM, K.PNEUMONIAE AND P.AURIGINOSA.
POSISSESS ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.EUMIGATUS,
A.BRASSICOLA, N. HEMATOCOCCA, F. CULMORUM AND F.OXYPORUM AND
AGAINST S.CEREVIASE AND C.ALBICANS YEAST. INACTIVE AGAINST
heterogeneities by mass spectrometry.";
Anal. Blochem. 274.69-80(1999).
-!- FUNCTION: PANGREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
RELEASE FROM THE PANGREAS.
                                                         -1- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE FROM CHROMAFFIN CELLS.
                                                                                                                                                                                                                                                                                                                                  MASS SPECTROMETRY: WW-8584.9; METHOD=MALDI; RANGE=19-94.
MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation;
                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
PHOSPHORYLATION (PARTIAL).
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0659; CHROMOGRANIN.
PROSITE; PSO0422; GRANINS_1; 1.
PROSITE; PSO0423; GRANINS_2; 1.
Signal; Amidation; Glycoprotein; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D-structure; Antibiotic; Fungicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOGRANIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANCREASTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASOSTATIN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATESTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR001990; Chromogranin_AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S79256; AAB21297 11; JOINED.
S79258; AAB21297 11; JOINED.
S79262; AAB21297 11; JOINED.
S79264; AAB21297 11; JOINED.
S79264; AAB21297 11; JOINED.
S79266; AAB21297 11; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M16971; AAA30765.1; EMBL; U73523; AAC48700.1; - PIR; A41520; A41520. PIR; A24175; A24175; PIR; A28033; A28033. PDB; ICFK; 22-MAR-99. GlycoSuiteDB; P05059; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S79270; AAB21297.1;
EMBL; S79256; AAB21297.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X04012; CAA27636.1;
X04298; CAA27841.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01271; Granin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
212
212
312
347
382
99
191
191
315
                                                                                                                                                                                                                                                                                          T.MENTAGROPHYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X04012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphism;
SIGNAL
                                                                                                         LUTEUS
                                                                                                                                                                                                                                                                                                                                                                                    FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
```

```
InterPro; IPR000475; Viral_infect
   NCBI_TaxID=11682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIF_HV1EL
P04597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIF_HV1EL
11D DDT TO DDT T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zaire: nucleotide sequence analysis identifies conserved and variable domains in the envelope gene."; Gene 52:71-82(1987).
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of human immunodeficiency virus from
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Srinivasan A., Anand R., York D., Ranganathan P., Feorino P., Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1). Viruses; Retrold viruses; Retroviridae; Lentivirus.
                             Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%; Score 41; DB 1; Length 188; 53.8%; Pred. No. 3.3; 2; Indels tive 4; Mismatches 2; Indels
                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA; 22159 MW; E3B67D89E0ACDB4F CRC64;
                             Score 43; DB 1;
Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                13-AG-1987 (Rel. 05, Created)
13-AG-1987 (Rel. 05, Last sequence update)
13-UJL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87248097; PubMed-3036660;
                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; K03458; AAA45379.1; -.
PIR; B26192; ASLJZR.
HIV; K03458; VIF$26.
                          48.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.00,
                      Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                           362 RSMRLSFRARGYGFRG 377
                                                                                                                                                   1 RGVSVSFRRRSYSLRG 16
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanchez-Pescador R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 VIE-HV126

TO VIE-HV126

TO 13-AUG-1987

DT 13-AUG-1987

DT 13-AUG-1987

DT 13-AUG-1987

DT 01-JUL-1993

DE VIRION INFE

GN VIE'N CONTROLINE-872

RA STAINWABAN

RA STAINWABAN

RA STAINWABAN

RA STAINWABAN

RA STAINWABAN

RA SANCHEZ-PEB

RY MODECULAT

RT MODECULAT

RT Gene 52:71-CC

CC This SWISS-CC

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIF_HV1B5
P04598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Institute are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILINE-88245056; PubMed-2424612;
ALIZON M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
Cell 46:65-74(1986).
-i- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                           MEDLINE=85111123; PubMed-2578615;
Ratner I., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumelster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                              Wong-Staal F.; "Complete nucleotide sequence of the AIDS virus, HTLV-III."; Nature 313:277-284(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 192 AA; 22520 MW; AC17E169F5354493 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                               -! - FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIRION INFECTIVITY FACTOR (SOR PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00349; VIRIONINFFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; K02012; AAA44654.1; -. HIV; K02012; VIF$BH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; K03454; AAA44326.1; -. EMBL; A07108; CAA00613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 53.0.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00559: Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|||::|||||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV; K03454; VIF$ELI.
SEQUENCE FROM N.A.
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration the European Boinformatics Institute of Bioinformatics and the EMBL outstation the Buropean Boinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spire B., Sire J., Zachar V., Rey F., Barre-Sinoussi F., Galibert F., Hampe A., Chermann J.C., "Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
-!- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                        Score 41; DB 1; Length 192; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%; Score 41; DB 1; Length 192; ilarity 53.8%; Pred. No. 3.4; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                    Indels
                                                                                  SEQUENCE 192 AA; 22689 MW; 169395846CCA2082 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 192 AA; 22556 MW; 15B9BDC424496D22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=90034200; Pubmed=2806917; Population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR00475; Viral_infect. Pfam; PF00559; Vif; 1. PRINTS; PR00349; VIRIONINFFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human immunodeficiency virus.";
Gene 81:275-284(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                 46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M27323; AAA44870.1; -. PIR; JQ0069; ASLJND. HIV; M27323; VIF$NDK.
                                                                                                                              Ouery Match
Best Local Similarity 53.8%
....nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                            :|||::|:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                    1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :[||::|:| ||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             VIF_HV1ND
P18805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIF_HV1RH
P05900:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                    RESULT 5
VIF_HYIND
DI VIE HYIND
DT 01-NOV
DT 01-NOV
DT 01-JUN
ON VIRION
ON CC 1-1- FU
CC 1-1- F
                                                                 AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIF_HVIRH
ID VIF_HV
AC P05900
DT 01-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
      SWE
                                                                                                                                                                                                                                  δŏ
                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                 Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                 Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow s
Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 192;
Pred. No. 3.4;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 AA; 22687 MW; F005E0AE621A5C6C CRC64;
01-NOV-1988 (Rel. 09, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIF_HV122 STANDARD; PRT; 192 AA. P12503; 01-0CT-1989 (Rel. 12, Created) 01-0CT-1989 (Rel. 12, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update) VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theodore T., Buckler-White A.;
Submitted (NOV-1988) to the HIV data bank.
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                            Submitted (XXX-1987) to the HIV data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M22639; AAA45367.1; -.
HY, M22639; VIF$2226.
InterPro; IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M17451; AAA45054.1; -.
HIV; M17451; VIF$RF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00349; VIRIONINFFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|||::|:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=11701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11683;
                                                                                                                                                                                                                                                                                                                                                                        Wong-Staal F.
```

```
NCBI_TakID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y303_HELPY
ID Y303_HELPY
AC O25074;
                                                                                                                                                                                                                                         Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Estruch J.J., Crossland L., Goff S.A.;
"Plant activating sequences: positively charged peptides are functional as transcriptional activation domains.";
Nucleic Acids Res. 22.3989.1994).
-I- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.1%; Score 41; DB 1; Length 202; 53.3%; Pred. No. 3.6; 1ve 3; Mismatches 4; Indels
                                                                                                       Length 192;
                                                                                                                                              2; Indels
                                         0294A76114C7C643 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 AA; 23391 MW; 522CB43CCD80A67E CRC64;
                                                                                                     Score 41; DB 1;
Pred. No. 3.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
60S RIBOSOMAL PROTEIN L13 (CLONE 6.2.1).
                                                                                                                                                                                                                                                                                                                                         202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L31416; AAA72054.1; -.
InterPro; IPR001380; Ribosomal_L13E.
Pfam; PF01294; Ribosomal_L13e; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probom; Proiss, Kidosomal_Li3e; 1.
Prodom; P0004443; Ribosomal_Li3E; 1.
PROSITE; PS01104; RIBOSOMAL_Li3E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. XANTHI; TISSUE-Seedling;
MEDLINE-95023159; Pubmed-7937121;
                                                                                                                                                                                                                                                                                                                                            PRT;
ProDom; PD000063; Viral_infect; 1.
                                         22572 MW;
                                                                                                       46.18;
                                                                                                                             53.8%;
                                                                               Ouery Match
Best Local Similarity 53.0-
المالية كالمالية كالمالية
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 GIAVDHRRRNRSLEG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GVSVSFRRSYSLRG 16
                                                                                                                                                                                        1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                  83 QGVSIEWRKRRYS 95
                                         192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein.
                                                                                                                                                                                                                                                                                                RESULT 8
RL13_TOBAC
ID RL13_TOBAC
AC P49627;
                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@licensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericensericenserice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-26695, ATCC 700392;
MEDLINE-97304467; PubMed-9222185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                          Alm R.A. Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Dolg P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001465; AAD05858.1; -.
InterFor: IRR00755; GTPL_OBG.
Pfam; PF01018; GTPL_OBG.
PROSTTE; PS00936; GTPLOBG.
Hypothetical protein; GTP-binding; Complete proteome.
NP_BIND 10 210 214 GTP (BY SIMILARITY).
NP_BIND 279 282 GTP (BY SIMILARITY).
SEQUENCE 360 AA; 38872 MW; 4C658B6479AA38FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
-- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1;
Pred. No. 6.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE GTP-BINDING PROTEIN HP0303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSFRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1|||| :::||
20 VSFREKFVIKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
```

```
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KESULT 12
INSI_ECOLI
                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Ganome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. ABS."; Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESOURNCE OF 229-334 FROM N.A.

MEDLINE-20245558; Pubmed-10781569;
Jimenez N., Gonzalez-Candelas F., Silva F.J.;
Jimenez N., Gonzalez-Candelas F., Silva F.J.;

"Prephenate dehydratase from the aphid endosymbiont (Buchnera) displays changes in the regulatory domain that suggest its desensitization to inhibition by phenylalanine.";
J. Bacteriol. 182:2967-2969(2000).

-: SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY. STRONG, TO E.COLI YHBZ OR H.INFLUENZAE H10877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%; Score 41; DB 1; Length 360; 53.8%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                           nding; Complete proteome.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 74FC579D9643DAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; gamma subdivision; Buchnera
pylori.";
Nature 388:539-547(1997).
-!- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y389_BUCAI STANDARD, PRT, 334 AA. P57469; Q97455; Q9L4J5; Q0-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update HYPOTHETICAL GTP-BINDING PROTEIN BU389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                InterPro; IPR000765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1OBG; 1.
Hypothetical protein; GTP-binding; NP_BIND 163 170 GTP (BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=TOKYO 1998;
MEDLINE=20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                     EMBL; AE000548; AAD07372.1; -. TIGR; HP0303; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                210 214 GT
279 282 GT
360 AA; 38707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8 هاندي 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||| : ::||
20 VSFRREKFVIKGG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VSFRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
  RAME AND DESCRIPTION OF THE STATE OF THE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dalrymple B., Caspers P., Arber W.; "Nucleotide sequence of the prokaryotic mobile genetic element IS30."; EMBO J. 3:2145-2149(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / W3110;
Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fikuda R., Ichihara S.,
Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
"Systematic sequencing of the Escherichia coli genome: analysis of the
4.0 - 6.0 min (189,987 - 281,416bp) region.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN+ELZ / MG1655;
MEDLINE-95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blattner F.R.;
Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92-8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSI_ECOLI STANDARD; PRT; 383 AA.
P37246; P77341;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSPOSASE INSI FOR INSERTION SEQUENCE ELEMENT IS30B/C/D.
(INSII OR B0256) AND (INSIZ OR B1404) AND (INSI3 OR B4284).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 1; Length 334;
Pred. No. 9.4;
1; Mismatches 4; Indels
EMBL; AP001119; BAB130>,
EMBL; AP001119; BAB130>,
EMBL; A7330443; GAB90993.1;
InterPro; IPR007055; GTP1_OBG;
Pfan; PF01018; GTP1_OBG; 1.

OR PRINTS; PR00326; GTP1_OBG; FALSE_NEG
PROSITE; PS009965; GTP1_OBG; FALSE_NEG

PROSITE; PS009965; GTP1_OBG; FALSE_NEG

ORD (BY SIMILARITY).

GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                    L -> P (IN REF. 2).
54F7A07404FA7E85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12;
MEDLINE=85027168; PubMed=6092059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 44.9%;
Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VSFRRSYSLRGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| | :||
21 VSFRREKYIPKGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                      NCBI_TaxID=562;
                         B3183.
                                                                                                                                                                     STRAIN-K12 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFES_PSEAE
Q04804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
NP_BIND
SEQUENCE
                         THBZ OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
      REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
PFES_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SO THE TAX A PART OF COURT OF A PART OF A PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prodom; PD00299; Transposase_1S30; 1.
PROSITE; PS01043; TRANSPOSASE_1S30; 1.
Transposition; Transposable element; DNA-binding; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                               MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.9%; Score 40; DB 1; Length 383; 50.0%; Pred. No. 11; tive 4; Mismatches 4; Indels
                                                                                                    Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L -> V (IN B0256).
F -> I (IN REF. 4).
A -> T (IN REF. 4).
; 6AADF2CD604B0F83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X00792; CAA25376.1; --
EMBL; U14003; AAA97180.1; --
EMBL; AE000133; AAC73359.1; --
EMBL; AE000337; AAC74486.1; --
EMBL; D8536; -; NOT_ANNOTATED_CDS.
EMBL; D90778; BAA15010.1; --
EMBL; D90778; BAA15010.1; --
PTR; S28740; S28740.
ECGGENE; EG40009; inst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001584; Rve.
InterPro; IPR001598; Transposase_IS30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 5 F
27 27 P
383 AA; 44281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: |||:||| ||
184 ENIQHLRRSHSLRHGR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE FROM N.A.
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                   Davis R.W.;
                                                                                                                                                                     STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
  ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=PAO;
MEDLINE-9336425; PubMed-8361354;
MEDLINE-9336425; PubMed-8361354;
Dean C.R., Poole K.;
"Expression of the ferric enterobactin receptor (PfeA) of Pseudomonas aeruginosa: involvement of a two-component regulatory system.";
Mol. Microbiol. 8:1095-1103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            MEDILINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coll K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: BELONGS TO THE GTP1 / OBG FAMILY. STRONG, TO
H.INFLUENZAR HIO877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 390;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nding; Complete proteome.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 3A6EBF56F24B7C47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PERSOR PROTEIN PFES (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U18997; AAA57984.1; -.
EMBL; AE000399; AAG76215.1; -.
ECOGENE: EG12795; yhbZ.
InterPro; IPR000765; GTP1_OBG.
Pfam; PF01018; GTP1_OBG; 1.
PRINTS; PR00326; GTP1_OBG; 1.
Hypothetical protein; GTP1_OBG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 217 G
283 286 G
390 AA; 43286 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111 | : ||
21 VSFRREKYIPKGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSFRRSYSLRGG 17
                                                                                                                                                                                         MG1655;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ************************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                          -!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM PFER/PFES.
STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Stover C.K., Other S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
Nature 406:959-964(2000)",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
[CORTROWGGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I)
[CONTAINS: VASOSTATIN I; VASOSTATIN II; EA-92; ES-43; PANCKBASTATIN;
SS-18; WA-8; WE-14; LF-19; AL-11; GV-19; GR-44; ER-37].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                         MAY ACTIVATE PFER BY PHOSPHORYLATION.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                        (POTENTIAL).
SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transduction; Transferase; Kinase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 446; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> E (IN REF. 1).
D1DA4FED1C222547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmenbrane; Inner membrane; Complete proteome.
DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L07739; AAA25930.1; -.
EMBL; AE004696; AAG06075.1; -.
InterPro: IPR0004010; Bctrl_sensor.
InterPro: IPR000406; DuP5.
InterPro: IPR003660; HAMP.
InterPro: IPR003661; His_kinA.
Pfam; PF00512; DuP5; 1.
Pfam; PF00512; Bupfase_c; 1.
Pfam; PF00512; Signal; 2.
SMARY; SW00304; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 GLGLAIARRAIELOGGR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00388; HiskA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GVSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
155
176
446
244
304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244
304
446 A
                                                                                                                                                                                                                                                                                                                                KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMGA_HUMAN
P10645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sensory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CMGA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
    RRARAR RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID DE DE OC OC OC OC
```

```
MEDLINE-90336639; PubMed-2165909;
Tamamura H., Ohta M., Yoshizawa K., Ono Y., Funakoshi A.,
Miyasaka K., Tateishi K., Jimi A., Yajima H., Fujii N., Funakoshi S.,
"Isolation and characterization of a tumor-derived human protein
related to chromogranin A and its in vitro conversion to human
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88059106; PubMed-2445752; Ronecki D.S., Benedum U.M., Gerdes H.H., Huttner W.B.; "The primary structure of human chromogranin A and pancreastatin."; J. Biol. chem. 262:17026-17030(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94165095; PubMed=8120054; Mouland A.J., Bevan S., White J.H., Hendy G.N.; "Human chromogranin A gene. Molecular cloning, structural analysis, and neuroendocrine cell-specific expression."; J. Biol. Chem. 269:6918-6926(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Adrenal gland; MEDLINE-86206941; PubMed-3704195; Wilson B.S., Phan S.H., Lloyd R.V.; Wilson B.S., Phan S.H., Lloyd R.V.; "Chromogranin from normal human adrenal glands: purification by monoclonal antibody affinity chromatography and partial N-terminal amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-22451; Pubmed-1577173; Curry W.J., Shaw C., Johnston C.F., Thim L., Buchanan K.D.; Curry W.J., Shaw C., Johnston C.F., Thim L., Buchanan K.D.; "Isolation and primary structure of a novel chromogranin A-derived peptide, WE-14, from a human midgut carcinoid tumour.";
                                                                                                                                     MEDLINE=88298816; PubMed=3403545;
Helman L.J., Ahn T.G., Levine M.A., Allison A., Cohen P.S.,
Cooper M.J., Cohn D.V., Israel M.A.;
"Molecular cloning and primary structure of human chromogranin A (secretory protein I) CDNA."
J. Blol. Chem. 263:11559-11563(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The spectrum of endogenous human chromogranin A-derived peptides identified using a modified proteomic strategy."; Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation of human pancreastatin fragment containing the active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sekiya K., Ghatei M.A., Minamino N., Bretherton-Watt D., Matsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orr D.F., Salmon A.L., Johnsen A.H., Chalk R., Buchanan K.D.,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 384-397.
Mouland A.J., Bevan S., White J.H., Hendy G.N.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
MEDLINE=88137586; PubMed=2830133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 191:33-39(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regul. Pept. 13:207-233(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence from a glucagonoma."
FEBS Lett. 228:153-156(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide, WE-14, from a human |
FEBS Lett. 301:319-321(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF DERIVED PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 134-319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 291-319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 342-355
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreastatin-48.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 19-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9852066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloom S.R.;
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shaw C.;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
Gadroy P., Stridsberg M., Capon C., Michalski J.-C., Strub J.-M., Van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.; Phosphorylation and O-glycosylation sites of human chromogranin A (CGA79-439) from urine of patients with carcinoid tumors."; J. Biol. Chem. 273:34087-34097(1998).

-I FUNCTION: PANCRESASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN RELEASE FROM THE PANCRESA.

-I SUBCELLUIAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
                                                                                                                                                                                                                                                                                                                                                                -1- MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
-1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
AMIDATION (G-320 PROVIDE AMIDE GROUP).
AMIDATION (G-457 PROVIDE AMIDE GROUP).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001819; Chromogranin_AB.
InterPro; IPR001990; Granin.
InterPro; IPR001271; Granin.
PROSTOR: PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00433; GRANINS_2; 1.
Suffani, Amidation; Glycoprotein; Calcium-binding; Phosphorylation; Suffanion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-LINKED (GALNAC. ..).
/FIIG-CAR_000116.
O-LINKED (GALNAC. ..).
/FIIG-CAR_000117.
O-LINKED (GALNAC. ..).
/FTIG-CAR_000118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOGRANIN A. VASOSTATIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION. PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ES-43.
PANCREASTATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, J03915; AAA52018.1; EMBL, J03483; AAA52017.1; EMBL, U03749; AAB53685.1; -1 EMBL, U03742; AAB53685.1; JOINED. EMBL, U03743; AAB53685.1; JOINED. EMBL, U03744; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03746; AAB53685.1; JOINED. EMBL, U03747; AAB53685.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LF-19.
AL-11.
GV-19.
GR-44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: 003749; AAB53685.1; EMBL: 003742; AAB53685.1; EMBL: 003743; AAB53685.1; EMBL: 003748; AAB53685.1; EMBL: 003748; AAB53685.1; EMBL: 003745; AAB53685.1; EMBL: 003747; AAB53685.1; EMR: AAS468; AAS468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
                                                                                                                                                                                                                                                                                                                               GRANULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
            RRRRA BARRA BARRA
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
S -> Y (IN REF. 1).

Q -> K (IN REF. 1).

E -> Q (IN REF. 1).

E -> Q (IN REF. 1).

N -> K (IN REF. 1).

E -> V (IN REF. 1).

A -> V (IN REF. 1).

SK -> TN (IN REF. 1).

SK -> TN (IN REF. 1).

SK -> TN (IN REF. 1).

N -> S (IN REF. 1).

A -> G (IN REF. 1).

B -> G (IN REF. 1).

C -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: February 12, 2002, 12:39:48
Job time: 801 sec
   44.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : :||| |:| ||
372 MKLSFRARAYGFRG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VSVSFRRRSYSLRG
                                          CONFLICT
CON
              ð
```

us-09-485-571-17.rsp

```
4.5
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2000
                                                                          OM protein - protein search, using sw model
```

February 12, 2002, 12:34:35; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec 1 RGVSVSFRRRSYSLRGGR 18 US-09-485-571-17 89 Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

219241

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	viral infectivity	chromogranin A pre	-		viral infectivity		viral infectivity	infecti	vif protein - huma	viral infectivity	viral infectivity	ribosomal protein	hypothetical prote	Ω	hypothetical prote	~													
SUMMARIES	OI	S42988	A41520	ASLJZR	ASLJND	S42999	S42966	S43000	S42997	S42998	S42968	S42980	S42959	S42945	S43004	S42974	S42958	S42979	S42961	S42965	S42955	S42940	S54379	S42954	S42953	S50116	915	G64557	B71952	52
	DB	7	П	٦	٦	7	~	7	7	~	7	~	7	~	7	7	~	~	~	~	~	~	~	7	7	7	7	-	~	7
	Length	192	449	188	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	192	202	289	360	360	445
æ	Query	49.4	48.3	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1	46.1
	Score	44	43	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
	esult No.	1	7	m	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

Similar to tuftel1	hypothetical prote	hypothetical prote	hypothetical prote	splicing factor PR	hypothetical prote	unknown protein en	hypothetical prote	unknown protein en	viral infectivity	IS30 transposase [	hypothetical prote	probable GTP-bindi	transposase - Esch	GTP-binding protei	probable GTP-bindi
E86306	E75278	T44045	T44231	T06077	B96832	D85844	A85629	D85680	S42967	A85911	D84975	C71286	F65241	A65109	A85982
7	~	7	7	7	7	7	7	7	~	~	~	~	٦	-	7
849	874	1513	1520	2352	2359	645	645	645	192	251	334	376	383	390	390
46.1	46.1	46.1	46.1	46.1	46.1	45.5	45.5	45.5	44.9	44.9	44.9	44.9	44.9	44.9	44.9
4.1	4.1	4.1	4.1	4.1	4.1	40,5	40.5	40.5	0	40	0;	0	0,*	0 †	40
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

NESULT I S42988
viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: S42988
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: S42940
A; Accession: S42988
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 <wie></wie>
A; Cross-references: EMBL: Z30679; NID:q459595; PIDN: CAA83159.1; PID:q459596
C;Superfamily: AIDS vif protein

Gaps ö Length 192; Indels Score 44; DB 2; Pred. No. 4.6; 5; Mismatches Query Match 49.4%; Best Local Similarity 47.1%; 8; Conservative

1 RCVSVSFRRSYSLRGG 17 δλ

ö

:|||::||::| 83 QCVSIEWRKRRYSTQVG 99

qq

Chromogranin A precursor [validated] - bovine
N; Alternate names: pituitary secretory protein I; secretory protein I
N; Contains: chromostatin; pancreastatin
C; Species: Bos primigenius taurus (cattle)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C; Accession: A41520, A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
R; Tacangelo, A.L.; Grimes, M.; Eiden, L.E.
Mol. Endocrinol. 5, 1651-1660, 1991
A; Title: The bovine chromogranin A gene: structural basis for hormone regulation an A; Reference number: A41520; MUID: 92140395
A; Status: not compared with conceptual translation
A; Accession: A41520
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-449 < AAC>
A; Cross-references: GB: S79270; NID: 9244423; PIDN: AAB21297.1; PID: 9244424
A; Residues: 1-449 < AAC>
A; Cross-references: GB: S79270; NID: 9244423; PIDN: AAB21297.1; PID: 9244424
A; Reference number: A28033; MUID: 97260925
A; Title: Primary structure of bovine pituitary secretory protein I (chromogranin A)
A; Reference number: A28033; MUID: 97260925
A; Molecule type: mRNA
A; Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 380-449 < ANN>
A; Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 1919163728

```
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S42999
                                                                                           g
                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
R. Weber is authors translated the codon Cod for residue 391 as Gin

A. Weber is an authors translated the codon Cod for residue 391 as Gin

A. Willier 2019 25 46, 1596 4.

A. Willier 2019 25 46, 1596 4.

A. Willier 2019 25 46, 1596 4.

A. Welesence munber: A2175, WID: 66311340 and distribution of its messenger RNA in endocrial Accession A4175.

A. Westerson C. A4175.

A. Westerson C. A4175.

A. Westerson A4175.

A. Westerson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F:142-161/Product: chromostatin #status predicted <MAT3>
F:266-312/Product: pancreastatin #status experimental <MAT2>
F:35-56/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.3%;
ilarity 50.0%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match'
Best Local Similarity
Matches 8; Conserv
```

```
Aslucian burners of protein protein control co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residuss: 1-188 <SRI>
A;Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45379.1; PID:g329402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S4299
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                               vif protein - human immunodeficiency virus 2r-6
N;Alternate names: orf-Q protein; sor protein
C;Species: human immunodeficiency virus 2r-6
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ore 41; DB 1
ed. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Gene: Vif
C;Superfamily: AIDS vif protein
C;Keywords: AIDS; immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%;
53.8%;
                                            | : :||| | | ||
362 RSMRLSFRARGYGFRG 377
RGVSVSFRRRSYSLRG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||::|:| ||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||: :|:| ||
83 QGVSIEWRKRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B26192
```

ó

Gaps

; 0

Length 449; 6; Indels

Score 43; DB 1; Pred. No. 16; Mismatches

```
œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                        RESULT
S42997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $42968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
S43000
viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: $43000
R; Wieland, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $43000
A; Accession: $43000
A; Accession: $43000
A; Accession: $43000
A; Residues: 1-192 <WIE>
A; Residues: 1-192 <WIE>
A; Residues: 1-192 <WIE>
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C; Accession: $42966
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: $42966
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: $42999
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-192 - VIIE>
A; Residues: 1-192 - VIIE>
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA_A;Mostures 1-192 CWIE>
A;Restidues: 1-192 CWIE>
A;Cross-references: EMBL:Z30627; NID:g459496; PIDN:CAA83104.1; PID:g459497
C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 192;
Pred. No. 15;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192;
                                                                                                                                                                                                                            Length 192;
                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                          Score 41; DB 2;
Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 2
Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%;
53.8%;
                                                                                                                                                                                                                            46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%;
53.8%;
                                                                                                                                                                                                     Query Match
Best Local Similarity 53.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||::|||||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                               83 OGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
C;Species: Numan immunodeficiency virus type 1, HIV-1 (C;Species: No. 1999) (C;Accession: S4297) (C;Accession: Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994 (A;Bescription: In vivo genetic variability of the HIV-1 gene. A;Reference number: S4294) (A;Accession: S4297) (A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: 842968
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. Subnitted to the EMBL Data Library, March 1994
A;Description: In vivo genetic variability of the HIV-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: 542998
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A;Bescription: In vivo genetic variability of the HIV-1 gene.
A;Reference number: 542940
A;Accession: 542998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-refexences: EMBL:230689; NID:g459615; PIDN:CAA83169.1; PID:g459616
C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule, type: DNA
A; Residues: 1-192 <WIE>
A; Cross-references: EMBL: 230629; NID: 9459500; PIDN: CAA83106.1; PID: 9459501
C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
viral infectivity factor vif - human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB :
Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB Pred. No. 15; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| |: :|:| ||
83 QGVSIEWRKRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||::||||
83 QGVSIEWRKRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S42968
```

Length 192

2;

46.1%; 53.8%;

4

```
A;Status: preliminary
A;Moleoule type: DNA
A;Residues: 1-192 - GNIE>
A;Residues: 1-192 - GNIE>
A;Cross-references: EMBL:Z30606; NID:g459456; PIDN:CAA83083.1; PID:g459457
C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 12, 2002, 12:34:36
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                     A; Accession: S42945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                 RESULT 11
S42980
viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: 842980
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. Submitted to the EMBL Data Library, March 1994
A;Bescription: In vivo genetic variability of the HIV-1 gene.
A;Reference number: $42940
A;Reference number: $42940
A;Accession: $42980
A;Accession: Draliminary
A;Molecule type: DNA
A;Residues: 1-192 <AHIED
A;Cross-references: EMBL:230641; NID:9459524; PIDN:CAA83118.1; PID:9459525
C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viral infectivity factor vif - human immunodeficiency virus type 1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Species: human immunodeficiency virus type 1, HIV-1
C; Accession: 542959
R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
Submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene.
A; Reference number: $42940
A; Accession: 542959
A; Cacssion: 542959
A; Cacssion: S42959
A; Cacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S42945

Viral infectivity factor vif - human immunodeficiency virus type 1

Viral infectivity factor vif - human immunodeficiency virus type 1

C; Species: human immunodeficiency virus type 1, HIV-1

C; Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999

C; Accession: S42945

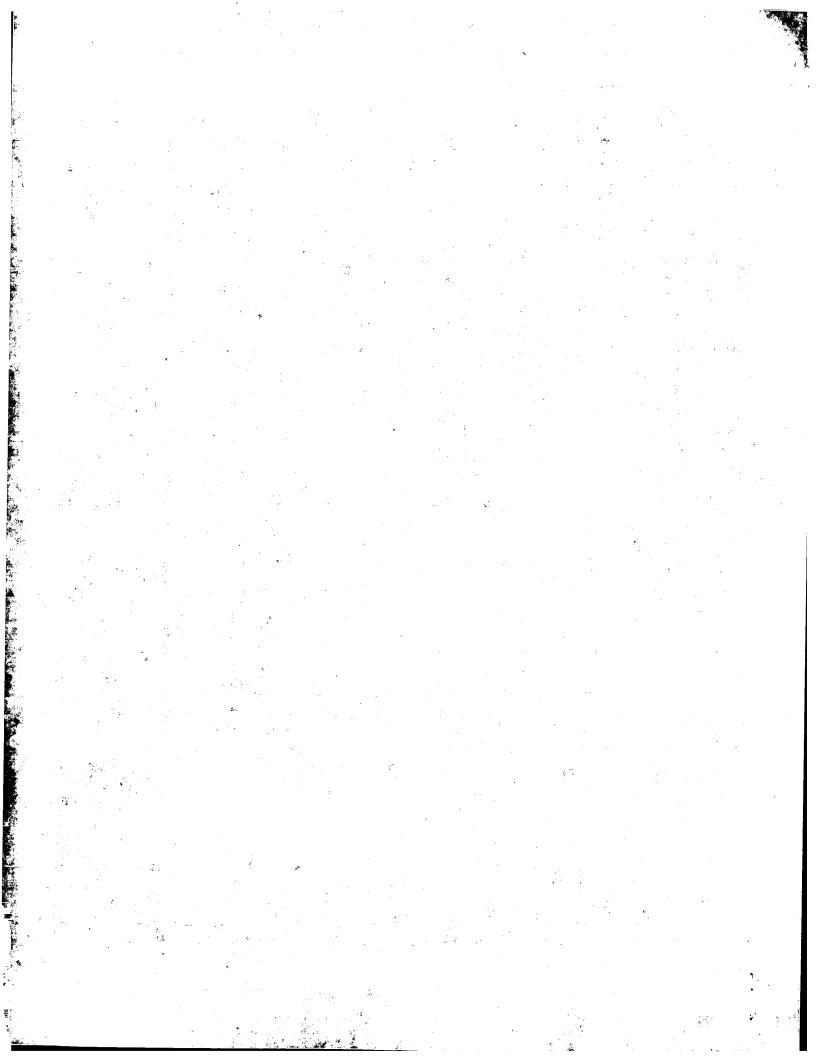
S; Wieland, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H,J; Kuehn, J.E. submitted to the EMBL Data Library, March 1994

A; Description: In vivo genetic variability of the HIV-1 gene.

A; Reference number: S42940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.J.; Kuehn, J.E.
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
          Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
       5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2;
Pred. No. 15;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 2
Pred. No. 15;
4; Mismatches
       Score 41; DB
Pred. No. 15;
                                                                      4; Mismatches
46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.18;
53.88;
                               Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                 1 RGVSVSFRRSYS 13
                                                                                                                                                                        :|||::||:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :[||::|:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                             Ωp
                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
S43004
viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: S43004
R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A;Description: In vivo genetic variability of the HIV-1 gene.
A;Reference number: S42940
A;Reference number: S43004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <WIE>
A;Residues: 1-192 <WIE>
A;Cross-references: EMBL:Z30695; NID:g459627; PIDN:CAAB3175.1; PID:g459628
C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral infectivity factor vif - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C;Accession: $42974
R;Wieland, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, J.E. Submitted to the EMBL Data Library, March 1994
A;Bescription: In vivo genetic variability of the HIV-1 gene.
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Residues: 1-192 <WIE>
A) Cross-references: EMBL:230635; NID:g459512; PIDN:CAA83112.1; PID:g459513
C) Superfamily: AIDS vif protein
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 192
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
Score 41; DB 2
Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2
Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%; Score 41; DB
53.8%; Pred. No. 15;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%;
53.8%;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 53.8
Matches 7; Conservative
                                                                                            13
                                                                                                                       :|||::|:|||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|||::||||
83 QGVSIEWRKRRYS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                         1 RGVSVSFRRSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 QGVSIEWRKRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGVSVSFRRRSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S42974
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
```

Job time: 554 sec



```
18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                      US-08-752-852A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME, KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7, Appli
7, Appli
2, Appli
2, Appli
1, Appli
2, Appli
1, Appli
1, Appli
1, Appli
1, Appli
4, Appli
                                                                                             (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, 7
Sequence 18, 8
Sequence 28, 8
Sequence 27, 8
Sequence 7, 8p
Sequence 7, 8p
Sequence 2, 8p
Sequence 2, 8p
Sequence 2, 8p
Sequence 17, 8p
Sequence 17, 8p
Sequence 2, 8p
Sequence 2, 8p
Sequence 2, 8p
Sequence 2, 8p
Sequence 17, 8p
Sequence 2, 8p
                                                                             February 12, 2002, 12:32:21; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-752-852A-15
US-08-752-852A-14
US-08-752-852A-11
US-08-752-852A-11
US-08-752-852A-15
US-08-6493A-93
US-08-6493A-93
US-08-6493-73
US-08-6493-73
US-08-647-7
US-08-886-269-1
US-08-886-269-1
US-08-886-269-1
US-08-886-269-1
US-08-886-269-1
US-08-886-269-1
US-08-886-269-1
US-08-167-647-1
                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-342-084-10
US-08-463-210-10
US-09-014-969-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-641-314C-2
                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                               RGVSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                    US-09-485-571-17
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of
                                                                                                                                                  Perfect score:
                                                                                                                                                                                          Scoring table:
                                                      ı
                                                     OM protein
                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
```

```
TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserve
                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21 CLASSIFICATION:
              US-08-752-852A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-752-852A-11
                                                                                                                                                                                                                                                                    CITY: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ĥ
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54.5; DB 2; Length 17; Pred. No. 0.0032; 0; Mismatches 4; Indels
                                                                               Length 18
; OTHER INFORMATION: all amino acids are D amino acids US-08-752-852A-15
                                                                          Score 69; DB 2; 1
Pred. No. 1.2e-05;
0; Mismatches 4,
                                                                                                                                                                                                                                                       Sequence 14, Application US/08752852A
Fatent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harwig Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARR: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION UNDABER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELERION: 212-790-9090
TELEX: 66141
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.2%;
72.2%;
                                                                        ch 77.5%;
1 Similarity 77.8%;
14; Conservative
                                                                                                                                           1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                1 RGVCVCFRRCYCLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGVSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGVCVCFRRCY-CRGGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.2
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS: unknown unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: peptide US-08-752-852A-14
                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                         US-08-752-852A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                           Matches
                                                                                                                                                                         OD
                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

RESULT

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.8%; Score 47; DB 2; Length 15; 71.4%; Pred. No. 0.053; tive 0; Mismatches 4; Indels
Sequence 10, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Gree, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer
APPLICANT: Leh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chang, Conway
APPLICANT: Chang, Chee-Liang
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/752,852A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
GAPPLICANT: Chang, Conway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,
FILING DATE: 21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-752-852A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGVCVCFRRCYCL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGVSVSFRRRSYSL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Taylor, Ethan W.

TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
SPRIOR FILING DATE: 1995-09-01
SROPHWARE: PALENTIN VET: 2.0
SEQ ID NO 93
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBLOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2;
Pred. No. 0.053;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 4
Pred. No. 3.9;
4; Mismatches
        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEX/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 93, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.18;
                                                                                                                                                                                                       TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 46.7.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-752-852A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGVSVSFRRRSYSLR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | |: : | | ||: |
9 KGSSIRYRSRCYSIR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGVSVSFRRRSYSL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGVCVCFRRCYCL 14
                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unl
TOPOLJGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-679-493A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-679-493A-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.8%; Score 47; DB 2; Length 15; ilarity 71.4%; Pred. No. 0.053; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Gu, Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DAS
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NAME:
FILING DATE:
ATONEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAX: 212-790-9990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTEM: DOS
SOFTWARE: FASTESCO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08752852A Patent No. 5994306 GENERAL INFORMATION:
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) MOLECULE TYPE: peptide US-08-752-852A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGVSVSFRRRSYSL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGVCVCFRRCYCL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
                                                                                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                   RY: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-752-852A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NY
                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
```

ö

```
Gaps
                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                               Score 40; DB 1; Length 18; Pred. No. 0.99;
                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%; Score 40; DB 1; Length 18;
44.4%; Pred. No. 0.99;
tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIN S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURAGHIGE, KARE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMULICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFRAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 48, Application US/08499523
; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-48; Sequence 48, Application US/09128345
                                                                                                                                                                                           44.98;
                                                                                                                                                                                                                                                                       1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                       Query Match
Best Local Similarity 44.4*
Pest Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 887-076.
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 18 amino acids
                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                              ; TOPOLOGY:
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                     US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 1; Length 18; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION : 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGBNT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
TELEPRAX: (202) 887-1500
TELEEX: 90-4030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/08243879A
Patent No. 5708145
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RATRISFSRRRFSVSVGR 18
                                                                                             ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                          CLIL
STATE: USA
COUNTRY: USA
TTD: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
```

ö

Gaps

```
GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Grieninger, Gerd
APPLICANT: Grieninger, Gerd
APPLICANT: Cao, Yiping
APPLICANT: Cao, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Monday, Mohamad Zaher
APPLICANT: Monday, Mohamad Zaher
TILE REFERENCE: Seq. ID #1 - 7 454-7 DIV
CURRENT APPLICATION NUMBER: US/09/167,647
CURRENT FILING DATE: 1996-06-07
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 27;
Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08799149C
Patent No. 6008195
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael E. Selsted
TITLE OF INVENTION: Antimicrobial Peptides and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSED for Windows Version 2.0
CURRNY APPLICATION DATA:
APPLICATION NUMBER: US/08/799,149C
FILING DATE: 14-February-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011 834
FILING DATE: 16-February-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 3;
Pred. No. 2.3;
0; Mismatches (
Score 39; DB 3;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson, P.C. STREET: 4225 Executive Square, Suite 1400
                                              0; Mismatches
                                                                                                                                                                                                                                        ; Sequence 7, Application US/09167647
; Patent No. 6025476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 43.8
Best Local Similarity 62.5
Matches 10; Conservative
                Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WWSFRGADYSLRAVR 18
                                                                                     3 VSVSFRRSYSLRGGR 18
                                                                                                                 3 VWVSFRGADYSLRAVR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-167-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-799-149C-5
                                                                                                                                                                                                                    US-09-167-647-7
  Query Match
                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Fu, xiping
APPLICANT: Grieninger, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Mohamad Zaher
APPLICANT: Mohamad Zaher
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
TITLE OF INVENTION NUMBER: US/08/886,269
CURRENT FILING DATE: 1997-07-01
EARLIER APPLICATION NUMBER: 08/479,755
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 4; Length 18;
Pred. No. 0.99;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8067-0054-999
                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LEUITA, A.
REGISTRATION NUMBER: 30,762
                APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOW, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08886269
Patent No. 6025148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGVSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.4*
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-886-269-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-09-128-345-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-886-269-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Gaps

2 GVSVSFRRSYSLRGGR 18

us-09-485-571-17.rai

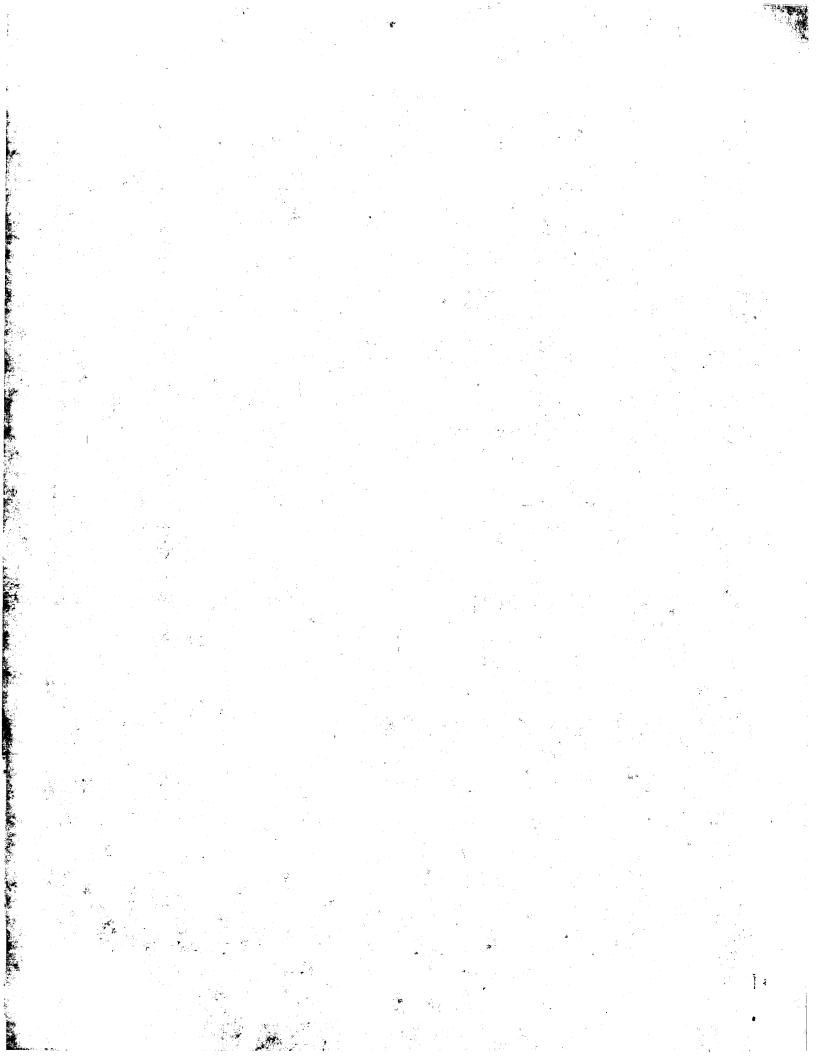
```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Georgiev, Georgii P.
APPLICANT: Kiselev, Sergei L.
APPLICANT: Kiselev, Sergei L.
APPLICANT: ProKhorchouk, Egor B.
APPLICANT: Ostermann, Elihoborg
TITLE OF INVENTION: Tumor Growth Inhibition- and Apoptosis-Associated
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                43.8%; Score 39; DB 3; Length 165; 47.1%; Pred. No. 17; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 4; Length 182;
Pred. No. 18;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,764
FILING DATE: (Herewith)
CLASSIFICATION: 515
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07306/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAS: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 515
ATTORNEY/AGENT INFORMATION:
NAME: ESEMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1630000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08893764
Patent No. 6172211
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                   ) NAME/KEY: Coding Sequence
; LOCATION: 36..521
US-08-799-149C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 GVSRGFLRSNYEVKGHR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GVSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-893-764-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-893-764-2
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
```

```
APPLICANT: Grieninger, Gerd
APPLICANT: Grieninger, Gerd
APPLICANT: Gao, Yan
APPLICANT: Cao, Yan
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad Zaher
APPLICANT: Ahadi, Mohamad J.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AGAINST A SUBUNIT OF FIBRINOGEN
FILE REPERENT: Septembers 1-7 for 454-7 CON/CPA
CURRENT APPLICATION NUMBER: US/08/886,269
CURRENT FILING DATE: 1997-07-01
EARLIER RIPLICATION NUMBER: 08/479,755
RALIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 3; Length 236;
Pred. No. 25;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 12, 2002, 12:32:22 Job time: 450 sec
                                                                                                                                   Sequence 1, Application US/08886269 Patent No. 6025148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.8%;
62.5%;
||| | | :| |
142 GVSRGFLRSNYEVKGHR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.8 Best Local Similarity 62.5 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VSVSFRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-886-269-1
                                                                                                                                                                           GENERAL INFORMATION:
                                                                                   RESULT 15
US-08-886-269-1
```

us-09-485-571-17.rai



```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:30:29; Search time 242.57 Seconds Run on:

(without alignments)
5.497 Million cell updates/sec

RGVSVSFRRRSYSLRGGR 18 US-09-485-571-17 89 Perfect score: Sednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched:

522463 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1992.DAT:*/SIDS8/gcgdata/geneseg/genesegp/AA1993.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT: A_Geneseq_1101:*

/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Protegrin derivati	Antimicrobial prot	A. thaliana enviro	HIV-1 subtype C pr	Zea mays protein f	Arabidopsis thalia	zea mays protein f				
	ID	AAW99404	AAW36214	AAW36213	AAW36209	AAW36210	AAW36215	AAY77962	AAB86197	AAG25990	AAG45699	AAG40714
	DB	20	18	18	18	18	18	21	22	21	21	21
	Query Match Length DB	18	18	17	15	15	15	366	3025	59	141	142
æ	Query Match	100.0	77.5	61.2	52.8	52.8	52.8	47.2	47.2	46.1	46.1	46.1
	Score	89	69	54.5	47	47	47	42	42	41	41	41
	Result No.	1	7	m	4	S	9	7	80	σ	10	11

ñ Ō-π	Arabidopsis thalia Protegrin peptide Human chromogranin Human ORFX ORF1593 TCCA Sequence. Sa Amino acid sequence Arabidopsis thalia Arabidopsis thalia
AAY01969 AAY01968 AAR01968 AAR01973 AAY01975 AAY01977 AAY01981 AAY01981 AAY01981 AAY01988 AAY01988 AAY01988 AAY01988 AAY01988 AAY01988 AAY01988 AAY01988 AAY01988 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY01970 AAY0198834 AAY01970 AAY0198834	AAG35853 AAX18776 AAX18363 AAX18362 AAB62758 AAK62758 AAG3797 AAG05623
00 00 00 00 00 00 00 00 00 00 00 00 00	21 20 20 21 21 21 21
00000000000000000000000000000000000000	849 18 26 31 112 374 439 114
44444444444444444444444444444444444444	41 044 044 044 033 044 040
11111111111111111111111111111111111111	7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

## ALIGNMENTS

AAW99404 standard; peptide; 18 AA. AAW99404; AAW99404 RESULT

(first entry) 08-JUN-1999 Protegrin derivative peptide SM1727.

Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier. 

Synthetic.

WO9907728-A2

18-FEB-1999,

98WO-FR01757. 06-AUG-1998;

97FR-0010297 12-AUG-1997;

(SYNT-) SYNT: EM SA.

Kaczorek M; Grassy G, Chavanieu A, Calas E,

WPI; 1999-190034/16.

Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells

"D-form residue" "D-form residue"

/note= Misc-difference 12

/note=

Misc-difference 13

Misc-difference

"D-form residue" "D-form residue"

'note= 'note=

"D-form residue"

'note=

/note= "D-form residue"

"D-form residue"

'note=

Misc-difference 18

WO9718826-A1

Misc-difference 17

'note= "D-form

Misc-difference 16

Misc-difference 15

2

```
RESULT
                    g
                                                                                           This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridge. The novel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to excland a deliver active agents to cytoplasm and nucleus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimiorobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; hry; human immunodeficiency virus; preservation; etrovirus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Hellcobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; blocidal; blostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; pendicillin resistant Stephylococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89; DB 20;
Pred. No. 3.9e-08;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "D-form residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "D-form residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "D-form residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial protegrin peptide (14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥
Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW36214 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "D-form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
AAW36214
     \overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\times}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}}{\cup}\overset{\mathsf{D}}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}}{\overset{\mathsf{D}}}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}}}{\cup}\overset{\mathsf{D}}{\cup}\overset{\mathsf{D}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCAMENTATION OF THE FORM OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

Steinberg DA;

Lehrer RI,

Gu CL,

Chen J,

Chang CC,

WPI; 1997-297871/27.

(INTR-) INTRABIOTICS PHARM INC

(REGC ) UNIV CALIFORNIA

95US-0562346. 96US-0649811.

96US-0690921

01-AUG-1996;

22-NOV-1995 17-MAY-1996

96WO-US18544 96US-0752852

22-NOV-1996; 21-NOV-1996;

29-MAY-1997

```
ö
                                                                                                                                                                                      The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodsuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcres associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant correspondence or facealis, penicillin resistant staphylococcus cureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 18; Length 18
Pred. No. 7.4e-05;
); Mismatches 4; Indels
                                                                                                                                      Claim 23; Page 104; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGVSVSFRRRSYSLRGGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

ï

Gaps

ij

Indels

4.

Mismatches

ö

Conservative

13;

```
Matches
                                                                                                                                          g
                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis.
                                                                                                                                                                                                                                                                                                                                                                                                              disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Staphylococcus neumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus penemoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                               Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehrer RI, Steinberg DA;
                                                                                                                                                                                                                                             Antimicrobial protegrin peptide (13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23; Page 104; 130pp; English.
                                    AAW36213 standard; peptide; 17 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0752852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gu CL,
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1996;
                                                                                                                                                                           12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                          AAW36213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AAW36213
```

Score 54.5; DB 18; Length 17; Pred. No. 0.016;

61.28; 72.28;

Query Match Best Local Similarity

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungl, protozoa and certain strains of viruses and retroviruses, e.g. HIV. it can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faccium or faccalis, penicillin resistant Staphylococcus
                                                                                                                                                                                                                                                                                     Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungl; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycun resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidassis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gu CL, Lehrer RI,
                                                                                                                                                                                                                                                      Antimicrobial protegrin peptide (9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 104; 130pp; English.
                                                                                                                                     Æ.
                                                                                                                                   AAW36209 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INTR-) INTRABIOTICS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0752852
RGVSVSFRRSYSLRGGR 18
                    12-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang CC, Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-1995;
17-MAY-1996;
01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09718326-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                        AAW36209;
  ~
                                                                                                                 AAW36209
                                                                                              RESULT
```

```
ö
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; protozoa; virus; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; blocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-postive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis,
                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                ö
                                                                                                Length 15;
                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steinberg DA;
                                                                                              DB 18; 1
0.24;
                                                                                                                            0; Mismatches
                                                                                              Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial protegrin peptide (10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 23; Page 104; 130pp; English.
                                                                                                                                                                                                                                                                   AAW36210 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0752852.
95US-0562346.
96US-0649811.
96US-0690921.
                                                                                             52.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gu CL,
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                           10; Conservative
                                                                                                                                                                            1 RGVSVSFRRRSYSL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-297871/27.
                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen J,
                                              AA;
                                              15
                                                                                                                                                                                                                                                                                                                                    12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                              Seguence
                                                                                                                                                                                                                                                                                                      AAW36210;
                                                                                                                         Matches
S X X X
                                                                                                                                                          δ
                                                                                                                                                                                      셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; pram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogon; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Staphylococcus aureus; systemic candidiasis.
keratitis, corneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus faecium and methicillin resistant staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                  52.8%; Score 47; DB 18; Length 15; 71.4%; Pred. No. 0,24; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehrer RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial protegrin peptide (15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 23; Page 104; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36215 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0562346.
96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0752852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0690921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                  14
                                                                                                                                                                                                                                                                                                                    1 rgvcvcfrrrcycl
                                                                                                                                                                                                                                                                                                   1 RGVSVSFRRRSYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-297871/27.
                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9718826-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang CC,
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36215;
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                   AAW36215
                                                                                                                                                                                                                                                                                                                                                                                  RESULT
   ACC
```

The present sequence is an antimicrobial protegrin peptide, which

us-09-485-571-17.rag

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Environmental stress; plant; transgenic plant; anaerobic; flooding; cold;
dehydration; drought; heat stress; salinity; osmotolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolation of coding sequences and/or genes involved in tolerance to environmental stress in plants. The sequences (AA299305-298365) are useful for producing a transgenic plant having enhanced tolerance or resistance to environmental stress conditions such as anaerobic, flocoding, cold, dehydration, drought, heat stress or salinity. This is useful for producing improved yield, growth, development and productivity under environmental stress conditions, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of polynucleic acids useful for producing transgenic plant by isolating genes involved in tolerance to environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV. It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, conneal ulcers, stomach ulcers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections,
                                                                                                                                                                                                            urinary tract infections, systemic candidiasis and oral mucositis. It is biostatic or biocidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomyoin resistant Enterococcus faecium or faecalis, penicillin resistant Streptococcus pneumoniae and methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. thaliana environmental stress tolerance related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 18; Length 15;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 236-238; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77962 standard; protein; 366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                           to 1 mg/kg/day, by injection.
                                                                                                                                                                                                                                                                                                                                                                                                                     52.8%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-EP05652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98EP-0202634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verbruggen N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-205726/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGVSVSFRRBSYSL
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ98342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200008187-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lee JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              용
     ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency virus type I subtype C/B' which can be used for the induction of specific humoral and cellular immune responses. (I) and pulpapetides (II) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus-I (HIV-I) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B' of HIV-I so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-I subtype C genome described in the method of the invention.
also provides growth of crops in areas where they cannot grow without the induced osmotolerance. Sequences AAY77925-984 represent polypeptide sequences from A. thaliana that are encoded by the genes involved in environmental stress tolerance.
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel polynucleotide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection; diagnosis; human; humoral immune response; antivicellular immune response; vaccine; treatment; gene therapy.
                                                                                                                                     DB 21; Length 366; 48;
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Xaa
/note= "Xaa represents a stop codon"
                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAO/; SHAO Y.
(GENE-; GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
                                                                                                                                   Score 42; DB Pred. No. 48; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                    AAB86197 standard; Protein; 3025 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     HIV-1 subtype C protein fragment #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 1..3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graf M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                   47.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2000; 2000DE-1056747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99DE-1055089
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                      Conservative
                                                                                                                                                                                                   4 SVSFRRSYSLRGGR 18
                                                                                                                                                                                                                      ||::||| || ||
52 svnyrrrelslisgr 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-336417/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wagner R, Wolf H,
                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                   366 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE10056747-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAO/) SHAO
                                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic
                                                                                                                                                                                                                                                                                                                                                     AAB86197;
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                    AAB86197
                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                     8888888
                                                                                                                                                                                                     ŏ
```

```
990S-0138094.
990S-0138540.
990S-0138147.
990S-0139452.
990S-0139452.
990S-01394545.
990S-01394545.
990S-0139456.
990S-0139456.
990S-0139456.
990S-0139456.
990S-0139460.
990S-0139460.
990S-0139460.
990S-0139460.
990S-0139460.
990S-0139460.
990S-013960.
990S-0140354.
990S-0140354.
990S-0140354.
990S-0141287.
990S-0141287.
990S-0141287.
990S-0142154.
990S-0142154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0143542

990S-0144085

990S-0144085

990S-0144335

990S-0144333

990S-0144333

990S-0144333

990S-0144335

990S-0144335

990S-0144335

990S-0144335

990S-0144335

990S-0144335

990S-014508

990S-014508

990S-014508

990S-014508

990S-014508

990S-0145185

990S-0145185

990S-0145185

990S-0145185

990S-014524

990S-014528

990S-014528

990S-0145386

990S-0145318

990S-0145318

990S-0145318

990S-0145318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0147192.
99US-0147260.
99US-0147303.
99US-0147416.
                                                                                                                                                                                                        18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                               Gaps
                                                                                                                             ;
0
                                                                      Score 42; DB 22; Length 3025;
Pred. No. 4.6e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 30276.
                                                                                                                                                                                                                                                                                                                                                AAG25990 standard; Protein; 59 AA
                                                                      47.28;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9905 - 0121825 - 9905 - 0121825 - 9905 - 0123548 - 9905 - 0125788 - 9905 - 0125785 - 9905 - 0125785 - 9905 - 0125785 - 9905 - 0132485 - 9905 - 0132485 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 0132486 - 9905 - 01324256 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 - 0134218 - 9905 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134221.
99US-0134370.
99US-0134768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0134941.
990S-0135124.
990S-0135529.
990S-0135629.
990S-0136621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0137502
99US-0137724
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000 (first entry)
                                            Query Match
Best Local Similarity 46.7.
The conservative
                                                                                                                                                                                                   :| |: :| | ||:|
557 kgssiryrsrxysir 571
                                                                                                                                                                      1 RGVSVSFRRRSYSLR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays subsp. mays
AA;
3025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
64-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    AAG25990;
                                                                                                                                                                                                                                                                                              AAG25990

AAG25990

XX

XX

AAG25990

XX

AAG25990

XX

AAG22

AA
g
                                                                                                                                                                                                                     g
                                                                                                                                                                            ŏ
```

```
pathway;
promoter;
                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 57406
                                                                                                                            AAG45699 standard; Protein; 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0130449
990S-0130510
990S-0131449
990S-01314407
990S-013248
990S-0132485
990S-0132485
990S-0132486
990S-0132487
990S-0134218
990S-0134218
990S-0134218
990S-0134218
990S-0134218
990S-0134218
990S-0134218
990S-0134333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0121825.
99US-0123180.
99US-0125788.
99US-0125788.
99US-0126785.
99US-0127462.
99US-0128234.
99US-0128734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0137528.
99US-0137502.
99US-0137724.
99US-0138094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0138540.
99US-0138847.
99US-0139119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139452.
99US-0139453.
99US-0139492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0137222
                                                                                                                                                                                              18-OCT-2000 (first entry)
       16
                                        42
                           |:|| ||: || |
gisvdhrrknksleg
       GVSVSFRRSYSLRG
                                                                                                                                                                                                                                                                                                         termination sequence.
                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999, 05-MAR-1999, 23-MAR-1999, 23-MAR-1999, 22-MAR-1999, 01-APR-1999, 06-APR-1999, 23-APR-1999, 23-APR-1999, 23-APR-1999, 06-MAY-1999, 06-MAY-1999, 06-MAY-1999, 14-MAY-1999, 19-MAY-1999, 19-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 - MAY - 1999;
25 - MAY - 1999;
27 - MAY - 1999;
28 - MAY - 1999;
01 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1999
                                                                                                                                                              AAG45699;
                                                                                           RESULT 10
     7
                                        28
                                                                                                         Db
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 2
Pred. No. 10;
3; Mismatches
990S - 0147493.
990S - 0147493.
990S - 0148171.
990S - 0148341.
990S - 0148341.
990S - 0148341.
990S - 0149368.
990S - 0149723.
990S - 0149923.
990S - 0149923.
990S - 0149930.
990S - 0149930.
990S - 0159368.
990S - 015686.
990S - 0151066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0159294
990S-0159295
990S-0159330
990S-0159331
990S-0159331
990S-0159638
990S-0159638
990S-0160741
990S-0160770
990S-0160814
990S-0160814
990S-0160980
990S-0160980
990S-0161406
990S-0161406
990S-0161360
990S-0161360
990S-0161933
990S-0161920
990S-0161920
990S-0161920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
13-AUG-1999;
13-AUG-1999;
13-AUG-1999;
17-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
21-AUG-1999;
21-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                           13. SEP - 1999

16. SEP - 1999

20. SEP - 1999

21. SEP - 1999

22. SEP - 1999

23. SEP - 1999

24. SEP - 1999

25. SEP - 1999

26. OCT - 1999

27. OCT - 1999

28. OCT - 1999

29. SEP - 1999

20. OCT - 1999

21. OCT - 1999

22. OCT - 1999

23. OCT - 1999

24. OCT - 1999

25. OCT - 1999

26. OCT - 1999

27. OCT - 1999

28. OCT - 1999

28. OCT - 1999

28. OCT - 1999

28. OCT - 1999

29. OCT - 1999

20. OCT - 1999
                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1999,
10-SEP-1999;
```

90S - 0139456 90S - 013945 90S - 013945 90S - 013945 90S - 013945 90S - 013946 90S - 013946 90S - 013946 90S - 013946 90S - 013975 90S - 013975 90S - 013975 90S - 013975	9905-0140825. 9905-0140821. 9905-0141287. 9905-0141284. 9905-0142055. 9905-0142063. 9905-0142803. 9905-0142803. 9905-0142803. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086. 9905-0144086.	UUS - 0144632 UUS - 0144884 UUS - 0145086 UUS - 0145088 UUS - 0145087 UUS - 0145087 UUS - 0145087 UUS - 0145187 UUS - 0145187 UUS - 0145218 UUS - 0145218 UUS - 0145218 UUS - 0145218 UUS - 0145218 UUS - 0145218 UUS - 0145318 UUS - 0145318 UUS - 0145318 UUS - 0145318 UUS - 0145318	US-0146389 US-0147038 US-0147038 US-0147302 US-0147302 US-0147302 US-0147303 US-0148171 US-0148311 US-0148341 US-0148341 US-0148341 US-0148341 US-0148341 US-0148341 US-0148341
8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999; 8-JUN-1999;	28 - 50N - 1999; 29 - 50N - 1999; 20 - 50N - 1999; 01 - 50L - 1999; 06 - 50L - 1999; 06 - 50L - 1999; 07 - 50L - 1999; 08 - 50L - 1999; 13 - 50L - 1999; 14 - 50L - 1999; 15 - 50L - 1999; 16 - 50L - 1999; 16 - 50L - 1999; 19 - 50L - 1999; 19 - 50L - 1999; 19 - 50L - 1999; 19 - 50L - 1999; 10 - 50L - 1	- JUL - 1999; -	- AUG-1999; - AUG-1999;
	2		

	Gaps
	0;
	1; DB 21; Length 141; o. 25; 4; Indels
	Score 41; Pred. No. 3; Mismat
990S-0149368. 990S-0149368. 990S-0149175. 990S-0149723. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0149929. 990S-0151303. 990S-015929. 990S-0159330. 990S-015929. 990S-015929. 990S-0159330. 990S-0159330. 990S-0159330. 990S-0159339. 990S-0159339. 990S-0159339. 990S-0159339. 990S-0159339. 990S-0159339.	similarity 53.3%; 8; Conservative
16-Aug-1999; 18-Aug-1999; 20-Aug-1999; 20-Aug-1999; 20-Aug-1999; 23-Aug-1999; 23-Aug-1999; 23-Aug-1999; 24-Aug-1999; 25-Aug-1999; 27-Aug-1999; 28-Aug-1999;	Query Match Best Local Simil Matches 8; C
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	OMX

RESULT 11 AAG40714

2 GVSVSFRRRSYSLRG 16 |:|| ||::|| || 28 gisvdhrrknrsleg 42

Qy Db

;

9

```
990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139463-990S-0139483-990S-0140354-990S-0140354-990S-0140354-990S-0140354-990S-0140332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141332-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-0141333-990S-
 99US-0139461
          18 - 70N - 1999)
22 - 70N - 1999)
23 - 70N - 1999)
23 - 70N - 1999)
24 - 70N - 1999)
26 - 70N - 1999)
27 - 70N - 1999)
28 - 70N - 1999)
29 - 70N - 1999)
20 - 70N - 1999)
20 - 70N - 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999
02-AUG-1999
03-AUG-1999
04-AUG-1999
05-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
11-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
                                                                                                                                                                                       1999;
                                                                                                                                                                                                                         .3-JUL-1999;
                                                                                                                                                      01-JUL-1
02-JUL-1
                                                                                                                                                                                                  09-JUL-1
12-JUL-1
                                                                                                                                                                                                                                                                              19-JUL-1
19-JUL-1
                                                                                                                                                                                                                                  14 - JUL- 1
  ************************
                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                mays protein fragment SEQ ID NO: 50555
AAG40714 standard; Protein; 142 AA
                                                                                                                                                                                                                     990S-0121825.
990S-0123180.
990S-0123180.
990S-0125788.
990S-0126764.
990S-0126764.
990S-0126764.
990S-0126714.
990S-0130871.
990S-0131449.
990S-0132486.
990S-0132486.
990S-0132486.
990S-0132486.
990S-0134218.
990S-0134218.
990S-0134218.
990S-0134218.
990S-013428.
990S-013468.
                                                                                                                                                                                                 2000EP-0301439
                                          (first entry)
                                                                                                                                 Zea mays subsp. mays
                                                                                                                                                                                                                     25 - FEB - 1999;
05 - MAR - 1999;
09 - MAR - 1999;
23 - MAR - 1999;
25 - MAR - 1999;
01 - APR - 1999;
06 - APR - 1999;
16 - APR - 1999;
                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                  19-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
04-MAX-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 - MAY - 1999;
14 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 - MAY - 1999
24 - MAY - 1999
24 - MAY - 1999
25 - MAY - 1999
27 - MAY - 1999
01 - JUN - 1999
04 - JUN - 1999
06 - JUN - 1999
06 - JUN - 1999
10 - JUN - 1999
                                         18-OCT-2000
                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                          06-SEP-2000
                      AAG40714;
                                                                  Zea
```

```
specification describes novel vif proteins (AAV01969-88) and genes encoding them (AAX35217-36). The vif gene is an accessory gene HIV-1 that has low functional mutagenicity and is conserved. In
                                                                                                                                                                                                                                                                                                                                                                                                   addition, attenuated, non functional vif clones are able to induce acids may be used to immunise memals. The attenuated, non-functional vif genes may be used in concert with other HIV-1 genes to produce vaccine that has a broad immune response against all viral components, and which minics many aspects of the immune responses induced by a live attenuated virus. Prophylactic vaccines which include viral acsape and contribute to lowering the viral set point during early infection stages.
                       Consensus sequence; attenuated; non-functional; accessory protein; vif; viral infectivity factor; HIV-1; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus sequence; attenuated; non-functional; accessory protein; vif;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                               New attenuated vif (viral infectivity factor) genes, used in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus sequence of a HIV-1 viral infectivity factor (vif) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 20; Length 190;
Pred. No. 35;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                    Weiner DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     viral infectivity factor; HIV-1; vaccine
                                                         Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01968 standard; protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 7A; 92pp; English.
                                                                                                                                                                                                                                Ayyavoo V, Nagashunmugam T,
                                                                                                                                                                97US-0060172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.18;
                                                                                                                                        98WO-US19478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US19478
                                                                                                                                                                                                        (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.1
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                              vaccines against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||::|:| ||
81 qgvsiewrkrrys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                        WPI; 1999-263380/22.
N-PSDB; AAX35217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 AA;
                                                                                    WO9913896-A1
                                                                                                                                                                26-SEP-1997;
18-SEP-1997;
                                                                                                                                        18-SEP-1998;
                                                                                                             25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9913896-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY01968;
                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 21; Length 142;
Pred. No. 26;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1 viral infectivity factor protein N13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY01969 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0161902.
99US-0149930.
99US-0150566.
99US-0150884.
99US-0151066.
99US-0151006.
99US-0151303.
                                                                                         99US-0151438.
99US-0151930.
99US-0152363.
99US-0153070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.18;
                                                                                                                                                                                                                                                                                                                 99US-0158232.
99US-0158369.
99US-0159293.
                                                                                                                                             99US-0153758
99US-0154018
                                                                                                                                                                       99US-0154039
                                                                                                                                                                                                                          99US-0155659
                                                                                                                                                                                                                                                  99US-0156596
                                                                                                                                                                                                                                                                            99US-0157753
99US-0157865
                                                                                                                                                                                                                                                                                                                                                                     99US-0159295
99US-0159329
                                                                                                                                                                                   99US-0154779
                                                                                                                                                                                                                                                                 99US-0157117
                                                                                                                                                                                                                                                                                                      99US-0158029
                                                                                                                                                                                                                                                                                                                                                          99US-0159294
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0159331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0160767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161406
99US-0161359
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0159584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0160814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39US-0160815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0160980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0161404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0161361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-016098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 53.3
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GVSVSFRRSYSLRG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1:|| ||:: || |
28 gisvdhrrknksleg
                                                                                                                                                                                                                     24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
                                                                                                                                                                                                                                                                                                               08-0CT-1999
13-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
12-0CT-1999
12-0CT-1999
13-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
                                                                                                                                                                                                                                                                                       06-0CT-1999
07-0CT-1999
                                                                                                                                                                                   20-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1999
```

Query Match

Best Loca Matches

ò q

22-OCT-1

AAY01969;

AAY01969 ID AAY0: XX AAC AAY0: XX DT 02-JI XX DE HIV-1

```
diagnosis of AIDS and pre-AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB, AAQ06635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9013630-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIV 1-NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR09302;
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spire B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR09302
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                        The present sequence represents the consensus sequence derived from attenuated, non-functional forms of the accessory protein vif (viral infectivity factor) of Human immunodeficiency virus type I (HIV-I).

The specification describes novel vif proteins (AAV01969-88) and the genes encoding them (AAX35217-36). The vif gene is an accessory gene for HIV-I that has low functional mutagenicity and is conserved. In addition, attenuated, non functional vif clones are able to induce immune responses capable of destroying native pathogen. Vif nucleic acids may be used to immunize mammals. The attenuated, non-functional vif genes may be used in concert with other HIV-I genes to produce vaccine that has a broad immune response against all viral components, and which mimics many aspects of the immune responses induced by a live attenuated virus. Prophylactic vaccines which include vif could limit both viral escape and contribute to lowering the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                New attenuated vif (viral infectivity factor) genes, used in genetic vaccines against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV; HTLV III; AIDS; diagnosis; vaccine; probe; hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 20; Length 190;
Pred. No. 35;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of lymphadenopathy associated virus (LAV) used for prodn. of DNA, antigens and antibodies used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montagnier L;
                                                                                                    Weiner DB;
                                                                                                                                                                                                                                           Disclosure; Page 57-58; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lymphadenopathy associated virus EL I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wain-Hobson S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoded by LAV EL I Q gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP81855 standard; protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%;
53.8%;
                                                                                                Ayyavoo V, Nagashunmugam T,
  97US-0060172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87WO-EP00326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86EP-0401380
                                                          (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.87
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGVSVSFRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 qgvsiewrkrrys 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sonigo P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-014396/02.
N-PSDB; AAN80436.
                                                                                                                                        WPI; 1999-263380/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AA;
26-SEP-1997;
18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8707906-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alizon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP81855
AAP8185
AAP81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
  ò
```

```
probes
                                                                                                                                                                                 viruses or related viruses or DNA proviruses in eg. biological samples. The proteins or peptides can be used for detection of antibodies induced in vivo and present in biological fluids. The DNA can also be used for the expression of LAV viral antigens for the prodn. of a vaccine against the detection of proteins related to the LAV viral entipodies for the prodn. of antibodies for the detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS.
                                                     LAV EL % (AAN80436) and LAV MA L (AAN80437) were isolated from the peripheral blood lymphocytes of patients. Different AlDS virus isolates concerned are designated by 3 letters of the patients name. Stable probe including the DNA sequences can be used for detection of the new LAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The HIV NDK virus was isolated from peripheral blood lymphocytes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an AIDS patient. A genomic library was prepd. from DNA extracted from CIBM cells infected with the virus. The library was screened with a pBTl probe corresp. to a fragment from HIV 1. The virus is more cytopathic than other strains and is not inhibited by OKT4A. It has been deposited as CNCM I-857. The sequence can be used to express proteins useful for diagnosing the presence of NDK and related viruses and in vaccines against immunodeficiency diseases. See also AAR09301-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sire J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New HIV-NDK retrovirus and protein component - used in vagainst immuno-deficiency disorders and in raising MAbs retro-virus detection in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rey F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence deduced from vif gene of HIV 1-NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Devaux C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB
Pred. No. 35;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR09302 standard; protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus; AIDS.
Claim 8; Fig 7A-7J; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chermann JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INRM ) INSERM INST NAT SANTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.18;
53.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-FR00312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89FR-0005914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 46.1
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||: :|:| ||
ggvsiewrkrrys 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGVSVSFRRRSYS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-361470/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barre-Sinnoussi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA;
```

ő

xx SQ Sequence 192 AA;

0; Gaps Query Match 46.1%; Score 41; DB 11; Length 192; Best Local Similarity 53.8%; Pred. No. 35; Matches 7; Conservative 4; Mismatches 2; Indels

ó

ολ

1 RGVSVSFRRRSYS 13 :|||::|:||| 83 qgvsiewrkrrys 95 Op

Search completed: February 12, 2002, 12:30:29 Job time: 362 sec

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
099140 bettongla p
099142 lagorcheste
09942 lagorcheste
09942 lagorcheste
09988 corynebacte
03686 llly sympto
091880 arabidopsis
09580 arabidopsis
09556 mus musculu
09557 conger myri
017484 plodia inte
017485 plodia inte
04444 poteto viru
09987 aeropyrum p
                                                                                                                                                                                                                                                                                                                                                          Qgaund oryza sativ
Qgaund oryza sativ
Qgayp5 mus musculu
Qgay47 mus musculu
Q52604 agrobacteri
Qg117 rattus norv
Qgan55 rhodobacter
Qg4f4 homo sapien
Q94f4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=1452; Nicolaisen M., Nielsen S.L.; Nicolaisen M., Nielsetide sequence of the 3'- terminal region of Kalanchoe latent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalanchoe latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=132477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.4%; Score 52; DB 12; Length 101; 56.2%; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AJ293570; CAB97501.2; -. InterPro; IPR002568; Carla_C4. I. Pfam; PF01623; Carla_C4; I. Hypothetical protein. NON_TER 101 101 SEQUENCE 101 AA; 11556 MW; C55F15AA3718BEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 11.6 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
099TUC2
09GLQ0
09GLQ1
09GLQ1
09E9R1
09E9R1
09E8R0
09E8R0
09F8R7
017484
017484
017484
017484
017484
017484
017484
017484
017484
017484
017487
090XPK
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
    Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:||| ::|:||
42 GRSTYARRRAISIGR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
  SEQUENCE FROM N.A.
    O91CW2
Q91CW2;
01-OCT-2000 (
01-OCT-2000 (
       OHIIIOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q91CW8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ICW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q9ICW2
    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ICW8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogicw8 kalanchoe 1 091cw2 kalanchoe 1 038024 potato viru 073508 potato viru 073512 potato viru 073514 potato viru 073529 potato viru 073531 potato viru 073531 potato viru 073525 potato viru 073525 potato viru 073525 potato viru 073525 potato viru 073526 potato viru 073525 potato viru 099109 potato
                                                                                                                                                                               (without alignments)
11.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                        February 12, 2002, 12:26:07; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         473505 segs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091CW8
0391CW2
0391CW2
073508
073512
073512
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
073513
                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 sv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                     US-09-485-571-15
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001
922
933
933
944
944
944
944
944
944
944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444444466666
```

Created) Last sequence update) Last annotation update)

(TrEMBLrel. 15, TrEMBLrel. 15, (TrEMBLrel. 17,

Score

Result Š 2

ö

Gaps

ö

Length 93; 3; Indels

```
11K PROTEIN (FRAGMENT).
Obtato virus S.
Viruses: ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.1%; Score 49; DB 12; Length 93; 52.9%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KARIA;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15611; CAA75698.1;
InterPro; IPR002568; Carla_C4.
InterPro; Carla_C4; I.
SPIGMS; CARIA_C4; I.
SEQUENCE 93 AA; 10537 MW; ACZFEZAOF98659B9 CRC64;
                                                   Matousek J., Schubert J., Dedic P.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. InterPro; IPR002568; Carla_C4.
InterPro; IPR01623; Carla_C4; 1.
NON_TER 93 A3: 10521 MW; 2DA6E2925A8C475D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ASCHERSLEBEN;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; V15615, CA75706.1; -.
InterPro; IPPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2DA6E2925A8C475D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          073509
073509;
073509;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 17, Last annotation update)
01-AUG-1998 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 12;
Pred. No. 0.86;
5; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 93 93
SEQUENCE 93 AA; 10521 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| :||:||: ||:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 55.1
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                       STRAIN-ASCHERSLEBEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                073512
073512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
073509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    073512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID DOT NO S S O S S O S S O S S O S S O S S O S S O S S O S S O S S O S S O S S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O S O 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HD DATE OF THE SECOND OF THE S
                       RC RA DR DR DR DR SO SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                           Nicolaisen M., Nielsen S.L.; "Nucleotide sequence of the 3^\prime\text{-} terminal region of Kalanchoe latent
HYPOTHETICAL 11.6 KDA PROTEIN (FRAGMENT).
Kalanchoe latent virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=132477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potato virus Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus. NCBL_TaxID=12167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 12; Length 101;
Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 12; Length 92;
Pred. No. 0.39;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; A7293571; CA897507.2; -. InterPro; IRR002568; Carla_C4. Ffam; PF01623; Carla_C4; 1. Pypochetical protein. 10. 10. SEQUENCE 101 AA; 11591 MW; 39BD224E73E3DBFA CRC64; SEQUENCE 101 AA; 11591 MW; 39BD224E73E3DBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caviler T.D., Corsini D.L., Berger P.H.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF023877; AAB81273.1; -.
InterPro; IPR002568; Carla_C4.
Fram: PF01623; Carla_C4; 1.
Hypothetical protein.
SEQUENCE 92 AA; 10319 MW; B0A9AC70B579A980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   073508;
01-AUG-1998 (TIEMBLIEL. 07, Created)
01-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 10.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.3%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.4%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 GGRSKYARRRRAIAAGR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 58.4
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:||| ::|:||
42 GRSTYARRRAISIGR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       STRAIN-PV-0290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-IDAHO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             038024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 038024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   073508
```

m

QQ

ò

ò pp

ö

Gaps

ö

Indels

ë.

93 AA.

```
Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; CarlavIrus. NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 12; Length 93;
Pred. No. 0.86;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                      STRAIN-VITAVA;
Matousek J., Schubert J., Dedic P.;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; VI5616; CAA757081.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON TER 93 ...
10507 MW; AC2FE2A0F98645C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matousek J., Schubert J., Dedic P.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; X15610; CAA75696.1; ... InterPro; IPR002568; Carla_C4. Pfam; PF01623; Carla_C4; 1. NON_TER 93 93 NA: 10333 MW; AB44F80C8018A5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PRCTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNU-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 12;
Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.1%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.1%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.1
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN "VITAVA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           073531 073531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093139
                                                              073529
                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
093139
                      RESULT
073529
                                                                                      SO DE RESERVA SO DE LA SO DEL SO DE LA SO DE LA SO DE LA SO DEL SO DE LA SO DEL SO DE LA SO DEL SO DEL SO DELA SO DEL SO DEL SO DE LA SO DEL SO DEL SO DEL SO DEL SO DEL SO DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8444G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                ö
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                    Score 49; DB 12; Length 93;
Pred. No. 0.86;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB 12; Length 93;
Pred. No. 0.86;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.1%; Score 49; DB 12; Length 93; 52.9%; Pred. No. 0.86; tive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAILM. Schubert J., Dedic P.;
Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; V15612. CAA75700.11.
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON TER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matour Manager J., Dedic P.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL; Y15609; CAA75694.1; -. InterPro; IPR002568; Carla_C4. Pfan; PF01023; Carla_C4; I. NON_TER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER 93 93 93
SEQUENCE 93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AGG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11K PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 AA.
                                                                                                                                                                                                                                                           93 A.A.
                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                    55.1%;
52.9%;
                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, 11K PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.1%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                        2 GGRLSYSRRRFSVSVGR 18
                                                                                                                                 |||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-VITAVA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Potato virus S.
                                                                                                                                                                                                                                                       073514 073514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    073527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
073527
AC 073527
AC 073527;
DT 01-AUG-
DT 01-UNG-
DE 11K PRC
OS POLATO
OC VITUSES
OX NCBL_TR
RN [1]
RN [1]
RN [1]
RN SCOUENC
RC STRAIN-
RA MALOUSE
RL SUBL! X
DR INTERPI
                                                                                                                                                                                                                                 g
                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

PRT;

ö

Gaps

ö

Length 93; 3; Indels ö

Gaps

ö

93 AA.

Gaps

ö

3; Indels

Length

```
InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10680 MW; 2241BD8D5D69865A CRC64;
                                                                                          Score 49; DB 12;
Pred. No. 0.87;
5; Mismatches 3;
                                                                                             55.1%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.9%;
                                                                                                                                                                         2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||| :| |:| | 38 GGRSTYGRKRRARSIGR 54
                                                                                             Query Match 55.1
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
'-bos 9; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potato virus M.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Potato virus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                11K PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S-RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joung Y.H.;
                                                                                                                                                                                                                                                                                                             041486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090NN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                             041486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00NO60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A PAC
DDT TO DDT
    DR
DR
SQ
                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=93033173; PubMed=1413539;
Foster G.D., Mills P.R.;
"The 3'-nucleotide sequence of an ordinary strain of potato virus S.";
Virus Genes 6:213-220(1992).
EMBL; S45593; AAB23462.1; -.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                    positive-strand viruses, no DNA stage; Carlavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                           12; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12; Length 94;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                               Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y15614; CAA75704.1; -.
InterPro: IRF00256; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
NON_TER 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matousek J., Schubert J., Dedic P.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; %15625; CAA75721.1; -.
InterProy IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
SEQUENCE 94 AA; 10665 WW; 5236BDFD583C830A CRC64;
                                                                                                                                                                                                                                  93 AA; 10565 MW; 11BD8D5D69865A75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                           DB 12
0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49;
Pred. No. (
                                                                                                                                                                                                                                                                                             Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.1%;
52.9%;
                                                                                                                                                                                                                                                                                           55.1%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLEEL. 01, 01-NOV-1996 (TrEMBLEEL. 01, 01-JUN-2001 (TrEMBLEEL. 17, 11 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                            ||| :|:|:| : |:||
38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                       2 GGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A.
Potato virus S.
Viruses; ssRNA po
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-KOBRA;
                                                                                                 STRAIN-KOBRA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11K PROTEIN.
                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q86541
Q86541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         073525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
Q86541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus NCBL_TaxID=12167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINTOWATO,
Grieco F., Di Franco A., Gallitelli D.;
Grieco F., Di Franco A., Gallitelli D.;
Grieco F., Di Franco A., Gallitelli D.;
J. Plant Pathol. 78:45-49(1997).
EMBL: X85114; CAA59434.1; -.
Interpro; IPR002568; Carla_C4.
Fran; PF01623; Carla_C4; 1.
SEQUENCE 108 AA; 12182 MW; F84956324A930699 CRC64;
                                                                                                                                                                                                                                                                                      Submitted (OCT-1996) to the EMBL/GenBank/DDBJ database
EMBL; U74376; AAB65087.1; -.
INTERPRO 1 PRO02568; Carla_C4.
Pfam; PF01623; Carla_C4; I.
SEQUENCE 94 AA; 10649 MW; C8CCDEF10F00A10A CRC64;
                  041486;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.9%; Score 48; DB 12;
52.9%; Pred. No. 1.5;
iive 3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 core 48; DB 1.
ed. No. 1.3;
Mismatches
94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09QNNO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
```

qq

Search completed: February 12, 2002, 12:38:34 Job time: 747 sec

. . .

· us-09-485-571-15.rsp

١

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:26:27; Search time 67.2 Seconds Run on:

(without alignments)
9.821 Million cell updates/sec

US-09-485-571-15 89 Perfect score:

1 RGGRLSYSRRRFSVSVGR 18 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P32194 sus scrofa	P32195 sus scrofa	P32196 sus scrofa	4			P37992 chrysanthem	P42142 macropus ru	P42131 caenolestes	P42135 dasyurus vi	37		_			4	P42140 murexia lon	-		-	P26788 conger myri		Q40504 nicotiana t	P04030 agrobacteri	028756 archaeoglob	Q40505 nicotiana t	-	_	O51526 borrelia bu	_	P29220 borrelia bu	16	Q04948 branchiosto
SUMMARIES	B ID	1 PG1_PIG		_		1 VNBP_PVMG	VNB	1 VNBP_CVB	- 1	1 HSP1_CAEFU	1 HSP1_DASVI	1 HSP1_MACAG	1 HSP1_ANTLA	1 HSP1_ANTSW	1 HSP1_PARBI	1 HSP1_SARHA	1 HSP1_DASRO	1 HSP1_MURLO	1 HSP1_ANTST	1 VNBP_LSV	1 HSP1_DROAU	1 LEG1_CONMY	1 PG4_PIG	1 FL1_TOBAC	1 YP6_AGRTU	1 SFSA_ARCFU		1 YAFH_ECOLI	1 PVDG_PLAKN	1 DP3A_BORBU	1 HRX_MOUSE	1 RL34_BORBU	1 HRX_HUMAN	1 IFE_BRALA
	Length DB	149					108	107	29	09	09			61	61	61	62	62	9	140	63	135	149	413	191	219	416	794	1070	1147	3866		9	464
de	Ouery Match	77.5	。	69.7	69.7	57.3	57.3	52.8	50.6	20.6		٠				50.6	50.6	90.9	50.6	49.4	٠		48.3	•	47.2	46.1	44.9	44.9	44.9	44.9	٠	43.8	43.8	43.3
	Score	69	63	62	62	51	51		45	45	45	45	45	45		45	45	45	45	44	43	43	43	43	. 43	41	40	40	40	40	40	39	m	38.5
	Result No.	1	7	m	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30		32	33

Eur. J. Biochem. 237:575-583(1996).

P16654 potato viru Q45486 staphylococ		Q9k8g8 bacillus ha P36420 lactobacill Q9w705 xenopus lae	P21238 arabidopsis P42145 pseudochiro Q9yic2 conger myri	P45952 mus musculu
VNBP_PVSP GATB_STASP	ERRZ_HUMAN IMDH_MYCTU GSP_ECOLI	SYV_BACHD SYV_LACCA NCO2 XENLA	RUBA_ARATH HSP1_PSECU LEG2_CONMY	ACDM_MOUSE
				7
93 475	500 529 619	880 901 1516	586 68 135	421
42.7	42.7	42.7 42.7 42.7	42.1 41.6 41.6	41.6
38 38	3888	888 866	37.5 37 37	37
34 35	36 37 38	8 4 4 0 0 t	4 4 4 4 3 2	45

## ALIGNMENTS

```
Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protectins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure of three cationic peptides from porcine neutrophils. Sequence determination by the combined usage of electrospray ionization mass spectrometry and Edman degradation."; FEBS Lett. 330:339-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Neutrophils;
BDLINE=23887466. Pubmed=8375505;
MITGORGSKAYA O.A., Shevchenko A.A., Abdalla K.O.M.A.,
Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokryakov V.N.,
                                                                                                                                          Sus scrofa (Pig).
Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB=Bone marrow;
MEDLINE-94283613; PubMed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5]
STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE-96235220; PubMed-8647100;
Aumelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,
Grassy G., Calas B., Chavanieu A.;
Synthesis and solution structure of the antimicrobial peptide protegrin-1.";
                                                          01-0CT-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PROTEGRIN 1 PRECURSOR (PG-1) (NEUTROPHIL PEPTIDE 1).
                                                                                                                                                                                                                                                                                                                                                                                                   C., Ganz T., Lehrer R.I.;
structure of porcine protegrin genes.";
Lett. 368:197-202(1995).
                               Š
                              149
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RED DUROC;
MEDLINE-95354835; PubMed-7628604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
                                                                                                                                                                                                                                                                                                                      FEBS Lett. 346:285-288(1994)
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 131-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 131-148.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Zhao C., Ganz T., "The structure of
                                                                                                                                                                                           NCBI_TexID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shamove 0.V.;
                            PG1_PIG
P32194;
                                                                                                                                                                                                                                                                                                         cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS
                PG1_PIG
RESULT
```

```
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PG3_PIG
P32196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PG3_PIG
AC PG3_PIG
AC PG3_PIG
DT 01-1
DT 01-1
DE PRO
CG MAM
CC MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
        ŏ
                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Bone marrow;
MEDLINE-94071989;
MEDLINE-94071989;
Storiol P., Zanetti M.;
"A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a cathelin-like pro-sequence.";
                                                                                                                                                           peptide from porcine leukocytes.";
Chem. Biol. 3:343-550(1996).
-!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA MONOCYTOGENES AND C.ALBICANS, IN VITRO.
-!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION (G-149 PROVIDE AMIDE GROUP). 6EFBA98429CD6EC4 CRC64;
                                                                                   Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                                                                        "Solution structure of protegrin-1, a broad-spectrum antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; PD001838; Cathelicidin; 1.
PROSTIE; PS00946; CATHELICIDINS_1; 1.
PROSTIE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Signal; Amidation; Multigene family; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEGRIN 1.
PYRROLIDONE CARBOXYLIC ACID
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-07T-1993 (Rel. 27, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3e-(
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1PG1; 27-MAY-98.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
[6]
STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE-97113279; PubMed-8807886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEGRIN 2 PRECURSOR (PG-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X79868; CAA56251.1; -. EMBL; X84094; CAA58890.1; -. PIR; S34585. PIR; S36820; S36820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 RGGRLCYCRRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
148
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
107
136
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PG2_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PG2_PIG

PG2_PIG

PG2_PIG

PG2_PIG

PG3_PIG

PG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                  -!- FUNCTION: MICROBICIDAL ACTIVITY. ACTIVE AGAINST E.COLI, LISTERIA
                                                                                                                        Kokryakov V.N., Harwig S.S.L., Panyutich E.A., Shevchenko A.A., Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.; "Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins."; FEBS Lett. 327:231-236(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-147 PROVIDE AMIDE GROUP). 698429DFFEC40466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Bone marrow;
MEDLINE-94283613; Pubmed-8013647;
Zhao C., Liu L., Lehrer R.I.;
"Identification of a new member of the protegrin family by CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEGRIN 2.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PEO0666; Cathelicidins; 1.
Probom; PEO01838; Cathelicidin; 1.
PROSITE; PSO0946; CATHELICIDINS_1: 1.
PROSITE; PSO0947; CATHELICIDINS_2: 1.
Antibiotic; Signal; Amidation; Multigene family.
SIGNAL 1 29 POTENTIAL.
PROPEP 30 130 PROTEGRIN 2.
MOD_RES 30 30 PROTEGRIN 2.
Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                        MONOCYTOGENES AND C.ALBICANS, IN VITRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 1;
Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001894; Cathelicidin.
                                                                            TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning.";
FEBS Lett. 346:285-288(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L24745; AAA31061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last se
01-NOV-1997 (Rel. 35, Last an
PROTEGRIN 3 PRECURSOR (PG-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.8%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 RGGRLCYCRRFFCICVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGGRLSYSRRRFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                    SEOUENCE OF 131-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P32194; 1PG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85
107
```

3

ì

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEGRIN 5.
PROTEGRIN 5.
PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-149 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (German isolate) (PVM).
positive-strand viruses, no DNA stage; Carlavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sl. 25, Last sequence update)
sl. 27, Last annotation update)
(PRI2) (NUCLEIC ACID-BINDING REGULATORY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91092429; PubMed=2265707;
Gramstat A., Courtpozanis A., Rohde W.;
"The 11 kba protein of potato virus M displays properties of nucleic acid-binding regulatory protein.";
FEBS Lett. 276:34-38(1990)
-1- FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SINILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER CAFLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.00053;
0.00053;
0.0053;
0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6CC7262429CD6B64 CRC64;
                                                                                                                                                    -i - FUNCTION: MICROBICIDAL ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; 332104; IPC1.
Cathelicidin.
Pfam. PF00666; Cathelicidins; 1.
ProDom: PD001838; Cathelicidins; 1.
PROSITE; PS00966; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Amidation; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                     Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.00
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                          STRAIN=RED DUROC;
MEDLINE=95354835; Pubmed=7628604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
01-OCT-1993 (Rel. 27, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 AA; 16604 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X84096; CAA58892.1; -. HSSP; 932194; 1PG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.7
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
130
148
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145
143
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=31710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
131
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136
138
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potato virus M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNBP_PVMG
Q01687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNBP_PVMG

ID VNBP_PVMG

DD VNBP_PVMG

DT 01-API

DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

SIMILARITY.

AMIDATION (G-149 PROVIDE AMIDE GROUP).

6F4BA98429CD6ED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metizoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEGRIN 3.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 62; DB 1; Length 149
Pred. No. 0.00053;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X83267; CAA58240.1; -.
EMBL; X84095; CAA58891.1; -.
HTK; S34587; S34587.
HTK; S342194; PTC1.
InterPro; IPR001894; Cathelicidin.
Probom; PD0066; Cathelicidins; 1.
PROSTTE; PS00946; CATHELICIDINS_1; 1.
PROSTTE; PS00946; CATHELICIDINS_2; 1.
Antibiotic; Signal; Amidation; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OVT-1997 (Rel. 35, Last annotation update)
PROTEGRIN 5 PRECURSOR (PG-5).
                                                                                     Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
FEBS Lett. 368:197-202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
                                     STRAIN-RED DUROC;
MEDLINE-95354835; PubMed-7628604;
                                                                                                                                                                                                 TISSUE=Leukocyte;
MEDLINE=93327946; Pubmed=8335113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.78;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 RGGGLCYCRRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
                                                                                                                                                                            OF 131-148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserv
                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
SEQUENCE
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PG5_PIG
P49934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                          The FEBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PG5_PIG

ID PG5

AC P49

DT 01-

DT 01-

DT 01-

DE PRO

GN NPG

OC Buk
```

ద

ò

ö

Gaps

00886E246A553B53 CRC64;

108 AA; 12183 MW;

SEQUENCE

S

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               ö
                                                     and for commercial
                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
     EMBL outstation
between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rupasov V.V., Morozov S.Y., Kanyuka K.V., Zavriev S.K.; "Partial nucleotide sequence of potato virus M RNA shows similarities to protexviruses in gene arrangement and the encoded amino acid
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
10.7 KDA PROTEIN (PUTATIVE NUCLEIC ACID-BINDING PROTEIN).
POCACO VILUS M (Strain Russian) (PVM).
Viruses; SSRNA positive-strand viruses, no DNA stage; Carlavirus.
                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: TO NUCLEIC ACID-BINDING PROFEINS FROM OTHER CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGISYNVRVAQFIDEGVTEVIPSVINKRE LVSLTMCAWRNLLMKE (IN REF. 1).
                                                                                                                                                                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Gen. Virol. 72:9-14(1991).
                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                           C4-TYPE (POTENTIAL).
86E80F8DC0B376E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zavriev S.K., Kanyuka K.V., Levay K.E.;
"The genome organization of potato virus M RNA.";
J. Gen. Virol. 72:9-14(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                          Score 51; DB 1;
Pred. No. 0.033;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gen. Virol. 70:1861-1869(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=91116326; PubMed=1990070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89293091; Pubmed-2738581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
                                                                                                                                       PIR, S12976, S12976.
InterPro: IPRO02568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                                           ZN_FING 57 78 C
SEQUENCE 108 AA; 12119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D14449; BAA03344.1; -.
                                                                                                                                                                                                                                                                             57.3%;
52.9%;
                                                                                                                       EMBL; X57440; CAA40689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X53062; CAA37237.1;
PIR; PN0006; WMVYP5.
PIR; S21606; S21606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zinc-finger; DNA-binding.
ZN_FING 57 78
CONFLICT 80 108
                                                                                                                                                                                                                                                                                                                                                                     40 GGRSKYARRRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                 2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=12168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNBP_PVMR
P17530;
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
VNBP_PVMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ά
                                                                                                                                                                                                                                                                                                                                                                                g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILINE=9201346; PubMed=1919520;
MEDILINE=9201346; PubMed=1919520;

"Nucleotide sequence and gene organization of the 3'-terminal region of Chrysanthemum virus B genomic RNA.";

of Chrysanthemum virus B genomic RNA.";

-1. Gen. Virol. 72:2333-237(1991).

-1. FUNCTION: MAY ACT AS A REGULATORY FACTOR DURING VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macropus rufus (Red kangaroo) (Megaleia rufa).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
NCBL_TaxID=12165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION.
-1- SIMILARITY: TO NUCLEIC ACID-BINDING PROTEINS FROM OTHER CARLAVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 1; Length 107; Pred. No. 0.17;
   Length 108
                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
12.6 KDA PROTEIN (PUTATIVE NUCLEIC ACID-BINDING PROTEIN).
Chrysanthemum virus B (CVB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4-TYPE (POTENTIAL).
674D16319920ED2F CRC64;
Score 51; DB 1;
Pred. No. 0.033;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AA.
                                                                                                                                                                                                                                                                                                                                                                107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JQ1251; JQ1251.
InterPro; IPRO02568; Carla_C4.
Pfam; PF01623; Carla_C4; 1.
Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 AA; 12576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.8%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S60150; AAB20081.1; -.
Query Match 57.3%;
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                2 GGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                 40 GGRSKYARRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.8
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ||:||| :: :||
40 GRSSYARRRALELGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP1_MACRU P42142;
                                                                                                                                                                                                                                                                                                                                                            VNBP_CVB
P37992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_MACRU
                                                                                                                                                                                                                                                                                                                                 VNBP_CVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                  DATA PARA BARANA BARANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

S

d

us-09-485-571-15.rsp

```
INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSP1_DASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
    ò
                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DACO
DACO
DARKEN NAMED DE PROPERTIES DE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       á
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                           Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsuplal protamine Pl genes.";
Proc. R. Soc. Lond. B, Biol. Sci. 259:7-14(1995).
-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein. INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazóa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 59;
Pred. No. 0.2;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AA; 8230 MW; 78F1AE592B4B2FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L35447; AAA74616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 69.2.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenolestes fuliginosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 RGRRRGYSRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFS 13
                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=37696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSP1_CAEFU
P42131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP1_CAEFU
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retief J.D., Krajewski C., Westerman M., Winkfeln R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsuptal protamine P1 genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259;7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING. THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBCELLULAR LOCATION: UNCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                   Promis PR00260; protamine_Pl; 1.
PROSITE; PS00048; PROTAMINE_Pl; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dasyurus viverrinus (Southeastern quoll), and Dasyurus hallucatus (Satanellus/Northern quoll). Eukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasyurus.
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 1; Length 60;
                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 60; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                            BY SIMILARITY.
7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :lear protein.
BY SIMILARITY.
615D3D85E7123025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 32, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.2; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                  InterPro; IPR000221; Protamine_P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP1_DASVI STANDARD; P
P42135; P42133;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                            50.6%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L35340; AAA74599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AA; 8246 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.68;
                                                                                                                                                                                                                                                    60 AA; 8514 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.28;
                                                    EMBL; L35332; AAA74598.1;
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 69.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L35341; AAA56795.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 RGRRRGYSRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
```

```
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 RGRRRGYSRRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP1_ANTSW
    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259-7-14 (1995).
-1- FUNCTION: PROTAMINES GUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                  Macropus agilis (Agile wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antechinomys laniger.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 1; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clear protein.
BY SIMILARITY.
96255C818921EB85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-97446280; PubMed-9299228;
Krajewski C., Blacket M., Buckley L.; Westerman M.;
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AA.
                                                                                                       60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO00221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Testis; DNA condensation; Nuclear INIT_MET 0 0 BY SI SEQUENCE 60 AA; 8338 MW; 96255
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL_1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L35451; AAA74615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                       STANDARD;
                                                                                                                                              (Rel. 32, (Rel. 32, 1) (Rel. 32, 1) (Rel. 35, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | | | |||||:|
RGRRGYSRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPERM PROTAMINE P1.
42 RGRRRGYSRRYS
                                                                                                                                                                                                             SPERM PROTAMINE P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=60701;
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9313;
                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Sperm
                                                                                                                                            01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998
                                                                                                                                                                                        01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSP1_ANTLA
                                                                                                       HSP1_MACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        018745;
                                                              T 11
                                                                                                                               P4213
                                                            HEREGOLLT AND THE PERSON TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=N.lorentzii, D.albopunctatus, D.geoffroii, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with cytochrome b, 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-: FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
                                                                                                                                QF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-A.swainsonii, and P.dorsalis; TISSUE-Sperm; MEDLINE-9521531; PubMed-7700877; Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
"A multigene assessment of phylogenetic relationships within the dasyurid marsupial subfamily Sminthopsinae.";
Mol. Phylogenet. Evol. 8:236-248(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN C SPERM DURING THE HADLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 61 AA; 8409 MW; E021567627E562B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dasyurus spartacus (Native cat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Antechinus.
NCBI_TaxID=9284, 9295, 32551, 32545, 63143, 32546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 61; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antechinus swainsonii, Phascolosorex dorsalis, Neophascogale Lorentzii (Long-clawed marsupial mouse), Dasyurus aloppunctatus (Native cat), Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF001587; AAB91377.1; -.
InterPro; DR000221; Protamine_Pl.
Pfam; PF00260; protamine_Pl; I.
PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANISM STANDAMC,
P42130; P42146;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watch 50.6%; Local Similarity 69.2%; nes 9; Conservative
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
SWISS-PROT entry is copyright. It is produced through a collaboration
                  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
"Reconstructing the taxonomic radiation of dasyurine marsupials with
Cytochrome D. 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-I- SUBCELLULAR LOCATION: UNCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                 Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Restls; DNA condensation; Nuclear protein.

INIT MET 0 BX SIMILARITY
SEQUENCE 61 AA; 8421 MW; C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parantechinus bilarni (Broad-footed marsupial mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
NCBI_TaxID=32555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Length 61;
Pred. No. 0.21;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                               0 0 BY SIMILARITY.
61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Testis; DNA condensation; Nuclear protein
                                                                                                                                                                                              EMBL: AF010267; AAB69297.1; -. EMBL: AF010272; AAB69302.1; -. EMBL: AF010274; AAB69304.1; -. EMBL: AF010275; AAB69304.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF010277; AAB69307.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                        EMBL; L35338; AAB95429.1; -. EMBL; L35339; AAA74601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || | | |||||:|
RGRREGYSRRYS 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSP1_PARBI
018768;
                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.harrisil; TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
Retief JD., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. F. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i - FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-D.maculatus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12s RRNA, and proteamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                Dasyurus maculatus (Tiger quoll).
Eukarycta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                   ö
                                                                                                                                                                                                                                                                                                                                                         Manmalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                   Indels
                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 0 BY SIMILARITY.
61 AA; 8410 MW; 4A215D3D85E71230 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1;
Pred. No. 0.21;
                  DB 1;
                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                               Sarcophilus harrisii (Tasmanian devil), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Testis; DNA condensation; Nuclear protein.
                  Score 45;
Pred. No.
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF010276; AAB69306.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; I.35324; AAA74608.1; -.
                  50.6%;
69.2%;
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                STANDARD;
                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                55
Query Match
Best Local Similarity
'... 9; Conservē
                                                                                                                                                                                                                                                                                SPERM FROTAMINE P1.
                                                                                                  43 RGRRRGYSRRRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | | || || || || || || || || || RGRRRGYSRRYS
                                                                                1 RGGRLSYSRRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                             HSP1_SARHA
P42151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                               HSP1_SARHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                   ò
                                                                                                                g
                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
```

Search completed: February 12, 2002, 12:39:48 Job time: 801 sec

```
February 12, 2002, 12:25:22 ; Search time 126.85 Seconds (without alignments) 10.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                     219241
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                       US-09-485-571-15
89
1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ij	7	S	٣	31d	12K protein - pota	nucleic acid-bindi	hypothetical 12.6K			protegrin 4 precur	FLO/LFY protein ho	aminopeptidase (EC	aminopeptidase (EC	hypothetical prote	hypothetical prote	hypothetical prote	¥	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	FLO/LFY protein ho	hypothetical prote		$\overline{}$	probable membrane	hypothetical prote	DNA polymerase III
SUMMARIES			0060NC	S57609	A53895	WMVY P5	S12976	B48549	JQ1251	G96537	S21102	B53895	1240	T30942	943	C72642	QQAG6T	A30832	1439	S53982		D81096	T06680	T03243	D71936	T42599	510	64746	÷	0172
	GI	557	JNC	S57	A53	MM	S12	B48	5	969	S21	B23	T03	T30	130	C72	Ŝ	A30	C69	S53	70°	D83	T06	T03	D7.1	T42	F85	F64	T16	B70
	80	7	7	7	7	Н	7	-	7	7	7	7							~							7	7	~	ď	7
	Query Match Length		147	149	149	108	108	94	107	627	135	149	413	1016	1016	118	191	186	219	447	1696	134	349	416	416	747	826	826	1030	1161
ď	Ouery Match	77.5	70.8	69.7	69.7		57.3	55.1	52.8	49.4	48.3	8	48.3		48.3	47.2	47.2	46.1	46.1	9	9	4.	44.9	44.9	44.9	44.9	44.9	44.9	44.9	44.9
	Score	9	63	62	62	51	51	49	47	44	43	43	43	43	43	42	42	41	41	41	41	40	40	40	40	40	40	40	40	40
	Result No.	П	7	m	4	ς.	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59

All-1 protein +GTE	probable tRNA intr	ribosomal protein	conserved hypothet	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	probable acyl-CoA	hypothetical prote	oxidoreductase, ac	acriflavine resist	hypothetical prote	hypothetical prote	trithorax homolog
A48205	B72545	G70154	E69554	B72739	T33652	T43147	T38308	S55626	H72730	A84265	D82164	G64595	T26377	E96505	A44265
~	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
3869	187	51	167	201	217	310	325	349	532	647	160	1028	1224	2114	3968
		80	8	æ	æ	8	80	ω.	43.8	œ.	ω.	ω.	₩.	8.	8.
44.9	44.4	43.	43.8	43.	43.	43.	43	43	43	43	43	43	43	43	43
40 44.9	39.5 44.4	_	_	39 43.	39 43.	39 43.	39 43	39 43	39 43		43	39 43	43	43	43

## ALIGNMENTS

Substitution of a momentary and a momentary of a momentary structure of three cationic peptides from portions of an animated carboxyl 1953 87807 87807 87808 87808 87808 87808 87808 87808 87807 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808 87808	RESULT 1 S57607 protegrin 1 precursor - pig N;Alternete names: neutrophil peptide 1
A; Title: The structure of porcline protegrin genes.  A; Accession: S66281; MUID:95354835  A; Accession: S66281; MUID:95354835  A; Accession: S66281; MUID:95354835  A; Accession: S66281; MUID:980642; PIDN:CAA58890.1; PID:9887643  A; Cross-references: EMBEL:X84094; NID:9807642; PIDN:CAA58890.1; PID:9887643  B; Zhao, C.; Liu, L.; Lehrer, R. I.  R; Zhao, C.; Liu, L.; Lehrer, R. I.  A; Accession: S45712  A; Accession: S5620	 C;Species: Sus scrout a Gomestic (Gomestic Pig) C;Date: 19-Oct-1995 #sequence_revision 03.Nov-1995 #text_change 16-Jul-1999 C;Accession: S66284; S45712; S36820; S34585; S57607 R;Zhao, C; Ganz, T; Lehrer, R.I. FEBS Lett. 368, 197-202, 1995
A Molecule type: DNA A Rocessium: 1-149 catha A Rocessium: 1-149 catha A Arcessium: 1-140 catha A Arcessium: 1-140 catha A Arcessium: 1-140 catha A Arcessium: 346, 286-288, 1994 A Artile: Identification of a new member of the protegrin family by CDNA cloning. A Rocession: 345712; MUID: 94283613 A Rocession: 345712; MUID: 94283613 A Recent cost unaber: 545712; MUID: 94283613 A Recent cost unaber: 545712; MUID: 94283613 A Residues: 1-149 catha A Residues: 1-149 catha A Residues: 1-140 catha A Reference number: 536820; MUID: 93387466 A Reference number: 536820; MUID: 93387466 A Residues: 11-140 catha A Reference number: 536820; MUID: 93337946 A Reference number: 534585; MUID: 93327946 A Rocession: 534585 A Rickyakov, V. N.; Harvig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M. A Reference number: 534585; MUID: 93327946 A Rocession: 534585 A Reference number: 534585; MUID: 93327946 A Rocession: 5673; 102/3; 126/3 A Repertamily: cathalin; cystatin homology C Superfamily: cathalin; cystatin homology C Superfamily: signal a Sequence #status predicted <sig> F: 21-2190chain: signal sequence #status predicted <arg< br=""> C Repertamily: signal a Sequence #status predicted <arg< br=""> F: 72-1290chain: propeptide #status predicted <arg< br=""> F: 71-146/Modified site: amidated carboxyl end (Arg) (amide in mature form from following type Matches 14; Conservative 0: Mismatches 4; Indels 0; Gaps 0;</arg<></arg<></arg<></sig>	 A;Title: The structure of porcine protegrin genes. A;Reference number: S66283; MUID:95354835
A. Cross-references: EMBLING 18987642; PIDN:CAA58890.1; PID:9887643 B. Zhoo, C.; Liu, L.; Lehrer, R.I. FEBS Lett. 346, 285-288, 1994 R.I. FEBS Lett. 346, 285-288, 1994 R.I. A.7Title: Identification of a new member of the protegrin family by CDNA cloning. A.Reference number: 845712; MuID:94283613 A.Rolecule type: mRNA A.Rocession: 845712 A.Rolecule type: mRNA A.Rocession: 836870 A.Title: Primary structure of three cationic peptides from porcine neutrophils. Seq. A.Residues: 134-148 CMR> A.Rocession: 836820; MuID:93387466 A.Rocession: 836820 A.Rocession: 836820; MuID:93387466 A.Rocession: 836820; MuID:93387466 A.Rocession: 836820; MuID:93387466 A.Rocession: 834885; MuID:93327946 A.Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A.Reference number: 834885; MuID:93327946 A.Rocession: 834885 A.Rocession: 834885; MuID:93327946 A.Rocession: 834885	 A; McCession : Sowica A; McJecule type: DNA A; Residues: 1-149 <2HA>
A: Title: Identification of a new member of the protegrin family by cDNA cloning.  A: Reference number: \$45712; MUID: 94283613  A: Accession: \$45712; MUID: 94283613  A: Accession: \$45712; MUID: 94283613  A: Accession: \$45712; MUID: 94283613  A: Residues: 1.149 C-2H2>  A: Residues: 1.149 C-2H2>  A: Residues: 1.149 C-2H2>  A: Residues: 1.140 C-2H2>  A: Residues: 1.140 C-2H2>  A: Residues: 1.140 C-2H2>  A: Residues: 1.300, 339-342, 1993  A: Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence number: \$36820; MUID: 93387466  A: Residues: 131-148 C-2H2>  A: Residues: 131-148 C-2H2>  A: Residues: 131-148 C-2H2>  A: Residues: 131-148 C-2H2>  A: Reference number: \$34585; MUID: 93327946  A: Reference number: \$34585; MUID: 93327946  A: Residues: 131-148 C-2H2>  A: Residues: 131-148 C-2H2>  A: Reference number: \$34585; MUID: 93327946  A: Reference number: \$34585; MUID: 93327946  A: Residues: 131-148 C-2H2>  A: Residues: 131-148 C-2H2>  C: Genetics: A: Residues: A: Residu	 L:X84094; NID:9887642; PIDN:CAA58890.1; hrer, R.I.
A; Accession: \$45712 A; Accession: \$45712 A; Accession: \$45712 A; Accession: \$45712 A; Accession: \$1.149 < czl2> A; Cross-references: GB:X79868; NID:9603035; PIDN:CAA56251.1; PID:9603036 R; Mirgorodskaya, O.a.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egg FEBS Lett. 330, 339-342, 1993 A; Title: Primary structure of three cationic peptides from porcine neutrophils. Seq A; Reference number: \$36820; MUID:93387466 A; Accession: \$36820 A; Molcoule type: protein A; Residues: 131-148 < AIXE. A; Accession: \$34585; MUID:93327946 A; Title: Protegrins: Letter antimicrobial peptides that combine features of cort A; Reference number: \$34585; MUID:93327946 A; Accession: \$34585 A; Molcoule type: protein A; Residues: 131-148 < KOK> C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Cancelics: A; Titlonali: propeptide #status predicted <sig> F; 12-2P/Domain: propeptide #status predicted <pro> F; 12-109/Domain: propeptide #status predicted <pro> F; 131-148/Product: protegrin # #status spredicted <pro> F; 131-148/Product: protegrin # #status spredicted <pro> F; 131-148/Product: protegrin # #status predicted <pro> F; 131-148/Product: protegrin # #status predicted <pro> F; 131-148/Product: protegrin # #status spredicted <pro> F; 131-148/Product: protegrin # #status predicted <pro> F; 131-148/Product protegrin # #status predicted <pro> F; 1</pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></pro></sig>	
A; Residues: 1-149 < 22H2> A; Residues: 1-149 < 22H2> A; Residues: 1-149 < 22H2> A; Construction of the cardion	A;Accession: S45712 A:Molecule type: mRNA
R; Mirgorodskaya, O.A.; Shevchenko, Ä.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egg FBES Lett. 330, 339-342, 1993 A; Title: Primary structure of three cationic peptides from porcine neutrophils. Seq A; Reference number: S36820 A; Molecule type: protein A; Residues: 131-148 <air> A; Residues: 131-148 <air 131-148="" <air="" a;="" residues:="" residues:<="" td=""><td>A;Residues: 1-149 <zh2> A;Cross-references: GB:X79868; NID:9603035; PIDN:CAA56251.1; PID:9603036</zh2></td></air></air></air></air></air></air></air></air></air></air></air>	A;Residues: 1-149 <zh2> A;Cross-references: GB:X79868; NID:9603035; PIDN:CAA56251.1; PID:9603036</zh2>
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Seq A; Accession: 836820; MUDD:93387466 A; Accession: 836820 A; Molecule type: protein A; Residues: 131-148 cMIR> B; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M FEBS Lett. 327, 231-236, 1993 A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A; Reference number: 834585; MUDD:93327946 A; Rolecule type: protein A; Reference number: 834585; MUDD:93327946 A; Redecile type: protein A; Residues: 131-148 cKOK> C; Genetics: A; Residues: 131-148 cKOK> C; Superfamily: cathelin; cystatin homology C; Keywords: amidated carboxyl end; antibacterial; neutrophil F; 129/Domain: signal sequence #status predicted cRIO> F; 22-129/Domain: signal sequence #status predicted cRIO> F; 21-129/Domain: cystatin homology cKTS> F; 30-130/Domain: propeptide #status experimental cMAT> F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form following that the coal Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egr FEBS Lett. 330, 339-342, 1993
A; Accession: S36820 A; Accession: S36820 A; Molecule type: protein A; Residues: 131-148 <amr> B; Rokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M FEBS Lett. 327, 231-236, 1993 A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A; Reference number: S34585; MUID:93327946 A; Accession: S34585 A; Molecule type: protein A; Residues: 131-148 <kok> C; Genetics: A; Gene: NPG1 A; Introns: 66/3; 102/3; 126/3 A; Introns: 66/3; 102/3; 126/3 C; Superfamily: cathelin; cystatin homology C; Keywords: amidated carboxyl end; antibacterial; neutrophil F; 1-29/Domain: signal sequence #status predicted <rig> F; 21-199/Domain: cystatin homology <cys> F; 30-130/Domain: propeptide #status predicted <pats #status="" 1="" 131-148="" <amt="" experimental="" f;="" product:="" protegrin=""> F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form following the coal Similarity 77.8%; Score 69; DB 2; Length 149; Best Local Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</pats></cys></rig></kok></amr>	A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequ. A; Reference number: S36820; MUID:93387466
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M. FEBS Lett. 327, 231-236, 1993 A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A; Reference number: S34585; MUID:93327946 A; Reference number: S34585; MUID:93327946 A; Recession: S34585 A; Molecule type: protein A; Residues: 131-148 < KOK> C; Genetics: A; Refene: NPG1 A; Introns: 66/3; 102/3; 126/3 A; Introns: 66/3; 102/3; 126/3 C; Superfamily: cathelin; cystatin homology C; Superfamily: cathelin; cystatin homology < C; Superfamily: cathelin; cystatin homology < C; Superfamily: cystatin homology < C; Siperfamily: C; Keywords: amidated carboxyl end; articled < C; Keywords: midated carboxyl end (Arg) (amide in mature form following that which the site: amidated carboxyl end (Arg) (amide in mature form following S; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form following Best Local Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	A;Accession: S36820 A;Molecule type: protein
A: 7:11e: Protegrins: leukocyte antimicrobial peptides that combine features of cort A; Reference number: S34585; MUID:93327946 A; Accession: S34585 A; Molecule type: protein A; Residues: 131-148 <kok> C: Genetics: A; Genetics: B; A; Genetics: A; Genet</kok>	
A; Accession: S34585; MULD:9332/946 A; Accession: S34585 A; Molecule type: protein A; Residues: 131-148 < KOK> C; Genetics: A; Gene 105: A; Introns: 66/3; 102/3; 126/3 A; Introns: 66/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3;	 FEBS Lett. 327, 231-236, 1993 A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort
A; Residues: 131-148 < KOK> C; Genetics: A; Residues: 131-148 < KOK> C; Genetics: A; Cenetics: A; Cathelin; cystatin homology C; Keywords: amidated carboxyl end; antibacterial; neutrophil F; 122-129/Domain: systatin homology < CYS. F; 30-130/Domain: cystatin homology < CYS. F; 30-130/Domain: cystatin homology < CYS. F; 131-148/Product: protegrin 1 #status experimental <art> F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form following that the coal Similarity 77.5%; Score 69; DB 2; Length 149; Best Local Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</art>	 A;Reterence number: S34585; MUID:93327946 A;Accession: S34585
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Introns: 66/3; 102/3; 126/3 C; Superfamily: cathelin; cystatin homology C; Keywords: amidated carboxyl end; antibacterial; neutrophil C; Keywords: amidated carboxyl end; antibacterial; neutrophil F; 22-129/Domain: signal sequence #status predicted <pro> F; 23-130/Domain: cystatin homology <cys> F; 30-130/Domain: propeptide #status predicted <pro> F; 131-148/Product: protegrin 1 #status experimental <amt> F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form following the follo</amt></pro></cys></pro>	 A;Molecule type: protein A;Residues: 131-148 <kok></kok>
A; Introns: 66/3; 102/3; 126/3  C; Superfamily: cathelin; cystatin homology C; Superfamily: cathelin; cystatin homology C; Superfamily: cathelin; cystatin homology C(S) E; 1-29/Domain: signal sequence #status predicted <sig> F; 22-129/Domain: propeptide #status predicted <pro> F; 31-134/Product: protegrin 1 #status experimental <pamp> F; 1148/Modified site: amidated carboxyl end (Arg) (amide in mature form following the mature form following the matches als matches of the matches o</pamp></pro></sig>	 C; Genetics:
C; Keywords: amidated carboxyl end; antibacterial; neutrophil F;1-29/Domain: signal sequence #status predicted <sig> F;22-129/Domain: cystatin homology <cys> F;30-130/Domain: cystatin homology <cys> F;31-148/Product: propeptide #status predicted <pro> F;131-148/Product: protegrin 1 #status experimental <mat> F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following that the corporation of the corpora</mat></pro></cys></cys></sig>	 A; Introns: 66/3; 102/3; 126/3 C:Superfamily: cathelin: cystatin homology
F;22-129/Domain: cystatin homology <cysperson an<="" and="" states="" td=""><td> C; Keywords: amidated carboxyl end; antibacterial; neutrophil</td></cysperson>	 C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F;30-130/Nomain: propeptide #status predicted <pro>F;30-130/Nomain: propeptide #status predicted <pro>F;131-140/Product: protegrin 1 #status experimental <pro>F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following the Match Match 77.5%; Score 69; DB 2; Length 149; Best Local Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</pro></pro></pro>	 F;22-129/Domain: cystatin homology <cys></cys>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following the property Match 17.5%; Score 69; DB 2; Length 149; Best Local Similarity 77.8%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	 F;30-130/Domain: propeptide #status predicted <pro> F;131-148/Product: protegrin 1 #status experimental <mat></mat></pro>
77.5%; Score 69; DB 2; Length 149; 77.8%; Pred. No. 0.00022; /ative 0; Mismatches 4; Indels 0; Gaps	F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
//.os; ried. NO. O.OOOzz; /ative 0; Mismatches 4; Indels 0; Gaps	 77.5%; Score 69; DB 2;
	 //.os, Fied. NO. O.OOOZZ, /ative 0; Mismatches 4; Indels 0; Gaps

2

```
C;Keywords: amidated carboxyl end; antibacterial F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                    69.78;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 RGGRLCYCRPRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 72.23
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: protein
A, Residues: 131-148 <MIR>
C, Genetics:
A, Introns: 66/3; 102/3; 126/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 131-148 <KOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S34587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S36821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS. Lett., 330, 339-447, 1938

A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A; Reference number: 536820; MUID:93387466

A; Rocession: 535822

A; Molecule type: protein
A; Residues: 131-146 (AIR)

R; Kokytyakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SF

R; Kokytyakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SF

R; Kokytyakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SF

R; Kokytyakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; SF

R; Kokytyakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G. Corticost
A; Reference number: 534585

A; Ritle: Protegrins: 1093327946
A; Rocession: 534586
A; Rocession: 5345
                                                                                                                                                                                                                                                                                                                                                                                              Protegrin 2 precursor - pig
NyAlternate names: cathelin-like protein precursor; neutrophil peptide 3
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice pig)
(Species: Sus scrofa domestice)
(Species: Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
557609
Protegrin 5 precursor - pig
N.Alternate names: cathelin-associated antimicrobial peptide
C.Species: Sus scrofa domestica (domestic pig)
C.Accession: S6688; S57609
R.Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A.;Title: The structure of porcine protegrin genes.
A.;Reference number: S66283; MUID:95354835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Residues: 1-149 < ZHA>
A Cross-references: BMBL:X84096; NID:g887646; PIDN:CAA58892.1; PID:g887647
A Cross-references: Leukocytes
C;Genetics:
A Gene. NPGS
A;Introns: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 2; Length 147
Pred. No. 0.0022;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.8%;
                                                                                                           131 RGGRLCYCRRRFCVCVGR 148
                                                     RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 RGGRLCYCRRFFCICVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 70.8
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΩD
                                                                                                                                                 q
                                                     á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
A; Molecule type: mRNA
A; Residues: 1-149 <-ZHX>
A; Cross-idues: 1-149 <-ZHX>
A; Cross-references: GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:g603038
B; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.
FEBS Lett. 327, 231-236, 1993
A; Title: Protegrins: leukocyte antimicrobial peptides that combine features of corti
A; Reference number: S34585; MUID:93327946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Mirgorodskaya, 0.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Ego FEBS Lett. 330, 339-342, 1939 Trible: Primary structure of three cationic peptides from porcine neutrophils. Sequ A; Reference number: S16820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                 in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X84095; NID:g887644; PIDN:CAA58891.1; PID:g887645
R;Zhao, C.; Liu, L.; Lehrer, R.I.
ERSE Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613
A;Accession: A53895
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protegrin 3 precursor - pig
NyAlternate names: neutrophil peptide 2
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecies: Sus scrofa domestica (domestic pig)
Cispecia: Sus scrofa domestica (domestic pig)
Rizhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835
A;Molecule type: DNA
A;Residues: 1-149 <2H3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.7%; Score 62; DB 2; Length 149; 72.2%; Pred. No. 0.0033; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;l-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 5 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide
                                                                                                                                                                                                                                                      Score 62; DB 2;
Pred. No. 0.0033;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =
=
=
=
=
```

```
hypothetical 12.6K protein - chrysanthemum virus B (Species: chrysanthemum virus B C;Species: chrysanthemum virus B C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999 C;Accession: JQ1251  
R;Levay, K.; Zavriev, S. Graviev, S. Gen. Virol. 72, 23337, 1991  
A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of A;Reference number: JQ1246; MUID:92013948
                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: potato vírus S
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999
C; Accession: B48549
R; Foster, G.D.; Mills, P.R.
Virus Genes 6, 213-220, 1992
A; Title: The 3'-nucleotide sequence of an ordinary strain of potato virus S.
A; Reference number: A48549; MUID: 93033173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F2J10.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:S45593; NID:g256417; PIDN:AAB23462.1; PID:9256419
A;Note: sequence extracted from NCBI backbone (NCBIN:114637, NCBIP:114639)
C;Superfamily: potato virus nucleic acid-binding protein
C;Reywords: DNA binding: zinc finger
F;55-75/Region: zinc finger
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:S60150; NID:g237315; PIDN:AAB20081.1; PID:g237321
C;Superfamily: potato virus nucleic acid-binding protein
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 107;
                                                                                   Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 94;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
     C; Superfamily: potato virus nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2;
Pred. No. 0.83;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB 1;
Pred. No. 0.34;
                                                                                     5
                                                                                     DB 2;
0.18;
                                                                                   Score 51; DB 2
Pred. No. 0.18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid-binding protein - potato virus S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.1%;
52.9%;
                                                                                   57.3%; 52.9%;
                                                                                                                                                                                                                               ||| |:||| ::|: |
40 @GRSKYARRRAISIAR 56
                                                                                                                                                                                               2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ||:||| :: :||
40 GRSSYARRRALELGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: genomic RNA A; Residues: 1-94 <FOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: genomic RNA A; Residues: 1-107 <LEV>
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JQ1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                               A. Accession: FS433

A. Moclesule type: genomic RNA
A. Residues: 1-108 < ZAV>
A. Moclesule type: genomic RNA
A. Residues: 1-108 < ZAV>
A. Cross-references: EMBL:X53062; NID:g61291; PIDN:CAA37237.1; PID:g61297
B. Rupasov, V. V. T. Morzov, S. Y.; Ranyuka, K. V.; Zavriev, S. K.
J. Gen. Virol. 70, 1861-1869, 1989
A. Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvi
A. Reference number: A92800; MUID:89293091
A. Title: Partial nucleotide sequence of potato virus M genomic RNA
A. Residueus: 1-79, VASCIMCAMRNILMEE < RUP>
A. Molecule type: MRNA
A. Reference number: PN0093; MUID:92049299
A. Title: The complete nucleotide sequence of potato virus M genomic RNA
A. Title: The complete nucleotide sequence of potato virus M genomic RNA
A. Reference number: PN0093; MUID:92049299
A. Accession: PN0095
A. Molecule type: genomic RNA
A. Residues: 1-108 < ZAZ>
A. Molecule type: genomic RNA
A. Residues: 1-108 < ZAZ>
A. Molecule type: genomic RNA
A. Residues: 1-108 < ZAZ>
A. Molecule type: genomic RNA
A. Residues: 1-79, 'LVSITMCAWRNILMKE' < ZAZ>
A. Molecule type: genomic RNA
A. Residues: 1-79, 'LVSITMCAWRNILMKE' < ZAZ>
A. Molecule type: genomic RNA
A. Residues: 1-79, 'LVSITMCAWRNILMKE' < ZAZ>
A. Cross-references: BMBL:X53062 in Blading; nucleotide binding; zinc finger
C. Superfamily: potate building; metal binding; nucleotide binding; zinc finger
F.57-78/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Gramstat, A.; Courtpozanis, A.; Rohde, W.
FEBS Lett. 276, 34-38, 1990
A;Title: The 12 Kba protein of potato virus M displays properties of a nucleic acid-bind
A;Reference number: $12975; MUID:91092429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12K protein - potato virus M
C;Species: potato virus M
C;Date: 19-Mar_1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
                                                                                                                                                                                                                         #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-108 <GRA>
A;Cross-references: GB:X57440; NID:g61400; PIDN:CAA40689.1; PID:g61402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 1; Length 108;
Pred. No. 0.18;
4; Mismatches 4; Indels
                                                                                                                                      nucleic acid-binding protein - potato virus M (strain Russian)
                                                                                                                                                          C; Species: potato virus M. A; Note: host Lycopersicon esculentum (tomato) C; Date: al-Mar-1990 #sequence_revision 23-Mar-1995 #tex C; Date: 31-Mar-1990 #sequence_revision 23-Mar-1995 #tex C; Accession: E54333; PN0006; PN0095; S21666 R; Zavriev, S.K.; Kanyuka, K.V.; Levay, K.E. J. Gen. Virol. 72, 9-14, 1991 A; The genome organization of potato virus M RNA. A; Reference number: A54333; MUID:91116326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.3%;
131 RGGGLCYCRRFCVCVGR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| |:||| ::|: |
40 GGRSKYARRRRAISIAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 19-Mar-1997 #
C;Accession: S12976
R;Gramstat, A.; Court
FEBS Lett. 276, 34-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
```

ö

chr

ő

```
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGRLSYSRRFSVSVGR 18
                                                                                                                                                                                    Query Match 48.39
Best Local Similarity 55.69
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 48.3
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||: |:||| :: |
555 GRLTISQRRFDIING 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GRLSYSRRFFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΩ
                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                         Op
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudnes, B.; Hudrar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <STO>A;Coss-references: GB:AE005173; NID:98569089; PIDN:AAF76434.1; GSPDB:GN00141
C;Genetics: F2210.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Conger myriaster
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
R;Muramoto, K.; Kamiya, H.
Biochim. Biophys. Acta 1116, 129-136, 1992
A;Title: The amino-acid sequence of a lectin from conger eel, Conger myriaster, skin much A;Reference number: S21102; MUID: 92256465
A;Reference number: S21102
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-135 cwurx
C;Superfamily: beta-galactoside-binding lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protegrin 4 precursor - pig
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: University and the sequence_revision 01-bec-1995 #text_change 16-Jul-1999
C.Accession: B53895
B.Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 288-288, 1994
A.Tile: Identification of a new member of the protegrin family by cDNA cloning.
A.Reference number: 845712; MUID:94283613
A.Reference number: 845712; MUID:94283613
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-149 <-ZHAA
A.Residues: 1-149 <-ZHAA
A.Residues: 1-149 <-ZHAA
A.Residues: 1-149 <-ZHAA
C.Coss-references: GB:X83268; NID:9603039; PIDN:CAA58241.1; PID:9603040
C.Superfamily: cathelin; cystatin homology
C.Superfamily: cathelin; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||||| | :|: |
279 KGGRLSLPRESLEISIAR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Conger myriaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGRLSYSRRFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :: | :||||:||
20 GGFINNSPQRFSVNVG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
S21102
lectin - eel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
```

```
F;22-129/Domain: cystatin homology <CYS>F;131-148/Product: protegrin 4 #status predicted <MAT>F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chacession: T03240

R/Kelly, A.J.; Bonnlander, M.B.; Meeks-Wagner, D.R.
Plant Cell 7, 225-334, 1995

R/Kelly, A.J.; Bonnlander, M.B.; Meeks-Wagner, D.R.
Plant Cell 7, 225-334, 1995

A/Title: NFL, the tobacco homologue of FLORICAULA and LEAFY, is transcriptionally ex A/Reference number: 214855; MUID:95276463

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-413 < KEL>

A/Cross references: EMBL:U16172; NID:9561681; PIDN:AAC48985.1; PID:9561683

A/Experimental source: cultivar Samsun

C/Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Accession: 130942
R; Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
Submitted to the EMBL Data Library, November 1997
A; Description: Molecular comparison of aminopeptidase cDNAs and gene structure betwee A; Reference number: 220942
A; Reference number: 220942
A; Actaus: preliminary
A; Molecule type: mRNA
A; Residues: 1-1016 <2HU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 154/1; 288/3
C;Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein
C;Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF034483; NID:92645992; PID:92645993; PIDN:AAC36148.1
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: alpha-aminoacylpeptide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aminopeptidase (EC 3.4.11.-) - Indian meal moth
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLO/LFY protein homolog NFL1 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Mar-2001
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 413;
                                                                                                                                              48.3%; Score 43; DB 2; Length 149; 55.6%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 14;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.3%; Score 43; DB
53.3%; Pred. No. 33;
ilve 4; Mismatches
                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                131 RGGRLCYCRGWICFCVGR 148
                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 GGRMKQRRRKKVVSTGR 202
```

```
Dypothetical protein APE0571 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Stacession: C72642
R;Kawarabayasi, X; Hino, Y; Horikawa, H; Yamazaki, S; Haikawa, Y; Jin-no, K; Takahawa, H; Takahaya, M; Masuda, S; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; M
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339
A;Accession: C72642
A;Acc
aninopeptidase (EC 3.4.11.-) - Indian meal moth
C.Species: Plodia interpunctella (Indian meal moth)
C.Species: Plodia interpunctella (Indian meal moth)
C.Accession: T3094
R; Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
Bubinited to the EMBL Data Library, November 1997
A; Description: Molecular comparison of aminopeptidase cDNAs and gene structure between the A; Reference number: Z20942
A; Accession: T30943
A; Accession: T30943
A; Status: preliminary
A; Molecular type: mRNA
A; Residues: 1-1016 < ZNANA
A; Residues: 1-1016 < ZNANA
A; Residues: 1-1016 < ZNANA
A; Cross-references: EMBL: ARONA minopeptidase
C; Superfamily: membrane alanyl aminopeptidase
C; Keywords: alpha-aminoacylpeptide hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.3%; Score 43; DB 2; Length 1016; 53.3%; Pred. No. 33; 1rdels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 2
Pred. No. 6.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: February 12, 2002, 12:34:35 Job time: 553 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.2
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||: |:||| :: |
555 GRLTISQRRFDITNG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GRLSYSRRRFSVSVG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 RGGRLRSSRRR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
QO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Appli Appli

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Total number of

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

е ::

Run

Scoring table:

2, 7

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

```
8, 13, 15)
/note= "x is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: O7-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURRAHIGE, KATE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SOO ID NO: 63:
SEQUENCE CHARACTERISTICS:
TEMMTON FOR SEO ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
           US-09-128-345-16

US-09-128-345-33

US-09-128-345-48

US-08-243-8734-48

US-08-243-8734-36

US-08-499-523-10

US-08-128-345-2

US-09-128-345-10

US-08-182-4834-17

US-08-243-8734-24

US-08-243-8734-24

US-08-499-523-45

US-08-499-523-45

US-08-128-345-37

US-08-33-45

US-08-33-45

US-09-128-345-45

US-09-128-345-45
                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/08499523; Patent No. 5804558; General INFORMATION: GENERAL INFORMATION: APPLICANT: LEHRER, ROBERT I. APPLICANT: HARWIG, SYLVIA S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR I
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: group(6, OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
US-08-499-523-63
 STATE:
59, Appl
1, Appli
2, Appli
28, Appl
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   App]
                                                                                                                       (without alignments)
3.817 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                        ; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2
Sequence 1
Sequence 1
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgn2_6/ptodata/2/iaa/PackfilesI.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-752-82A-23

US-09-128-145-63

US-09-128-145-67

US-08-1499-523-53

US-08-1499-523-58

US-09-128-345-58

US-09-128-345-58

US-09-128-345-58

US-09-128-345-59

US-09-128-345-59

US-09-128-345-59

US-08-128-345-59

US-08-138-345-28

US-08-138-348-28

US-08-138-348-38

US-08-243-879A-1

US-08-243-879A-1

US-08-243-879A-1

US-08-499-523-16

US-08-499-523-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-08-499-523-11
5-08-499-523-16
5-08-499-523-33
5-08-499-523-48
                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              212252 seqs, 22503292 residues
                                                                                                      February 12, 2002, 12:24:52
                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                     US-09-485-571-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
```

Length 18;

Score 73; DB 1; Pred. No. 1.4e-05;

82.0%; 77.8%;

Query Match Best Local Similarity

US-08-499-523-63

123,

Sequence 1 Sequence 1 Sequence Sequence Sequence

-08-752-852A-1

Score

Result Ş -08-752-853-2

Matches

g

```
Score 73; DB 2; Length 10; Pred. No. 1.4e-05; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas CITY: New York CUTYE: New York COUNTRY: USA ZIP: 10036-2711 COMPUTER READABLE FORM:
                                                                                                      ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/752,852A
21-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-128-345-63; Sequence 63, Application US/09128345; Patent No. 6159966; Patent INFORMATION:
                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/752.
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
77.8%;
                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLCYARREFAVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 82.0
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                      STATE:
          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: group(6, 8, 13, 15) .
CTHER INFORMATION: /note= "X is a hydrophobic, a other information: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
            4; Indels
                                                                                                                                       RESULT 2
US-08-499-523-67
Sequence 67, Application US/08499523
Sequence 67, Application US/08499523
Sequence 67, Application US/08499523
Sequence 67, Application US/08499523
APPLICANT: LEHRER, ROBERT I.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MONRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/499,523
FILING DATE: 07-JUL-1995
TARGETER TOTALION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73; DB 1;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELESAX: 90-4030
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-752-852A-230
; Sequence 230, Application US/08752852A
; Patent No. 5994306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen, Jie
Steinberg, Deborah
          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang, Conway
Gu, Chee-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                        1 RGGRLXYXRRFFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRFFSVSVGR 18
                                                 1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
```

RESULT

g ò

ö

Gaps

;

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                            ) NAME/KEY: Modified-site

) LOCATION: group(6, 8, 13, 15)

OTHER INFORMATION: /note= "% is a hydrophobic, a

); OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-67
                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "X is a hydrophobic, a
small, or a large polar amino acid"
                                                                                                                                                                                         Score 73; DB 4; Length 18;
Pred. No. 1.4e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/08499523
Fatent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: FORRYARCO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
CORRESPONDENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOBESTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 71; DB 1; 1
Pred. No. 2.9e-05;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-0540.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,599
REFRENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.8%;
77.8%;
                                                                                                                                                                                           Query Match 82.0%;
Best Local Similarity 77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
8..13
                                                                                                                                                                                                                                                                                                   1 FGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                         1 FGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; orher information: smal. us-08-499-523-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2000 Penr
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
          TOPCLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-499-523-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                             COCATION: group(6, 8, 13, 15)
CTHER INFORMATION: /note= "X is a hydrophobic, a cother information: small, or a large polar amino acid" US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73; DB 4; Length 18;
Pred. No. 1.4e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORREY/AGENT INFORMATION:
NAME: CORUZZI, LAURA, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: COTUZZI, LAUTA, A.
REGIGTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741
FELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                             8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
      US/09/128,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67, Application US/09128345 Patent No. 6159936
                     FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA, A.
REGISTRATION UNDHER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741
TELEX: (6141 PENNIE
INPORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: MOdified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
77.8%;
APPLICATION NUMBER: US/09
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLXYXRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.0
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-128-345-67
```

õ a

ò q

```
: LOCATION: group(6, 15)

; OTHER INFORMATION: /note= "X is a hydrophobic, a

; OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CCRUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 71; DB 4; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212) 790-999
TELEFAX: (212) 869-9741
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS ILP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LERRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/09128345 Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLXYCRRFFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.8
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10036-2711
                                                                                                            CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-128-345-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: group(8, 13)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%; Score 71; DB 1; 1
77.8%; Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REBERGE/CETORNER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: shalloness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-128-345-53
Sequence 53, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                 Sequence 58, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHERE, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROFEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Disulfide-bond LOCATION: 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site LOCATION: group(8, 13)
  RGGRLSYSRRFFSVSVGR 18
                         |||||| | |||| | ||||
RGGRLXYCRRRFCVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLCYXRRFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.8
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07 CLASSIFICATION:
                                                                                                         RESULT 7
US-08-499-523-58
```

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                              COCATION: group(6, 15)
COTHEN INFORMATION: /note= "X is a hydrophobic, a
INFORMATION: Small, or a large polar amino acid"
US-08-499-5:3-54
                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 1; Length 18;
Pred. No. 4.2e-05;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-499-523-59
US-08-499-523-59
Sequence 59, Application US/08499523
Sequence 59, Application US/08499523
Sequence 59, Application US/08499523
SENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORRYAKOV, VLADIMIR N.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISSON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
LOCATION: group(8, 13)
OTHER INFORMATION: /note= "X is a hydrophobic, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20006-1812
COMPUTER READABLE FORM:
COMPUTER TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.7%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLXYCRRRFCIXVGR 18
                                                                                                                                                                                                                         NAME, KEY: Modifled-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                              18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
  INFORMATION FOR SEQ ID NO:
                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              roPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                        NAME, KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : LOCATION: group(8, 13)

: OTHER INFORMATION: /note= "X is a hydrophobic, a

: OTHER INFORMATION: small, or a large polar amino acid"

US-09-128-345-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71; DB 4; Length 18;
Pred. No. 2.9e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORNTAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE 3.76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORNISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: WRRASHIGE, KATE H,
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERAX: (202) 887-0763
TELEX: 90-4030
                                                                                                                                                                             8067-0054-999
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-499-523-54
; Sequence 54, Application US/08499523
; Patent No. 5804558
                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA, A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 58:
SEQUIENCE CHARACTERISTICS:
LENGTH: 18 amino acids
STRANDEDNESS: single
TOPPOCCGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond 6..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLCYXRRFFXVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.8
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
```

ö a

```
/note= "X is a hydrophobic, a small, or a large polar amino acid"
                                                                                                                                                                                                                                               Score 70; DB 4; 1
Pred. No. 4.2e-05;
1; Mismatches 4;
                                                                                                                                                                                                    ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                     GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KORMYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                      Sequence 59, Application US/09128345 Patent No. 6159936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08095769A; Patent No. 5464823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFRAX: (212) 869-9741
TELES: 6641 PENNE: 6641 PENNE: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.7%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTHER INFORMATION: /not / OTHER INFORMATION: /not / US-09-128-345-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLCYXRRFFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.7
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                       JS-09-128-345-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-095-769A-1
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
 small, or a large polar amino acid"
                                                                    Score 70; DB 1; Length 18; Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: group(6, 15)
CTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 4; Length 18; Pred. No. 4.2e-05; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 10036-2711

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-AUG-1998

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COLUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-909
TELEFAX: (612) 869-9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                          Sequence 54, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LERRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                    78.7%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.7%;
Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Disulfide-bond LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                        1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                1 RGGRLCYXRRFXICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||| | |||| : |||
RGGRLXYCRRRFCIXVGR 18
                                                                                Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
; OTHER INFORMATION:
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                          RESULT 12
US-09-128-345-54
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                     Db
                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
GENERAL INFORMATION:
APPLICANT: LEBRER, ROBERT I.
APPLICANT: ROKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL MAMMALIAN ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W. Ste. 5500
```

Gaps

ö

4; Indels

Length 18;

```
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 1; Length 18;
Pred. No. 6e-05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-08-182-483A-2
IS-GQUENCE 2, Application US/08182483A
Fatent No. 5693486
GENERAL INFORMATION:
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION:
NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPENDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STRRET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ITPE: DC
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-JAN-1994
CLASSIFICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
          COUNTRY: USA

2 IP: 2006-1812

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,769A
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MREASHIGE 729,959
REFERENCE/DOCKET NUMBER: 220002054020
FELEPAX: 90-4030
TELEFAX: 90-4030
TELEFAX: 90-4030
TELEFAX: 90-4030
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
STOPOLOGY: linear
US-08-095-769A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.5%;
Best Local Similarity 77.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLCYCRRRFCVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSVSVGR 18
Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
```

prot prot PG-1. S peptide

Protegrin pept Antimicrobial Antimicrobial

Protegrin

Antimicrobial protections: antimicrobial pept Cationic, antimicrobial pept Cationic, antimicrobial pept Cationic protegrin peptide Antimicrobial pept Antimicrobial comp Antimicrobial peptide protegrin peptide Cationic protegrin peptide Cationic, antimicroficial comp Antimicrobial peptide Cationic, antimicroficial comp Antimicrobial peptide Cationic, antimicroficial cationic cation

```
Linear: protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaczorek
                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                     AAW09073
AAW29556
AAW2918
AAY3170
AAY93170
AAY91757
AAY91757
                                                                                                                                                                           AAB35050
AAW25081
AAW09087
AAR78773
                                                                                                                                                                                                                                      AAW18148
AAW18149
AAW18150
AAY93669
AAW36285
AAW18153
AAR78751
AAR78776
AAW36322
AAW36208
                                                                  AAW18144
AAW18130
                                                                                                                                                                                                                           AAW18147
AAW18148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         છે
                                                                                                                                                                                                                                                                                                                                                                                                       AAW99403 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grassy
  98WO-FR01757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97FR-0010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
  AAW99403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calas B,
                                                                                                                                                                                                                                                                                                                                                                                               AAW99403
  Protegrin derivati
Peptide which may
Protegrin-like pep
Protegrin-like pep
Peptide which may
Antimicrobial prot
Cationic, antimicr
                                                                           (without alignments)
5.497 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                 February 12, 2002, 12:24:27; Search time 242.57 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                 /SIDS8/9cgdata/geneseq/geneseqp/AA1999.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1990.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1990.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1991.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1993.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1993.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1995.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1995.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1995.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1997.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1997.DAT:
/SIDS8/9cgdata/geneseq/geneseqp/AA1999.DAT:
                                                                                                                                                                                                                                                                                            | SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDS8/gcgdata/geneseqp/GeneseqpAAA1981.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1982.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1983.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1985.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1986.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1988.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1989.DAT:*
| SIDS8/gcgdata/geneseqg/geneseqp/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS8/gcgdata/geneseg/genesegp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gcgdata/geneseq/geneseqp/AA2000.DAT
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                           522463 seqs, 74073290 residues
                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW99412
AAY93177
AAY93179
                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW99403
AAY93616
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                           RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Π
                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                        US-09-485-571-15
89
                                                                                                                                                                                                                                                                                     A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11881188
11881188
11881188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000000000000
```

Post-processing:

Database :

sed

Minimum DB : Maximum DB :

Total number of

Searched:

Perfect score:

Sequence:

OM protein

.. 0

Scoring table:

Antimicrobial pept Antimicrobial pept Antimicrobial prot Cationic, antimicr Protegrin peptide

- used

Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells

WPI; 1999-190034/16

AAW36429 AAW09084 AAW09085 AAW18151 AAW18152

AAY93615

89 81 81 81 73 73 72

Score

Result Š

15: 17: 17: 18: 20: 22:

Ξ

antimicr

Cationic,

Peptide which may Antimicrobial prot

18 AA;

Sequence

```
This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotics family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the addisulphide bridge. The newell derivatives are linear and lack the agents to an organism. e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antitumour agents, and intivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, marticularly produced by chemical synthesis, can be coupled easily to the agent, cross anamalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 89; DB 20; I
100.0%; Pred. No. 8.5e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93616 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 8; 34pp; French.
Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-FR02939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 rggrlsysrrrfsvsvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Temsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY93616:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93616
\overset{\mathsf{P}}{\times} \overset{\mathsf{P}}{\times
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotics family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibudies antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive including crossing the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                            Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm; nucleus; blood-brain barrier.
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Derivatives of antibiotic peptides lacking disulfide bridges as carriers to deliver active agents into cells
     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 81; DB 20; Length 18
Pred. No. 1.6e-06;
); Mismatches 2; Indels
 100.0%; Score 89; DB 21; 100.0%; Pred No. 8.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaczorek M;
                              0; Mismatches
                                                                                                                                                                                                                                  Protegrin derivative peptide SM2196.
                                                                                                                                                AAW99412 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-FR01757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            97FR-0010297
                                                                     1 rggrlsysrrrfsvsvqr 18
                                                     1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chavanieu A,
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                            WO9907728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1998;
                                                                                                                                                                                                        08-JUN-1999
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                             AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                              ŏ
                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1-X16; are amino acids (aa), of which 6-10 of them are hydrophobic and X0 must be Trp; each B is an acntaining a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be retro forms of (a)-(c) containing D and/or L-form aa, or a fragment containing at least 7 consecutive aa from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, reptyplesins, transportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (ii) peptides with alpha-helices, beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with the presence of fall into the peptide antibiotic categories defined above: (a)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on creptesents as synthetic linear peptide designed on peptides are based on the BBB and is conjugated to a doxorubicin molecule by a succipate.
                                                                                                                                                                                   Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conjugates of the linear peptides and the active agent are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linker. The peptide may also be linked to a benzylpenicillin molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier .
                                                                                                                                                                                                                                                                                                                                                                _note= "linked to doxorubicin via a succinate
(-CO-(CH2)2-CO-) linker; optionally linked
to benzylpenicillin by a glycoamide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to treat, prevent or diagnose brain cancer, Alzheimer's or
Parkinson's diseases, depression, pain and meningitis, but also for
studying drug behaviour in BBB models.
                                                                                                                                             Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temsamani J;
                       AAY93177 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example I; Page 13; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98FR-0015074
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clair P, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-422871/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a glycoamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200032236-A1.
                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1998;
                                                                                                     06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2000
                                                                                                                                                                                                                                                                                        Synthetic.
                                                             AAY93177;
AAY93177
```

18 AA;

Sequence

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system The linear peptide preferably has the formula: (a) X1-X16; (b); BXXBXXXXBBXXXXXBXXXXBXBX, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be Trp: each B is aa containing a side chain that includes a basic group, and each X is an aliphatic or aromatic aa. The linear peptide may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the use of linear peptides, coupled to an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retro forms of (a)-(c) containing D- and/or L-form as, or a fragment containing at least 5, preferably at least 7 consecutive as fragment containing at least 5, preferably at least 7 consecutive as fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrims, Antennapedia, tansportan, etc. Of these several families have cytolytic effects and are termed peptide antibiotics. They fall into 3 main categories based on their structure: (i) peptides with alpha-helices, e.g. cerropins and maganins; (ii) peptides with disulphide bond-linked beta-sheets, e.g. protegrin, tachyplesins, defensins; (iii) peptides with no major structure but containing bends due to the presence of pro-residues, e.g. bactericins and RR39: The peptides of the invention fall into the peptide antibiotic categories defined above: (a)-peptides are based on
                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                               blood-brain barrier; diagnostic; central nervous system; protegrin;
Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;
cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                ö
          Length 18;
                                              Indels
Score 81; DB 21; LP Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                         Protegrin-like peptide antibiotic Dal-SynBl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example II; Page 20; 54pp; French.
                                                                                                                                                                                                                         AAY93179 standard; peptide; 18 AA
                                              ö
          91.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-FR02938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98FR-0015074
                                                                                                         RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                    06-DEC-2000 (first entry)
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-422871/36.
          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200032236-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                               AAY93179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clair F,
                                                                                                                                                                                    S
                                                                                                                                                                                                                                             g
                                                                                       9
```

Antimicrobial protegrin peptide (229).

13-FEB-1998 (first entry)

AAW36429;

AAW36429 standard; peptide; 18 AA.

AAW36429

1 rggrlsysrrrfststgr 18

g

1 RGGRLSYSRRFSVSVGR 18

```
;
0
protegrins; and (c)-peptides are based on tachyplesins. This sequence the BBB and is conjugated to a dalargin molecule by a disulphide linker. Conjugates of the linear peptides and the active agent are particularly used to treat, prevent or diagnose brain cancer, Alzheimer's or Parkinson's diseases, depression, pain and meningitis, but also for studying drug behaviour in BBB models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly produced by chemical synthesis, can be coupled easily to the agent, performed by chemical synthesis, can be coupled easily to the agent, receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anticancer agent; cancer cell; resistance; P-glycoprotein pump;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                       Score 81; DB 21; Length 18;
Pred. No. 1.6e-06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93615 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                   91.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-FR02939,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98FR-0015073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Temsamani J, Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                       A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200032237-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000.
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY9361
AAY 9361
AAY 
      88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
```

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram positive and gram negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It infections or diseases in plants and animals, e.g. conjunctivitis, can also be used for the prophylaxis or treatment of microbial cartitis, corneal ulcers, stomach ulcers associated with seriatis, corneal ulcers, stomach ulcers associated with sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis.

It is biostatic or biocidal against clinically relevant pathogens carbibiting multi-drug resistance, e.g. vancomycin resistant stephylococcus care december of according methicillin resistant Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5
                                                                                                                                                                                                disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; enjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; blocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; pensiratory insesistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant Straphylococcus aureus; systemic candidiasis.
                                                                                                                                       Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J, Gu CL, Lehrer RI, Steinberg DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 110; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0562346.
96US-0649811.
96US-0690921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US18544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0752852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                            W09718826-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang CC,
```

ó

Gaps

0;

Score 81; DB 21; Length 18; Pred. No. 1.6e-06; ); Mismatches · 2; Indels

.; 0

91.0%; 88.9%;

Best Local Similarity 88.9 Matches 16; Conservative

Query Match

Ŋ

```
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harwig SSL,
                                                                                                                                                                                                                                                                                                                     11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                AAW09085;
                                                                                                                        Seguence
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                               AAW09085
                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                     ŏ
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinantly produced, corresponding to the generic formula:

A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

where A1 = a basic amino acid; A2 and A3 = a small amino acid; A4 = a

basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino

acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino

acid or proline; A17 may be absent or a basic, neutral/polar,

hydrophobic or small amino acid; and A18 may be absent or a basic,

neutral/polar, hydrophobic or small amino acid. This has a charge of at

least +3 and its N-terminal acylated and/or C-terminal amidated or

esterified forms, all of which may contain a disulphide bond to give a

cystellne bridge. Peptides of this formula are designated protegrins and

are useful as anti-bacterial, anti-viral and anti-fungal agents in
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                        Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                           ö
                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin IB-288.
                                                                                                                                                                                                                                                               Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                      Length 18;
                                         Score 73; DB 18; Length 10
Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                               /note= "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                           Ą.
                                                                                                                                                                                                                                                                                                                                                                        'note= "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 65; 106pp; English.
                                                                                                                                                                          AAW09084 standard; peptide; 18
to 1 mg/kg/day, by injection.
                                                      82.08;
                                                                 77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0499523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kokryakov VN,
                                                                                                1 RGGRLSYSRRFFSVSVGR 18
                                                                                                            |||||| |:||||:| |||
| rggrlcyarrrfavcvgr 18
                                                                                                                                                                                                                     (first entry)
                                                                          14; Conservative
                                                                 Local Similarity
                       AA;
                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                      18
                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1996;
                                                                                                                                                                                                                    11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1996
                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                               AAW09084;
                      Sequence
                                                      Query Match
                                                               Best Loca
Matches
 2 × 8
                                                                                                ò
                                                                                                                    8
```

```
plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydla trachomatis, Treponema pallidum and Neisseria gonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: A1-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Nelsseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cationic, antimicrobial, virus-neutralising protegrin IB-289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73; DB 18; Length 18;
Pred. No. 3.1e-05;
Wismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6..15
/note= "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CALIFORNIA LOS ANGELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW09085 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 65; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.08;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0499523
95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||| |:||||:| ||||
| ragricyarrrfavcvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
```

us-09-485-571-15.rag

```
where Al = a basic amino acid; A2 and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; This has a charge of at least +3 and its N-terminal acylated and/or C-terminal amidated or esterified forms, all of which may contain a disulphide bond to give a cre useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gram-negative bacteria. The protegrins are particularly useful for the treatment of sexually transmitted disconnatis, Treponema pallidum and Neisseria gonorchocae. They can also be used in eye care solutions and as preservatives for food. The conference of serum) than certain antiblotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cationic, antimicrobial, virus-neutralising protegrin PC-55.
                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 73; DB 18; Length 18; 77.8%; Pred. No. 3.1e-05; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW18151 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 64; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harwig SSL, Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0451832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGGRLSYSRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Thes 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                         18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9637508-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW18151;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
       à
```

```
The presum: Sequence is a specificatly cialmed example on a peptide, the presum: Sequence is a specification of the generic formula:

Al-A2-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where A1 = a basic amino acid; A2 and A3 = a small amino acid; A9, A12 and A16 = a basic, hydrophobic, meutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, meutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, meutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, meutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, meutral/polar, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid. This has a charge of a clast +3 and its N-terminal acylated and/or C-terminal amidated or seterified forms, all of which may contain a disulphide bond to give a cystine residues are replaced by a hydrophobic, small or give a cystine residues are replaced by a hydrophobic, small or diright and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins of growth of a virus or microbe and inactivate the endotoxin of gramnestance to microbial or viral infection in plants by preventing the treatment of sexually transmitted disease caused by microorganisms e.g. Candida albicans, HIV-1, Chlamydia trachomatis, Treponema pallidum and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
present sequence is a specifically claimed example of a peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cationic, antimicrobial, virus-neutralising protegrin peptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic, antimicrobial, virus-neutralising protegrin PC-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 18;
Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW18152 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.9%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US07594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0499523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||:::||||:||||
| rggrlawarrrfavavgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW18152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18152
δλ
```

; 0

G

```
20-JUL-1993;
26-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR78751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                       The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula:

A1-A3-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-A17-A18)

where A1 = a basic amino acid; A5, A7 and A14 = a hydrophobic amino acid; A6 and A14 = a hydrophobic amino acid; A7 and A14 = a hydrophobic amino acid; A7 and A14 = a hydrophobic amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A18 may be absent or a basic, hydrophobic or small amino acid; A10 and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; A10 and A18 may contain a disulphide bond to give a cleast 43 and its N-terminal acylated and/or C-terminal amidated or settified forms, all of which may contain a disulphide bond to give a cysteine residues are replaced by a hydrophobic, small or large polar anion acid (e.g. alanine in this case). Peptides of this formula are call the cystance do protegrins and are useful as anti-bacterial, anti-viral and anti-fungal agents in plants and animals. The protegrins confer creatment of a virus or microbe and inactivate the endotoxin of gramners and autiched albicans, HIV-1. Chlamydia trachomatis, Treponema pallidum and Nesseria gonorrhoeae. They can also be used in eye care solutions and asserial condition of the protegrins are more effectives under a pallidum and nesserial gonorrhoeae. They can also be used in eye care solutions are asserved to the protegrins are more effectives or an expective of a secondarion of the care more effectives or an expective or also the protegrins are more effectives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; antiviral; antifungal; antibiotic; endotoxin; Candida albicans; gram-negative bacteria; STD; sexually transmitted disease; HIV-1; Chlamydia trachomatis; Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cationic, antimicrobial, virus-neutralising protegrin PC-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.9%; Score 72; DB 18; Length 18; 72.2%; Pred. No. 4.4e-05; ive 5; Mismatches 0; Indels
useful for the treatment of microbial infection, as food
                     preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CALIFORNIA LOS ANGELES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW18153 standard; peptide; 18 AA.
                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US07594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0499523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                            Claim 6; Page 64; 106pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9637508-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-1995;
26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW18153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW18153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
```

ð

```
The present sequence is a specificative training the period of the generic formula:

Al-A2-33-A4-A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18)

Where all a basic amino acid; A2 and A3 = a small amino acid; A9, A12 and A16 = a hasic, hydrophobic, neutral/polar or small amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid;
A9, A12 and A16 = a basic, hydrophobic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contextral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, contextral/polar, hydrophobic, small of which may contain a disulphide bond to give a cysteine bridge. This peptide is in snake form where all the cysteine bridge. This peptide is in snake form where all the canno acid (e.g. alanine in this case). Peptides of this formula are designated protegrins and are useful as anti-bacterial, anti-viral and anino acid (e.g. alanine in this case). Peptides of this formula are context of mino acid gents in plants and anino acid confer resistance to microbial or viral infection in plants by preventing the growth of a virus or microbe and inactivate the endotoxin of gramrestament of sexually transmitted disease caused by microorganisms ergonorrhoeae. They can also be used in eye care solutions and as preservatives for food. The protegrins are more effective under physiological conditions (e.g. in the presence of serum) than certain antibiotics and are non-toxic to the cells of higher organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a specifically claimed example of a peptide,
                                                                                                                                              Cationic, antimicrobial, virus-neutralising protegrin peptide(s) useful for the treatment of microbial infection, as food preservatives and in eye care solutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70; DB 18; Length 18;
Pred. No. 9.3e-05;
; Mismatches 1; Indels
Harwig SSL, Kokryakov VN, Lehrer RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR78751 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                           Claim 5; Page 64; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.78;
72.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94WO-US08305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0093926
93US-0095769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 72.2
Matches 13; Conservative
                                                                         WPI; 1997-033984/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protegrin PG-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR78751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

"protegrins". The

```
peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and hydrophobic amino acids and/or (2) being isolatable from animal (e.g. pyrchhobic amino acids and/or (2) being isolatable from animal (e.g. cys residues is/are replaced by Mydrophobic or small amino acids. The perchies can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by N-acylation and/or C-terminal amidation acid residues can be present.

The present sequence is a specific example of the protegrin relative sources and residues can be present.

The present sequence is a specific example of the protegrin relative sources and real acid residues can be present.

The present sequence is a specific example of the protegrin relative sources and real acid residues in which Cys(6, 8, 13, 15) have all been replaced by Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation; disinfection; prophylaxis; treatment; infection; disease; conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD; Helicobacter pylori; sexually transmitted disease; oral mucositis; gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic; respiratory infection; urinary tract infection; MRSA; protozoan; vancomycin resistant Enterococcus; pathogen; multi-drug resistance; penicillin resistant Streptococcus pneumoniae; pig; porcine; methicillin resistant (Staphylococcus aureus; systemic candidiasis.
                                                                                                                                                    Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections and as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 16; Length 10
Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                 are disclosed which are designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                               Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial protegrin peptide (122).
                                                                                                                                                                                                                                                                        Disclosure; Page 19; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36322 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0752852.
95US-0562346.
96US-0649811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US18544.
                                            ΛN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRRFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                            Kokryakov
                                                                                               WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AA;
                                                                                                                                                                                                                                                                                                                              peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09718826-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1996;
22-NOV-1995;
17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW36322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36322
              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or esterification, and can be in linear or cystine-bridged form. D-Amino acid residues can be present.

The present sequence is a specifically claimed example of the protegrins, designated PG-1. It can be synthesised; or it can be isolated from porcine leukocytes, in which case it is in amidated and in dicystine bridged form. A synthetic version in which all the amino acids have D-configuration is also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides are disclosed which are designated "protegrins". The peptides are useful as antibacterial, antiviral and antifungal agents in both animals and plants. The peptides are 16-18 amino acids in length and are characterised by four invariant Cys residues at positions 6, 8, 13 and 15 and either (1) by a characteristic pattern of basic and portine) amino acids and/or (2) being isolatable from animal (e.g. portine) leukocytes; or analogues of these peptides in which 1-4 of the peptides can be produced synthetically and some can be produced recombinantly or can be isolated and purified from their native sources. The peptides can be modified by Nacylation and/or C-terminal amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                      Antibiotic peptide-based cpds. designated protegrin(s) - are useful for treating and preventing viral and microbial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protegrin; antibiotic; antimicrobial; antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69; DB 16; Length 18; Pred. No. 0.00013; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                       Claims 1, 9, 10; Pages 56, 59; 80pp; English.
                                                                                                                                                 Lehrer RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR78776 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0093926.
93US-0095769.
94US-0182483.
94US-0243879.
94US-0182483
94US-0243879
                                                                                                                                           Kokryakov VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US08305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 rggrlcycrrrfcvcvgr 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protegrin peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRFFSVSVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 77.8
les 14; Conservative
                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                               and as preservatives
                                                                                                                                                                                                 WPI; 1995-075188/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AA;
13-JAN-1994;
17-MAY-1994;
                                                                                                                                           Harwig SSL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9503325-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1994;
17-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR78776
AAC AAR7
AAC AACA
AAC AAR7
AAC AACA
AA
```

ò g ą.

ö

Gaps

ó

Length 18;

```
The present sequence is an antimicrobial protegrin peptide, which has a broad spectrum of activity against microbial targets, including gram-positive and gram-negative bacteria, yeast, fungi, protozoa and certain strains of viruses and retroviruses, e.g. HIV.

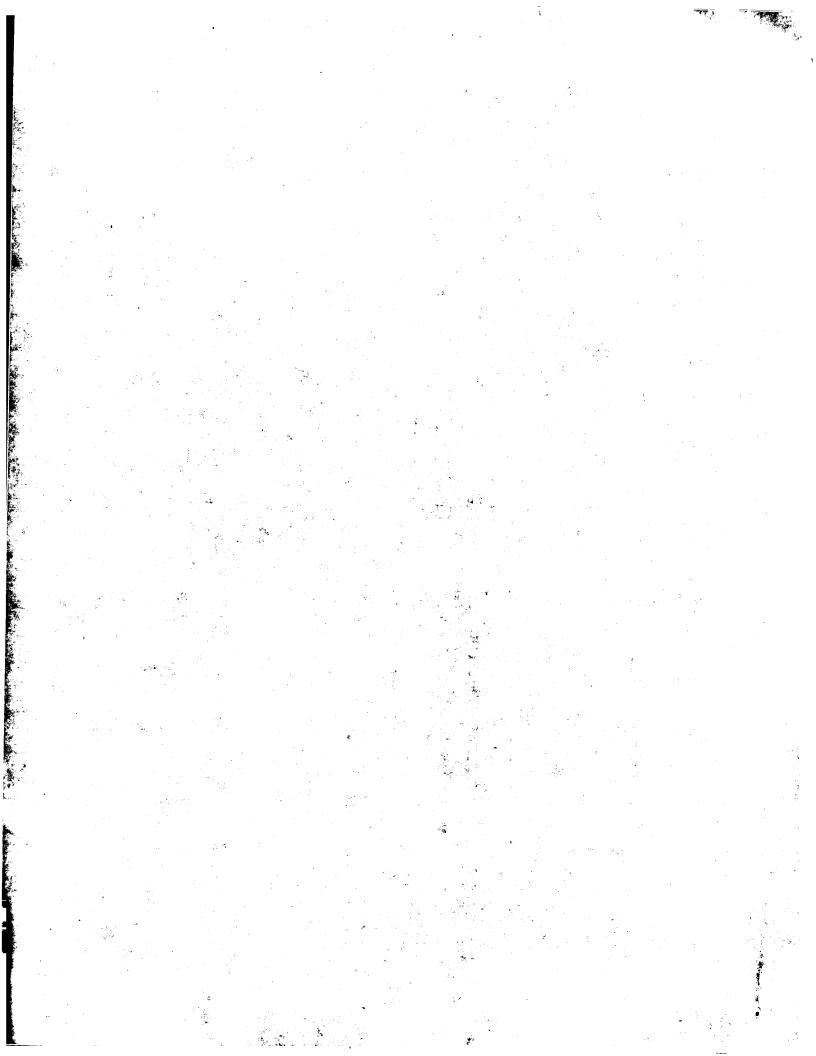
It can be used to preserve or disinfect a variety of materials, including medical equipment, foodstuffs, cosmetics, contact lens solutions, medicaments or other nutrient containing materials. It can also be used for the prophylaxis or treatment of microbial infections or diseases in plants and animals, e.g. conjunctivitis, keratitis, corneal ulcres, stomach ulcrers associated with Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis, endocarditis, pneumonia and other respiratory infections, urinary tract infections, systemic candidiasis and oral mucositis. It is blostatic or blooidal against clinically relevant pathogens exhibiting multi-drug resistance, e.g. vancomych resistant can be interococcus faccilis, penicillin resistant Staphylococcus are ureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5 to 1 mg/kg/day, by injection.
                                                                                                                                                                                               New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g. HIV)
                                                                                                            Lehrer RI, Steinberg DA;
                                                                                                                                                                                                                                                                                  Claim 23; Page 107; 130pp; English.
                                         (INTR-) INTRABIOTICS PHARM INC. (REGC ) UNIV CALIFORNIA.
01-AUG-1996; 96US-0690921.
                                                                                                         Chang CC, Chen J, Gu CL,
                                                                                                                                                     WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
```

Gaps ö Score 69; DB 18; Length 18; Pred. No. 0.00013; 0; Mismatches 4; Indels Query Match 77.5%; Best Local Similarity 77.8%; Matches 14; Conservative 1 RGGRLSYSRRRFSVSVGR 18 ô

ö

g

Search completed: February 12, 2002, 12:30:29 Job time: 362 sec



OM protein

Run on:

Sequence:

Searched:

Database

. ∾

Result

Appl Appl Appl Appl Appl Appl Appl

Appli Appli Appli Appli

```
Sednence Sed
                      Sequence
Sequence
Sequence
Sequence
                                                                                                  Sequence
Sequence
Sequence
      Sequence
US-09-128-345-53
US-09-128-345-54
US-09-128-345-59
US-09-128-345-59
US-08-752-852A-66
US-08-752-852A-64
US-08-752-852A-64
US-08-752-852A-63
US-08-752-853-23
US-08-752-853-23
US-08-182-483A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 8067-034-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMFUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids
      ZIP: 10036-2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPCLOGY: unknown
; MOLECULE TYPE: pept1
US-08-752-852A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-752-852A-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
    Sequence 65, Appl
Sequence 80, Appl
                                                                                                                                                         (without alignments)
2.121 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                    February 12, 2002, 12:32:23; Search time 106.12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4
Sequence 4
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3
Sequence 4
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*/
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-752-852A-65
US-08-752-852A-80
US-08-182-483A-24
US-08-243-893A-28
US-08-243-893A-27
US-08-499-523-48
US-08-182-483A-19
US-08-499-523-64
US-08-499-523-64
US-08-499-523-64
US-08-499-523-64
US-08-499-523-67
US-08-499-523-67
US-08-499-523-67
US-08-499-523-67
US-08-128-345-67
US-08-128-343-81
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                US-09-485-571-23
                                                                                                                                                                                                                                                       1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 : . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
```

```
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FIRE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
 Chang, Conway
Gu, Chee-Liang
                                   Chen, Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RRLCYCRRRF 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-752-852A-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-182-483A-28
                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
Score 40; DB 2; Length 14; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                    RESULT 2
US-08-752-862A-80
Sequence 80. Application US/08752852A
Sequence No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Steinberg, Deborah
APPLICANT: Harwig, Sylvia
TITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCES: 242
CORRESPONDENCE ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 2
Pred. No. 0.24;
0; Mismatches
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV 1996
CLASSIFICATION: 435
PRIOR APPLICATION UMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-08-752-852A-242
Sequence 242, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
Query Match 80.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RRLCYCRRRF 10
                                                                     1 RRLSYSRRFF 10
                                                                                         New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-752-852A-80
                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2; Length 17;
Pred. No. 0.26;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28, Application US/08182483A
Patent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 SOFTWARE: DOS DOS OCTUBER: DOS DOS OCTUBERT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A FILING DATE: 21-NOV-1996 CLASSIFICATION: 435 PRIOR APPLICATION: 435 APPLICATION: ASPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                8067-034-999
                ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-909
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.v.
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                               CIAL
STATE: NI
COUNTRY: USA
TTD: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2000 PeniCITY: Washington STATE: DC
```

```
Gaps
                                                                                                        Gaps
                                                                                                     ö
                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEBRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HORRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STRIET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPRY disk

COMFUTER: IBM PC compatible

OPEFATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/499,523

FILING DATE: 07-JUL-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MORASHIGE, KATE H.

RESTERENCE/DOCKET NUMBER: 2000-0540.24

TELECOMMUNICATION: NUMBER: 2000-0540.24
                                            Score 39; DB 1;
Pred. No. 0.41;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1;
Pred. No. 0.41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-00-128-345-48
Sequence 48, Application US/09128345
Patent No. 6159936
GENERAL INFORMATION:
APPLICANT: LEHERER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            US-08-499-523-48
Sequence 48, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (202) 887-1500
(202) 887-0763
                                            78.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.07
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 887-076:
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                         Query Match 78.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                              2 RLSYSRRFF 10
                                                                                                                                                                                            2 RESYSRRE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|:|||||
4 RISFSRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-74N-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURACAHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FLING DATE: 17-MAY-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, SYLVIA S.L.
ATTLE COF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.0%; Score 39; DB 1 77.8%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
RECISTRATION NUMBER: 299,959
RECEDENCE/DOCKET NUMBER: 2000-0540.22
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
INFORMATION FOR SEQ ID NO: 27:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08243879A Patent No. 5708145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.8°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Single;
TOPOLOGY: linear
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|:|||||
4 RISFSRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-08-243-879A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 16;
                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SURTENT APPLICATION TO NOT NOT STATE STATE STATE STATES STATE STATES STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1;
Pred. No. 0.83;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC COMPATIBLE
COMPUTER: AVSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08243879A Patent No. 5708145 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-499-523-40; Sequence 40, Application US/08499523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,59
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 887-1500
(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
77.8%;
(202) 887-0763
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 16 amino acids amino acid
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.0
Local 7; Conservative
                                                                                                                     16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                          single
                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || | | ||||
4 RLGYGRRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || | | ||||
4 RLGYGRRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-243-879A-19
                                                                                                                                                                                                         ; TOPOLOGY:
US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-243-879A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                     LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NDER: US/08/182,483A
FILING DATE: 13-3AN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CORRYAKOV, VLADIMIR N.
APPLICANT: ROKRYAKOV, VLADIMIR N.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                        ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 4;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: DATORNAME CONTROL ATTORNEY AND THE COLUZZI, LAULA, A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.21
TELECOMBUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                               1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08182483A patent No. 5693486 GENERAL INFORMATION:
      PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAN: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.0
7; Conservative
                                                          New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|:||||||
|4 RISFSRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   usa
                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-08-182-483A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
07-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STREANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RLXXXRRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-128-345-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

EDION TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: BM PC COMPATIBLE
SUCHANE: PATENTIN Release #1.0, Version #1.30
CURRENT ON TOWNER: US/08/499,523
FILING DATE: 07-JUL.1995
CLASSIFICATION NUMBER: US/08/499,523
FEGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-163
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aning acids
MANDE: MISSIONERE MANDER: LENGTH: LENGTH
                                                 APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: WORRTAGNO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMORRICON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPTRY: USA
2IP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHERER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOWNTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 74.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                CITY: Was
STATE: DC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-499-523-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
TCLASSIFICATION STATE AND ALL AND AND ALL AND AND ALL AND AND ALL AND AND AL
```

g

```
: LOCATION: group(6, 8, 13, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 37; DB 1; Length 18; 77.8%; Pred. No. 0.92; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                             SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: US/08/499,523 CLASSIFICATION: 514
ATTOREX/AGENT INFORMATION:
NAME: WRRASHIGE: 29,959
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPEAS: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington
                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: KOKENAKO, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAROV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 887-076:
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
                                                                                                                                                                   STREET: Zuvu communitation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20006-1812
  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-499-523-67
                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                              Score 37; DB 4; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : LOCATION: group(6, 8, 13, 15);
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 4; Length 16;
Pred. No. 0.83;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFA: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  ; Sequence 64, Application US/09128345; Patent No. 6159936; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-08-499-523-63
Sequence 63, Application US/08499523
; Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%;
77.8%;
                                                              74.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 74.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
                                                                                                                                                  2 RLSYSRRFF 10
                                                                                                                                                                          2 RLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RLXYXRRF 12
                                                                                                                                                                                                                                                          RESULT 13
US-09-128-345-64
US-09-128-345-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
```

ó

Gaps

. 0

```
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/499,523

FILING DATE: 07-UUL-1995

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:
NAME: WURSHIGE, RATE H.

REFERENCE/OCKET NUMBER: 29,959

FELENCH NUMBER: 20,059

FELENCH NUMBER: 20,059

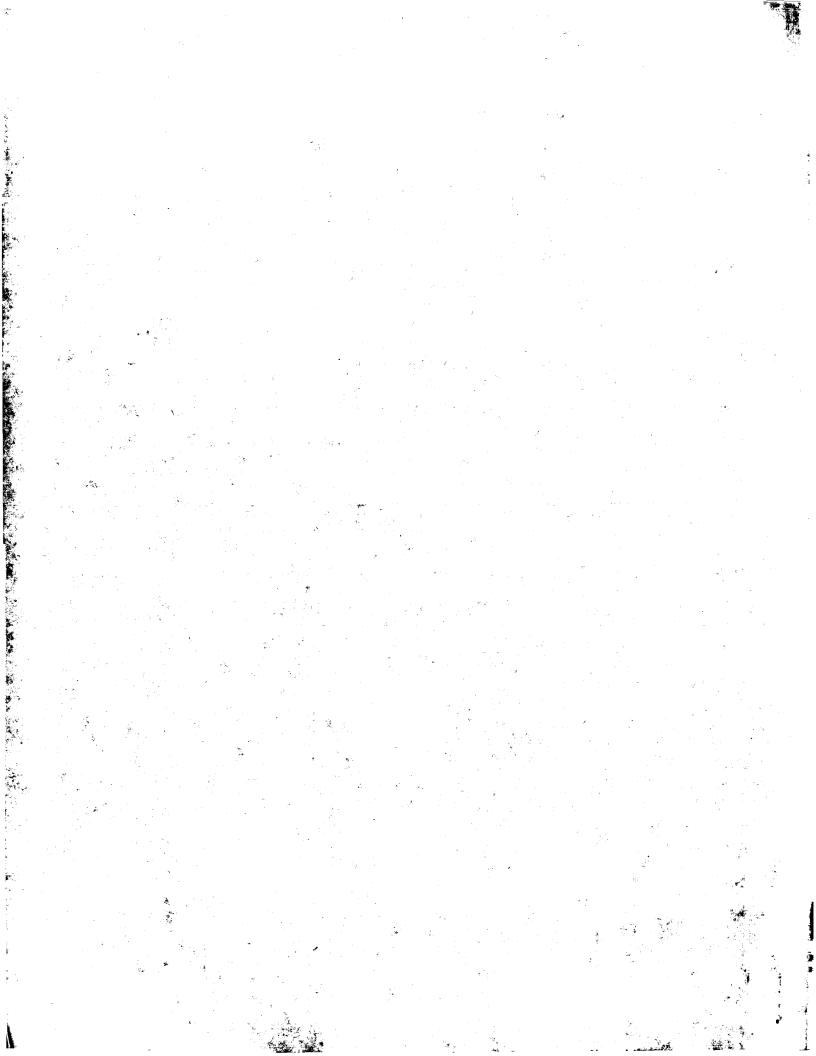
FELENCH SECONDINICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEO ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acid
STRANDEDNESS: Single
STARM Est amino acid
STRANDEDNESS: Single
FRATUR: 91 coup(6, 8, 13, 15)
COUPEY NAME/KEY: Modified-site
COUPER INFORMATION: Mamil, or a large polar amino acid
COUPER INFORMATION: Mamil, or a large polar amino acid
US-08-499-523-67

OUBEY MATCH
BEST LOCAL SIMilarity 77:8%; pred, No. 0.92;
MATCHES 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 RISYSTRER 10

DA A RIXXYRERF 12
```

Search completed: February 12, 2002, i2:32:23 Job time: 451 sec



```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

model
3
using
search,
protein s
•
protein
W _O

(without alignments)
6.005 Million cell updates/sec February 12, 2002, 12:34:39; Search time 126.85 Seconds Run on:

.us-09-485-571-23 50

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 RRLSYSRRFF 10 Title: Perfect score: Scoring table: Sequence:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ď			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
1	41	82.0	77	7	B40973	spermatid-specific
7	41	82.0	7	7	A40973	spermatid-specific
m	41	82.0		7	S56116	spermatid-specific
4	38	76.0		7	S56117	spermatid-specific
ស	38	76.0		7	D96798	hypothetical prote
9	36	72.0		~	JC5795	
7	35	70.0	113	7	S77123	ribosomal protein
89	35	70.0		7	0060NF	
σ	35	70.0		7	S57607	protegrin 1 precur
10	35	70.0		7	G84693	probable proline-r
11	34	68.0		?	B86273	hypothetical prote
12	34	68.0		7	JQ1873	BR1 protein - toma
13	34	68.0		7	B54575	35K GTP-binding pr
14	34	68.0		7	149117	Ras-like protein K
15	34	68.0		7	T00533	probable DNA2-NAM7
16	33	0.99		~	PN0641	hypothetical prote
17	33	99		7	C53234	globulin-10 - maiz
18	33	0.99		7	E72281	hypothetical prote
19	33	0.99	264	~	JC6125	U2 small nuclear r
20	33	0.99		7	D81896	Neisseria meningit
21	33	99		7	A86443	probable major int
22	33	99		7	T19144	hypothetical prote
23	33	99	430	~	G96594	unknown protein, 5
24	33	99			H72516	hypothetical prote
25	33	99			S19252	1-aminocyclopropan
26	33	0.99	518		S31442	1-aminocyclopropan
27	33	0.99				probable ribosomal
28	33	99				DNA topoisomerase
29	32	64.0			T10370	protein p6.9 - Org

protamine P1 - duc ribosomal protein	transcription fact rfbP protein homol hypothetical prote	pre-mRNA splicing sugar transport sy	probable membrane		hypothetical prote hypothetical prote	hypothetical prote hypothetical prote	AcOrf-140 protein	homeotic protein g
S39425 T11985	S30049 C56146 R69398	A48133 E86810	S55084	T50996	T34024 E96683	T25635 T25634	E72867	S35226
00	200	000	70	9 77 6	20	0 0	7	7
61 103	4 4 4 7 4 4 4 7 4 4 4 9 9	494	612	924	1006	1129	9	209
64.0 64.0	64.0 0.4.0	64.0	64.0	64.0	64.0 64.0	64.0 64.0	62.0	62.0
32	322	35	32	32	32	32 32	31	31
30 31	3 8 8 2 8 8	32.	37	0 G G	40 41	42 43	44	45

## ALIGNMENTS

SULT 0973	-	
ວດ	<u>.</u>	m
2 6	4	7
າ ဝ	⊃	σ
	ŭ	0

Special Specific protein T2 precursor - common cuttlefish
N;Alternate names: arginine-rich protamine; testis-specific protein T2
C;Species: Septa officialalis (common cuttlefish)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13·Sep-1998
C;Accession: B40973; S14086
R;Wouters-Tyrou, D.; Chartier-Harlin, M.C.; Martin-Ponthleu, A.; Boutillon, C.; Van
J; Biol. Chem. 266, 17388-17395, 1991
A;Title: Cuttlefish spermatid specific protein T. Molecular characterization of two
A;Reference number: A40973; MUID:9137359
A;Accession: B40973
A;Molecule type: protein
A;Residues: 1-77 <WOU>
R;Martin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.
Eur. J. Biochem. 195, 611-619, 1991
A;Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct varia
A;Reference number: S14085; MUID:91153298
A;Accession: S14085
A;Residues: 22-77 <MAR>
A;Residues: 22-77 <MAR>

C;Superfamily: sperm histone C;Reywords: Dhosphoprotein; spermatogenesis E;1-21/Domain: signal sequence #status predicted <SIG>F;22-77/Product: proteamine variant Sp2 #status experimental <MAT>

Gaps ö Length 77; 1; Indels Score 41; DB 2; Pred. No. 0.5; 1; Mismatches 82.0%; 80.0%; Query Match 82.0 Best Local Similarity 80.0 Matches 8; Conservative

ö

1 RRLSYSRRFF 10 ò

| |||||||: 64 RRRSYSRRY 73 q

### RESULT A40973

National Specific protein T1 precursor - common cuttlefish
Naternate names: argininerrich proteinie; testis-specific protein T1
C;Species: Sepia officinalis (common cuttlefish)
C;Species: Sepia officinalis (common cuttlefish)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998
C;Accession: A40973: S14085
R;Wouters-Tyrcou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van
B;Wouters-Tyrcou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van
A;Title: Cuttlefish spermatid-specific protein T. Molecular characterization of two
A;Reference number: A40973; MUD:91373359
A;Molecule type: protein
A;Residues: 1-78 &WOUT
B;RMartin-Ponthieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.
Eur. J. Bicchem. 195, 611-619, 1991

```
A;Molecule type: mRNA
A;Residues: 1-1045 <KOY>
A;Cross-references: DDBJ:AB008430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.0%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.08;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 60.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||::|||||
| 1053 RRVRFSRRF 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:||: |:||
267 RKLSFKRKRF 276
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1108 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDEP protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: JC5795
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nge factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S77123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatid-specific protein T2 precursor - longfin squid
N;Alternate names: sperm protemin SP
C;Species: Loligo pealeii (longfin squid)
C;Species: Loligo pealeii (longfin squid)
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jagquinod, M.; S Biochem J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami A;Reference number: S56116; WUID:95351983
A;Accession: S56117
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-118 <WOUS
                                                                                                                                                                                                                                                                                                                                                                                Spermatid-specific protein T1 - longfin squid
Spermatid-specific protein T1 - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S56116
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; S Biochem. J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami A;Accession: S56116
A;Accession: S56116
A;Status: preliminary
A;Status: protein
A;Resiques: 1-79 <WOU>
C;Superfamily: sperm histone
A,Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants. A;Reference number: S14085; MUID:91153298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                      A.Accession: S14085
A.Molecule type: protein
A.Residues: 22-78 (AMR)
C.Superfamily: sperm histone
C.Steywords: DNA binding; nucleus; phosphoprotein; spermatogenesis
F.1-21/Domain: signal sequence #status predicted <SIG>F:22-78/Product: protamine variant Sp1 #status experimental <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                              Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
0.51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                            Score 41; DB 2;
Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB Pred. No. 2.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.51
1; Mismatches
                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%;
80.0%;
                                                                                                                                                                                                                82.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                Query Match 82.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || ||||||:
66 RRRSYSRRRY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                              65 RRRSYSRRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RRLSYSRRR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                            δ
```

```
hypothetical protein F22K20.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C;Acsion, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hudzar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kiml C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzin Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talli kar, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719
A;Accession: D96798
A;Steatus: precliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Koyano, Y.; Kawamoto, T.; Shen, M.; Yan, W.; Noshiro, M.; Fujii, K.; Kato, Y.
Biochem. Biophys. Res. Commun. 241, 369-375, 1997
A;Title: Molecular cloning and characterization of CDEP, a novel human protein conta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: This protein is involved in the adhesion, proliferation, and differentian C;Superfamily: pleckstrin repeat homology; protein 4.1 membrane-binding domain homology; profession: ezrin-like status predicted verse. F;42-316/Domain: ezrin-like status predicted verse. F;42-316/Domain: protein 4.1 membrane-binding domain homology <B41> F;931-1027/Domain: pleckstrin repeat homology <PLK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005173; NID:g2829910; PIDN:AAC00618.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein S6 - Synechocystis sp. (strain PCC 6803)
N.Alternate names: protein s111767
C.Species: Synechocystis sp.
A.Variety: PCC 6803
C.Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 2;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2
Pred. No. 50;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Reference number: JC5795; MUID:98086358
A; Accession: JC5795
```

134 RLCYCRRRF 142

q

```
A; Molecule type: DNA
A; Residues: 1-149 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-149 <ZH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 FLCYCRRFF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S36820
                                                                                                                                                                                                                                                                                      A; Accession: S66284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: NPG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Reference number: $74322; MUID:97061201
A; Reference number: $74322; MUID:97061201
A; Reference number: $77123
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-113 < KANY
A; Cross-references: EMBL:090908; GB:AB001339; NID:g1652725; PIDN:BAA17681.1; PID:g165276
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Start codon: GTG
C; Superfamily: Escherichia coli ribosomal protein $6
C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cat
C;Accession: S77123
Kšaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
                                                                             A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protegrin 2 precursor - pig
N;Alternate names: cathelin-like protein precursor; neutrophil peptide 3
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Way-1994 #sequence_revision 19-Way-1994 #text_change 16-Jul-1999
C;Accession: JN0900; S36822; S34586
R;Storici, P:: Zanetti, M.
Biochem. Blophys. Res. Commun. 196, 1363-1368, 1993
A;Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a A;Reference number: JN0900; MUID:94071898
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 35; DB 2; Length 147; 77.8%; Pred. No. 13; 2; Indels Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 35; DB 2; Length 113; 70.0%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 77.0%
The conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 RRLAYQIRRF 57
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

Gaps

ö

RLSYSRRRF 10

ò

```
A,Cross-references: GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:g603036 R:Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Eg FEBS Lett. 330, 339-342, 1993 A.F. Three cationic peptides from porcine neutrophils. Seq A;Reference number: S36820; MUID:93387466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M FEBS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of cort A;Reference number: S34585; MUID:93327946
A;Reference number: S34585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A) Introns: 66/3; 102/3; 126/3

A) Introns: 66/3; 102/3; 126/3

C) Superfamily: cathelin: cystatin homology

C; Reywords: amidated carboxyl end, antibacterial; neutrophil

C; Reywords: amidated carboxyl end, antibacterial; neutrophil

E; 1-29/Domain: status sequence #status predicted <SIG>
F; 22-129/Domain: propeptide #status predicted <PRO>
F; 13-148/Product: protegrin 1 #status experimental <MAT>
F; 148/Modified site: amidated carboxyl end (Arg) (amide in mature form from followi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable proline-rich protein [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C; Accession: G84693 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallo euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vent Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; WUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X84094; NID:g887642; PIDN:CAA58890.1; PID:g887643
R;Zhao, C.; Liu, L.; Lehrer, R.I.
ERBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613
A;Accession: S45712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                              #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
Protegrin 1 precursor - pig
N.Alternate names: neutrophil peptide 1
C.Species: Sus scrofa domestica (domestic pig)
C.Species: Sus scrofa domestica (domestic pig)
C.Species: 19-Oct-1995 #sequence_revision 03-Nov-1995 #
C.Accession: S66284; S45712; S36820; S34585; S57607
RK:Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
A.Title: The structure of porcine protegrin genes.
A.Reference number: S66283; MUID:95354835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 131-148 <MIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 131-148 <KOK>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
```

Length 257;

1;

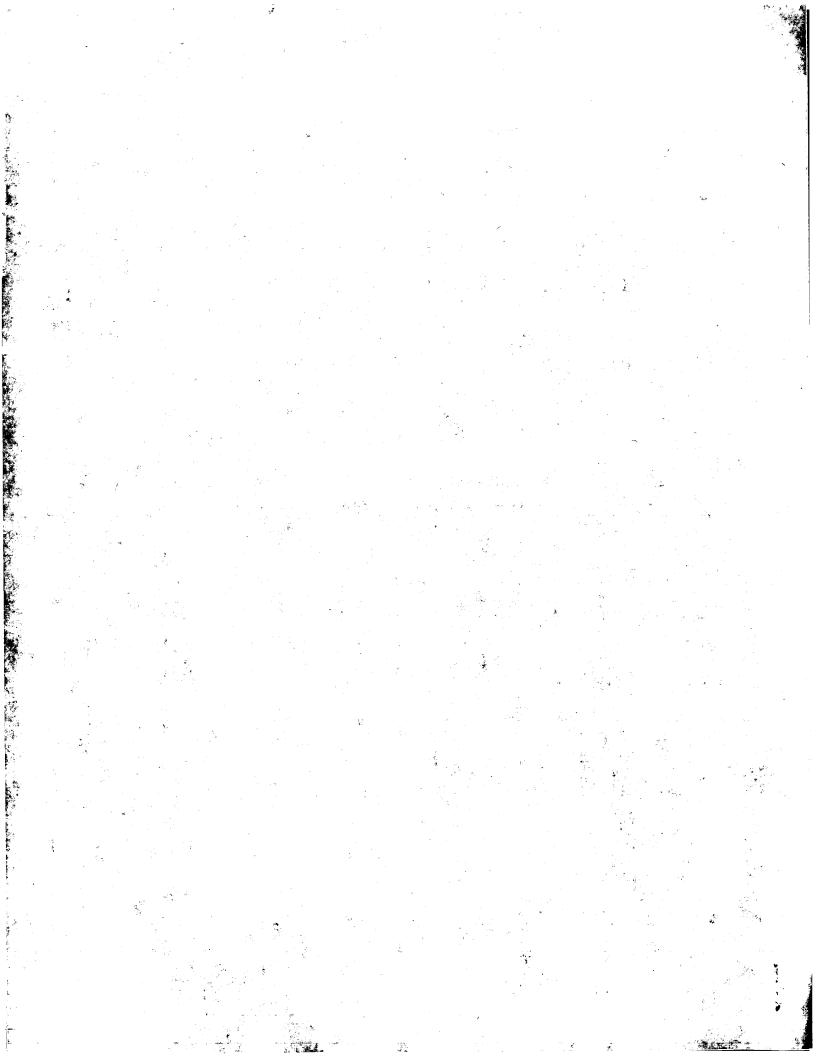
```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.0%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                 68.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                          Conservative
                                 Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-295 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:||:||
250 RRLAYQKRR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 RRLAYQKRR 258
                                                                                                       10
                                                                                                                               | || || || || 8 RGFSYSNRRF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRLSYSRRR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRLSYSRRR 9
                                                                                                       RRLSYSRRRF
                 Query Match
Best Local S
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
T00533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
JO1873
BRI protein - tomato mottle virus (isolate Florida)
C; Species: tomato mottle virus
C; Species: tomato mottle virus
C; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 23-Jul-1999
C; Accession: JQ1873
R; Abouald, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A; Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from A; Reference number: JQ1873
A; Accession: JQ1873
A; Reference number: JQ1873
A; Retauns: translation not shown
A; Molecule type: DNA
A; Residues: 1-257 <ABO>
A; Conserreferences: GB:L14461; NID:g1200530; PIDN:AAC32418.1; PID:g295328
C; Genetics:
A; Map position: segment B
C; Superfamily: tomato golden mosaic virus BRI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AAD39285.1 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: B86273
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chuqy, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tile: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                          ö
                 A Status: preliminary
A Modecule type: DNA
A Mesidues: 1-891 <STO>
A; Cross-references: GB:AE002093; NID:g3980411; PIDN:AAC95214.1; GSPDB:GN00139
C; Genetics:
A; Gene: At2g2210
A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-249 <STO>
A;Cross-references: GB:AE005172; NID:g5080775; PIDN:AAD39285.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                Length
                                                                                                                                                                                                                2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                Score 35;
Pred. No.
                                                                                                                                                                                                              70.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.0
Best Local Similarity 77.9
Matches 7; Conservative
                                                                                                                                                                                                                Query Match 70.0
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              RRISISRRR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRR 9
                                                                                                                                                                                                                                                                                                     1 RRLSYSRRR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B86273
A; Status: preliminary
A; Accession: G84693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                           g
```

```
B54575
B54575
B54575
B54575
Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-NOv-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 02-Feb-2001
C;Accession: B54575
R;Maguire, J; Santoro, T; Jensen, P; Siebenlist, U; Yewdell, J; Kelly, K.
Science 265, 241-244, 1994
A;Title: Gem: an induced, immediate early protein belonging to the Ras family.
A;Reference number: A54575; MUID:94294787
A;Accession: B54575
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: 149117
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable DNA2-NAM7 helicase family protein [imported] - Arabidopsis thaliana N;Alternate names: SEN1 protein homolog T20K24.14 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ras-like protein Kir/Gem - mouse
N;Alternate names: Kinase-inducible ras-like (kir)
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U13053; NID:g563155; PIDN:AAC52145.1; PID:g563156
C;Genetics:
A;Gene: kir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 295,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
,
Score 34; DB 1
Pred. No. 33;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2
Pred. No. 37;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34;
Pred. No. 3
```

ö

```
C; Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C; Accession: T0033; G84522
R; Rounsled (S. Lin, X.); Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, Submitted to the EMBL Data Library, July 1997
A; Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A; Recession: T00533
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1090 cROU>
A; Roulsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
R; Lin, X.; Kaul, S.; Rouusley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Russ, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
A; Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Residues: 1-1090 cSTO>
A; Cross-references: GB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
A; Tatle: Sequences: GB:AECO2093; NID:93176714; PIDN:AADI2029.1; GSPDB:GN00139
A; Throns: 250/1; 310/1; 342/1; 383/2; 427/3; 1016/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

68.0%; Score 34; DB 2; Length 1090;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 12, 2002, 12:34:39 Job time: 557 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRLSYSRRF 10
|::|||:|
209 RKVSYSQRSF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```



```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 12, 2002, 12:39:51; Search time 67.2 Seconds (without alignments) 5.456 Million cell updates/sec Run on:

US-09-485-571-23 50 1 RRLSYSRRF 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	sepia			P42131 caenolestes	P42135 dasyurus vi		macropus	O18745 antechinomy	P42130 antechinus	P42138 macropus eu	_		P42151 sarcophilus		P42134 dasykaluta		P42129 antechinus	P73636 synechocyst	P32195 sus scrofa	P32194 sus scrofa	Q06661 tomato mott	P55041 mus musculu	Q9y216 homo sapien	P42145 pseudochiro	Q94535 drosophila	_		P50494 plasmodium			_	14	P42132 dromiciops
SUMMARIES		PRT2_SEPOF	PRT1_SEPOF	HSP1_MACRU	HSP1_CAEFU	HSP1_DASVI	HSP1_MACAG	HSP1_MACGI	HSP1_ANTLA	HSP1_ANTSW	HSP1_MACEU	HSP1_MACRG	HSP1_PARBI	HSP1_SARHA	HSP1_TRIVU	HSP1_DASRO	HSP1_MURLO	HSP1_ANTST	RS6_SYNY3	PG2_PIG	PG1_PIG	VBR1_TMOV	GEM_MOUSE	YA13_HUMAN	HSP1_PSECU	U2AG_DROME	YQ37_CAEEL	1A1C_DIACA	PVDG_PLAKN	YNCA_CAEEL	BVCP_NPVOP	HSP1_ORNAN	HSP1_PLAIN	HSP1_DROAU
	ength DB	77			60 1					61 1		_	<del>, -</del>	61 1	_	~	7					257 1								-	0	0	_	63 1
di	Query Match Length	82.0	82.0	74.0	74.0	4	ͺ	4	4	4	4	4	74.0	74.0	74.0	74.0	74.0	74.0	70.0	70.0	70.0	68.0	68.0	68.0	0.99	0.99	0.99	0.99	0.99	0.99		64.0	•	64.0
	Score		41	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	35	35	35	34	34	34	33	33	33	33	33	33	32	32	32	32
	Result No.	-	7	m	4	S	9	7	æ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

	O19917 cyanidium c	Q48460 klebsiella	Q08170 homo sapien	Q03153 saccharomyc	P41699 autographa	Q03416 nicotiana t	Q03488 petunia hyb	Q07474 petunia hyb	Q03378 antirrhinum	P23706 antirrhinum	Q07472 petunia hyb	
J	RR6_CYACA	YC14_KLEPN	SFR4_HUMAN	YMY8_YEAST	Y140_NPVAC	GLOB_TOBAC	FBP1_PETHY	MAD2_PETHY	GLOB_ANTMA	DEFA_ANTMA	MAD1_PETHY	AP3_ARATH
	7	-	٦	-	-	Н	٦	-	-	-		<del></del>
	103	465	494	612	9	209	210	212	215	227	231	232
	64.0	64.0	64.0	64.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0
	32	32	32	32	31	31	31	31	31	31	31	31
	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	g	oct	38 C	
	tio	re P., two distinct	ERIZED BY A DOUBLE TID-SPECIFIC PROTAMINES COMPACT INACTIVE COMPLEX.  ES. THE 2. SP2 APPEARS TO PHOSPHORYLATED IN	PROTEIN TI -binding; ;;
	nthieu A., Ir characterizat sperm protamine	P.,	ZED BY A DOU P-SPECIFIC PTAMINES COM CTIVE COMPLI THE SP2 APPEARS	OTE:
.NE SP2]. Sepioida	۸., cte: rota	re e	BY ZIF:	PR - b.
NE S	eu / arac	tie	SPECTIVE THE SPECTIVE	FIC DN TION
AMI.	thi ch peri	Sautiere es of two	RIZ ID- ROT NAC NAC S.	ECI 18; yla yla TEI TEI
ROT	Pon lar if s	Ö	CTE PO I	D-SPEC enesis phoryl PROTE 2.
M P	ecu ecu	ne D	JARA SPER SPER TH S AN	ATIL SOSP
SEPOF PERZ_SEPOF STANDARD; PRT; 77 AA. 01.FEB-1991 (Rel. 17, Created) 01.NOV-1991 (Rel. 20, Last sequence update) 01.NOV-1991 (Rel. 40, Last annotation update) SPERMATID-SPECIFIC PROTEIN T2 (COWTAINS: SPERM PROTAMINE SEPIA officinalis (Common cuttlefish). ENGATYOCKS; Metazoa; Mollusca; Cephalopoda; Coleoidea; Segialidae; Sepia. NCBL_TAXID-6610;	SEQUENCE. MEDLINE-91373359; PubMed-1894625; MEDLINE-91373359; PubMed-1894625; Woutters-Tyrou D., Chartier-Harlin MC., Martin-Ponthieu A., Boutillon C., van Dorsselaer A., Sautiere P.; Guttilefish spermatid-specific protein T. Molecular characterization of two variants T1 and T2, putative precursors of sperm protamine variants Sp1 and Sp2."; Variants Sp1 and Sp2."; J. Biol. Chem. 266:17388-17395(1991).	[2] SEQUENCE OF 22-77. MEDLINE-91153298; PubMed-1999185; MATLIN-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautie Schindler P., van Dorsselaer A.; "Cuttlefish sperm protamines. 1. Amino acid sequences of	ants."; J. Biochem. 195:611-619(1991). J. Biochem. 195:611-619(1991). CUTLEER PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC NUCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC NUCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX. SUBCELLUIAR LOCATION: NUCLEAR. DEVELOPMENTAL STAGE: SPERMIOGENESIS. DEVELOPMENTAL STAGE: SPERMIOGENESIS. PRIME: PHOSPHORYLATION OCCURS AT DIFFERENT DEGREES. THE TRIPHOSPHORYLATED FORM MAY BE PREDOMINANT IN 72. SP2 APPEARS TO PROSPHORYLATED IN BLONGATED SPERMATIDS, BUT DEPHOSPHORYLATED IN	-i. Similariy: High, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN T TREE SI4086; S14086. PIR: S14086; S14086. PIR: H40973; B40973. Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein; Phosphorylation; Testis; DNA condensation; Nuclear protein; Prosphorylation; CHAIN 22 77 SPERMATID-SPECIFIC PROTEIN T2. CHAIN 22 77 SPERM PROTAMINE SP2. CHAIN 1 21 HYDROPHOBIC. DOMAIN 1 22 77 ARC-RICH (HIGHLY BASIC). VARIANT 1 1 MISSING (IN T2B). SEQUENCE 77 AA; 10485 MW; 0F2C1B215292E0D7 CRC64;
PRT; 77 AA. ed) sequence update) annotation update t2 (CONTAINS: SPE uttlefish). ex; Cephalopoda; C.	ere T.	Bela	S ISES 1778 STA	Spein spin spin spin spin spin spin spin sp
up on AIN h).	utlutt utluetn etn pr	· · ·	619(1991). SPERMIOGENESIS SITION: HISTONES RROTAMINES (SPL/ ILY CONDENSED, S NUCLEAR. ESTIS. SPERMIOGENESIS. OCCURS AT DIFFE UM MAY BE PREDOM NGATED SPERMATI	FICINALIS SP me core; Spe lear protein SPERMATID-SP SPERM PROTAM SPERM PROTAM ARG-RICH (HI MISSING (IN 0F2C1B21529
PRT; uence otati [CONT lefis Cepha	n M Sa prot	A D	HIS HIS HES JES JENS JENS AT AT AT SE P	FICINALI me core; lear pro SPERMATI SPERM PR HYDROPHO ARG-RICH MISSING
PF 1) eque anot inot ctle	1625 A., A., IC F	)185 [yrc A.;	MICONE CONE CONE CONE CILER CANE CANE CANE CANE CANE CANE CANE CANE	SPE SPE SPE SPE SPE ARC MIS
atec r se N T3 cut	1894 r-Ha saer cifi	1999 rs-7 aer nes	SPED SPED ITIC INIC LY ( LY ( NUCATA MA MA	S.OI eosc Nuc
SEPOF STANDARD; PRT; P80002; 01-FEB-1991 (Rel. 17, Created) 01-NOV-1991 (Rel. 20, Last sequence up 01-NOV-1991 (Rel. 40, Last annotation SPERMATID-SPECIFIC PROTEIN T2 (COWTAIN Sepia officinalis (Common cuttlefish). ENKATYOCA: Metazoa; Mollusca: Cephalop SEDIATANID-6610;	1373359; PubMed-1894625; Yrou D., Chartier-Harlin M C., van Dorsselaer A., Saut sah spermatid-specific proteil riants Tl and T2, putative p Spl and Sp2.",	[2] SEQUENCE OF 22-77. MEDILINE-91153298; PubMed-1999185; MATLIN-Ponthieu A., Wouters-Tyrou Schindler P., van Dorsselaer A.; "Cuttlefish sperm protamines. 1.	ants."; J. Biochem. 195:611-619(1991). J. Biochem. 195:611-619(1991). FUNCTION: CUTTLEFISH SPERMIOGEN NUCLEAR PROTEIN TRANSITION: HIS PROFEINS (TI/T2) -> PROTAMINES SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS. DEVELOPMENTAL STAGE: SPERMIOGEN PYM: PHOSPHORYLATION OCCURS AT TRIPHOSPHORYLATED FORM MAY BE P PHOSPHORYLATED IN ELONGATED SPE	TO S.OFFICINALIE TO S.OFFICINALIE Nucleosome core; To SPERMATIE SPERM PRC HYDROPHOP HYDROPHOP HYDROPHOP HYDROPHOP HYDROPHOP H&BS MW; OFZCIB21
STANDARD; 1. 17, Cr 1. 20, La 1. 40, La FIC PROTE is (Commo	11373359; PubMec Yrou D., Chart. T.C., van Dorsten 1.C., van Dorsten s.b. spermatid-sk rriants Tl and Spl and Spl."; Chem. 266:1738	ubM Wo Ors	auts."; J. Biochem. 195:611- S. Biochem. 195:611- BROTEIN CUTLEFISH NUCLEAR PROTEIN TRANS PROTEINS (T1/T2) -> E PROTEINS (T1/T2) -> E PROTEINS (T1/T2) -> E SPERM DNA INTO A HIGH SUBCELLULAR LOCATION TISSUE SPECIFICITY: DEVELOPMENTAL STAGE: PHOSPHORYLATED IN ELC PHOSPHORYLATED IN ELC PHOSPHORYLATED IN ELC	H, TO  Nucl  77  77  77  77  77  77  71  10485
TAN 1 2 2 4 4 1 1 C 4 5 1 C 6 3 5 6 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5 6 9 5	1; P , C in D in D T T T T T S P	7. 4. 6. F. 7. P.	19 TTTI TTTI TTO TTO TLOC IFIC SRYI	22 122 122 132 133 134 134 134 135 135 135 135 135 135 135 135 135 135
T 1 SEPOF STP PRIZZ SEPOF STP P80002; 01-FEB-1991 (Rel. 01-NOV-1991 (Rel. SPENMATID-SPECIFIC SEPIA Officinalis ENKATYOCK; MEVEZZO SEPIA OFFICINALIS NELKATYOCK; MEVEZZO SEPIA OFFICINALIS SEPIA OFFICINALIS NELZ SEPOFICINALIS	SEQUENCE. SEQUENCE. MEDLINE-91373359; Wouters-Tyrou D., Boutillon C., van "Cuttlefish sperme of two variants Tl variants Sp1 and Sv2 J. Biol. Chem. 266	[2] SEQUENCE OF 22-77. MEDLINE=91153298; Mathin-Ponthieu A. Schindler P., van "Cuttlefish sperm	CT)  (T)  (T)  (T)  (T)  (T)  (T)	-1 - SIMILARITY: HIGH. PIR: \$14086; \$14086. PIR: \$14086; \$14086. PIR: \$140973. Chromosomal protein; Nutigene family. CHAIN 22 77 CHAIN 22 77 CHAIN 22 77 VARIANT 1 21 VARIANT 1 1 21 SEQUENCE 77 AA; 104
F 91 ( 01 ( 1cir 1cir Ser	1373 rrou C., sh s sh s riar riar Sp1	OF 2 1153 nthi P.,	iochiochiochiochiochiochiochiochiochioch	-:- SIMILARIDE DE CONTROL DE CONT
SEPOF P80002, SEPOF P80002, SEPOF 01-FEB-1991 01-NOV-1991 SPERMATID-S Sepia offic Eukaryota, Sepiae, Sepiae, S	CE. S-Ty lon lon efis vai	CE ( E=9 -Pol ler efit	variants."; Eur. J. Bio -!- Broclear PROTEIN PROTEIN PROFEN SUBCELL -!- TISSUE -!- DEVELOP -!- PTM: PH TRIPHOS PHOSPHO MATTIER	-!- SIMILARS -!- SIMILARS PIR; \$14086 PIR; \$14087 PIR;
T 1 SEPOF PRT2_SE P80002; 01-FEB- 01-NOV- 20-AU3- SPERMAT Sepia Sepia	1   SECUENCE. SECUENCE. MEDLINE=9 Wouters-T Boutillor "Cuttlefi of two vs variants	UEN LIN Lind Ltl	Lan Span Span Span Span Span Span Span Sp	-!- SIMI PIR; SIM PIR; B40 Chromcso Testis; Multigen CHAIN DOMAIN WARIANT
PRT2_SEPOF ID PRT2_ AC P8T02 DT 01-F0 DT 01-NO DE SPERM OS SEPIA OC SEUKAT	[1] SEQ MED Wou Bou Bou Cu of var	SEQ MAD MAR Sch	Buria Furi	PIR; PIR; PIR; Chrom Testi: Multi CHAIN CHAIN DOMAII
RESULT PRT2_S IID P DT O DT O DT S DE S OS S OS S OX N	x a x d d fi fi fi d	ZQXddi	H J D D D D D D D D D D D D D D D	000000000000000000000000000000000000000
OCC OCC OFF	RY RA RY RT	RN RX RA RA RA	#4000000000000	CCC CCC KWW KWW KWW KWW KWW KWW KWW KWW

82.0%; Score 41; DB 1; Length 77; 80.0%; Pred. No. 0.11;

Query Match Best Local Similarity

```
HSP1_CAEFU P42131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_CAEFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRIPHOSPHORYLATED FORM MAY BE PREDOMINANT IN TI. SPI APPEARS TO BE PHOSPHORYLATED IN ELONGATED SPERMATIDS, BUT DEPHOSPHORYLATED IN
                                                                                                                                                                                                                                                                                                                               Martin-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautiere P., Schindler P., van Dorsselaer A.; "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                          Boutillon C., van Dorsselaer A., Sautiere P.; "Cuttlefish spermatid-specific protein T. Molecular characterization of two variants T1 and T2, putative precursors of sperm protamine variants Sp1 and Sp2.";
                                                                                                                                                                                                                                                                                                                                                                       EUT. J. Biochem. 195:611-619(1991).

-!- FUNCTION: CUTTLEFISH SPERMIGGEMESIS IS CHARACTERIZED BY A DOUBLE NOCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC PROTEINS (TJ/T2) -> PROTAMINES (SPL/SP2). THE PROTAMINES COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
Testis; DNA condensation; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Sepioida;
 ;
0
                                                                                                                                                SPERWATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTAMINE SP1]. Sepia officinalis (Common cuttlefish).
                                                                                                                                                                                                                         MEDLINE-91373359; PubMed=1894625;
Wouters-Tyrou D., Chartier-Harlin M.-C., Martin-Ponthieu A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPERMATID-SPECIFIC PROTEIN T1
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: TESTIS.
DEVELOPMENTAL STAGE: SPERMIOGENESIS.
PTM: PHOSPHORYLATION OCCURS AT DIFFERENT DEGREES. THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 78; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN T1B).
09FE3EDBF0DCED33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARG-RICH (HIGHLY BASIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM PROTAMINE SP1.
 Ϊ;
                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                              78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROPHOBIC
                                                                                                                                                                                                                                                                                      Biol. Chem. 266:17388-17395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                       MEDLINE=91153298; PubMed=1999185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10631 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATURE SPERM CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
78
21
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S14085; S14085.
PIR; A40973; A40973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRRF 10
                                  || |||||||:
64 RRRSYSRRRY 73
                                                                                                                                                                                                                                                                                                           SEQUENCE OF 22-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Testis; DNA conde
Multigene family.
                                                                                                                                                                                          NCBI_TaxID=6610;
                                                                                                                                                                                  Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP1_MACRU
ID HSP1_MACRU
                                                                                              PRT1_SEPOF
P80001;
 ώ
ώ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               variants.
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                          RESULT 2
PRT1_SEPOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                               g
                       ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPOLD PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                          Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
-I- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                    (Megaleia rufa).
Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1; Length 59;
Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testis; DNA condensation; Nuclear protein.

By SIMILARITY

O 0 BY SIMILARITY

SEQUENCE 59 As, 8230 MW; 78FIAE592B4BAFA2 CRC64;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                       kangaroo)
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L35447; AAA74616.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenolestes fuliginosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32, 01-NOV-1997 (Rel. 35,
                                                                                                                                                                       Macropus rufus (Red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPERM PROTAMINE P1.
                                                                                                   P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 RRRGYSRRY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=37696;
                                                                                                                                                                                                                                                                   NCBI_TaxID=9321;
                                                                                                   SPERM PROTAMINE
```

615D3D85E7123025 CRC64;

8246 MW;

60 AA;

SEQUENCE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dasyurus viverrinus (Southeastern quoll), and Dasyurus hallucatus (Satanellus/northern quoll). Eutaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Metaheria: Dasyuromorphia; Dasyuridae; Dasyurus.
                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                      74.0%; Score 37; DB 1; Length 60; 70.0%; Pred. No. 0.53; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                           0 0 BY SIMILARITY.
60 AA; 8514 MW; 7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSP1_DASVI STANDARD; PRT; 60 AA. P42135; P42133; Ol-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro; IPR000221; Protamine_P1.
                                                                                                                                                               EMBL; L35332; AAA74598.1; -.
InterPro; PR000221; prochamine_Pl.
Pfam; PF00260; prochamine_Pl; Il.
PROSITE; PS00048; PROTAMINE_Pl; I.
SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L35340; AAA74599.1; -. EMBL; L35341; AAA56795.1; -.
                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 70.0.
ابر 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP1_DASVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.,
"Molecular phylogeny and evolution of marsupial protamine Pl genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION. PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.0%; Score 37; DB 1; Length 60; 70.0%; Pred. No. 0.53;
   Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testis; DNA condensation; Nuclear protein.
INIT_MET 0 0 BY SIMILARITY.
SEQUENCE 60 AA; 8338 MW; 96255C818921EB85 CRC64;
Score 37; DB 1;
Pred. No. 0.53;
1; Mismatches
                                                                                                                                                                                                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
SPERM PROTAMINE Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AA
                                                                                                                                                                                60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                            Macrcpus agilis (Agile wallaby).
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Sperm;
MEDLINE=95215351; PubMed=7700877;
   74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L35451; AAA74615.1; -
   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                            SPERM PROTAMINE P1.
                                                               1 RRLSYSRRRF 10
                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9313;
                                                                                    01-NCV-1995
01-NCV-1995
01-NCV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal
                                                                                                                                                                              HSP1_MACAG
P42137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSP1_MACGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P42139;
                                                                                                                                              RESULT 6
HSP1_MACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
HSP1_MACGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                              g
                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BHHH
                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
HSP1_ANTSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metalbria; Dasyuromorphia; Dasyuridae; Antechinomys.
NCBI_raxID=60701;
               Macropus giganteus (Eastern gray kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1; Length 60; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
1DC25C80C490BC90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L35333; AAA74604.1; -. InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA; 8415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=9317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                               TISSUE-Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSP1_ANTLA
018745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP1_ANTLA
AC O18745
DT 15-JUL
DT 16-JUL
DT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
   á
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES-N.lorentzii, D.albopunctatus, D.geoffroii, and D.spartacus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
Reconstructing the taxonomic radiation of dasyurine marsupials with cytochrome b, 12s rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DUKING THE HALDID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECTES—A.Swainsconii, and P.dorsalis; TISSUE—Sperm;
MEDIINE—95215351; PubMed=7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                   Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasyurus spartacus (Native cat).
Kakaryota: Metazoca: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Metatheria: Dasyuromorphia; Dasyuridae; Antechinus.
NCBL_TAXID=9284, 9295, 32551, 332545, 63143, 32546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 61;
Pred. No. 0.54;
L; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antechinus swainsonii, Phascolosorex dorsalis,
Neophascogale lorentzii (Long-clawed marsupial mouse),
Dasyurus albopunctatus (Native cat),
                                                                                                                                                                                                                                                                                                                                                                                                                                    Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY.
SEQUENCE 61 AA; 8409 MW; E021567627E562B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dasyurus geoffroii (Chuditch/western quoll), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSP1_ANTSW STANDARD; PRT; 61 AA. P42130; P42146; 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                      EMBL; AF001587; AAB91377.1; -.
InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L35338; AAB95429.1; -.
EMBL; L35339; AAA74601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L35339; AAA74601.1; -.
EMBL; AF010267; AAB69297.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 RRRGYSRRY
```

```
HSPI_PARBI

AC 0181_P

DT 15-JUL

DT 15-JUL

DT 15-DE

DE SPERM

GN PRMI.

GN PRMI.

GN PRMI.

OC BARATY

OC MAMMAI

OC MAMMAI

OC MAMMAI

OC MAMMAI

NCBLT

RN [1]

RN [1]

RR KRAJØW

RT RROJØW

RT 
                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIATO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                        Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 61;
Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 61;
Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                    0 0 BY SIMILARITY.
61 AA; 8390 MW; E021472785E71221 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58C2925C80C49AIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Testis; DNA condensation; Nuclear protein.
EMBL; AF010272; AAB69302.1; -.
EMBL; AF010274; AAB69304.1; -.
EMBL; AF010275; AAB69305.1; -.
InterPro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95215351; PubMed-7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chromosomal protein; Nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%;
70.0%;
                                                                                                                                                                                                                                                                             74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L35450; AAA74614.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA; 8495 MW;
                                                                                                                                                                                                                                                                          Query Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                           SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRRGYSRRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_MACEU
P42138:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INIT_MET
SEQUENCE
                                                                                                                                                                                    INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
       g
                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molevular phylogeny and evolution of marsupial protamine PI genes."; Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14(1995).

- PUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.; Rreconstructing the taxonomic radiation of dasyurine marsupials with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                          Wallabia bicolor (Swamp wallaby).
Sukaryota: Metacoa: Chordata: Craniata: Vertebrata; Euteleostoml;
Mammalia: Metatheria: Diprotodontia: Macropodidae; Macropus.
NCBI_PaxID=9320, 9330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parantechinus bilarni (Broad-footed marsupial mouse)..
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Parantechinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B822925C80C490BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1;
Pred. No. 0.54;
                                                                                                                                                                                                                             Macropus rufogriseus (Red-necked wallaby), and
P42141; P42153; PA1-MACRG STANDARD; PRT; 61 AA. P42141; P42153; 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.54
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 135329; AAA74610.1; -.
EMBL; L35328; AAA74609.1; -.
InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AA; 8571 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                               SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=32555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSP1_PARBI
O18768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INIT_MET
SEQUENCE
```

Usage by

```
and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIT_MET
       modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
HSP1_TRIVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF
SEGUENCE FROM N.A.
SPECIES-D. maculatus;
Krajewski C., Young J., Buckley L., Woolley P.A., Westerman M.;
"Reconstructing the taxonomic radiation of dasyurine marsupials with
cytochrome b, 12S rRNA, and protamine Pl gene trees.";
J. Mammal. Evol. 4:217-236(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: PROTABINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN C
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dasyurus maculatus (Tiger quoll).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sarcophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 1; Length 61;
Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condensation; Nuclear protein.
0 BY SIMILARITY.
51 AA; 8421 MW; C02857DF087FC9A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NoV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SPERM PROTAMINE Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarcophilus harrisii (Tasmanian devil), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR. TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES-S.harrisii; TISSUE-Sperm;
MEDLINE-95215351; PubMed-7700877;
                                                                                                                             -!- SUBCELLULAR LOCATION: NUCLE
-!- TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF010277; AAB69307.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AA; 8421 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9305, 9281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || ||||||
45 RRRGYSRRY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Testis; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSP1_SARHA
P42151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSPI_SARHA
TO HSPI_SARHA
TO HSPI_SARHA
DT PAIDLIS
DT DI-NOV
DT DI-
              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            ö
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Molecular phylogeny and evolution of marsupial protamine Pl genes.", Proc. R. Soc. Lond., B., Biol. Sci. 259-7-14(1995).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                   Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 61;
Pred. No. 0.54;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                 Length 61;
                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
802287E627EE816C CRC64;
                                                                                                                                                                                                                                                                                                 Score 37; DB 1;
Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichosurus vulpecula (Brush-tailed possum).
                                                                                                                                                                                                                                                                                                                                                Mismatches
                          or send an email to license@isb-sib.ch).
           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L32744; AAA99479.1; -. Interpro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AA; 8571 MW;
                                                                                                                                                                                                                                                                                                      74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 3
01-NOV-1997 (Rel. 3
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSP1_TRIVU
P42152;
```

us-09-485-571-23.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                      Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.; "Modecular phylogeny and evolution of marsupial protamine Pl genes."; Proc. R. Soc. Lond., B, Biol. Sci. 259.7-1411995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
                                                                                                                                                                         Dasykaluta rosamondae, Parantechinus apicalis (Dibbler), and Pseudantechinus macdonnellensis (Fat-tailed marsupial mouse). Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Dasykaluta. NCBI_TaxID=33560, 9291, 9299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%; Score 37; DB 1; Length 62; 70.0%; Pred. No. 0.54; 2; Indels live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Testis; DNA condensation; Nuclear protein.

INIT_MET 0 0 BY SIMILARITY.

SEQUENCE 62 AA; 8585 MW; 99C02857DF087FC9 CRC64;
                                  HSPI_DASRO STANDARD; PRT; 62 AA. P42134; P42144; P42149; 01-NOV-1995 (Rel. 32, Created) 15-JUL-1999 (Rel. 32, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                          MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - TISSUE SPECIFICITY: TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L35325; AAA74605.1; -. EMBL; L35326; AAA74607.1; -. EMBL; L35337; AAA74603.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 70.0
ابر 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 TISSUE-Sperm;
RESULT 15
HSP1_DASRO
                                      ò
```

Search completed: February 12, 2002, 12:39:52 Job time: 805 sec

45 RRRGYSRRY 54

g

			•	10
		•		
	•.			
		•• • • • • • • • • • • • • • • • • • •		
		A company of the comp		
		Marie de la Marie	in the state of th	
		tarian di salah di s		ŝ.
		No.		116
				, Mar
			ing the state of	
				* *,
				*
				e de la companya de l
				1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
				2
	. *			
	•		1	
	en e		and the second of the second o	
				e to
			***	
		*		,
			en e	t fact
				**************************************
				1 21.54.4
**************************************		***		
		•		
	in the second of			i kananan jarah dari
	And the second of the second o			
24 - 24 - 24 - 24 - 24 - 24 - 24 - 24 -		t Programa		
	<b>□ □</b> □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □ □		, gr	
			· ·	
				- 14 A
		•	•	4. Fa
			•	k W
		•	\$ .	

Q9nyf9 homo saplen Q9fhx1 arabidopsis Q9z59 rattus norv Q9v5q4 drosophila Q9l0x6 streptomyce Q9x88 arabidopsis Q9ap92 uncultured Q9mf9 arabidopsis

O9zw08 arabidopsis O9fyb2 arabidopsis

Q9avh0 pisum

Ogvn68 drosophila Ogdwel rat cytomeg Ogesp9 mus musculu Ogy216 homo sapien

O64476 arabidopsis

Q9ncq0 acies aegyp Q9ncq0 acies aegyp Q9ng4 drosophila Q91q1 hypsiprymno Q0363 aca mays (m Q91cw4 streptomyce Q9xou2 thermotoga Q9ng4 caenorhabdi Q9n37 homo saplen Q9yu17 neisseria m Q9ccs9 arabidopsis

sed

Minimum DB Maximum DB

Database

Searched:

Perfect score: Sequence: Scoring table:

OM protein

Run on:

```
SEQUENCE FROM N.A.
MEDLINE-93139780; PubMed-8423448;
Gilbertson R.L., Hidayat S.H., Paplomatas E.J., Rojas M.R., Hou Y.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maxwell D.P.;

"Pseudorecombination between infectious cloned DNA components of tomato motitle and bean dwarf mosaic geminiviruses.";

J. Gen. Virol. 74.23-31(1993).

EMBL; LO2618; AAA47940.1; -.

InterPro: IPR000263; Gemini_Coat_ARl_BRl.

InterPro: IPR001530; Gemini_BRl.

InterPro: IPR001530; Girlinil_BRl.

Pfam; PF01489; Gemini_BRl; 1.

Pfam; PF01489; Gemini_BRl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TOMATO MOTTLE GEMINIVIRUS (CLONE PTFB-1) BR1 (CLONE PTFB-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 12; Length 256;
Pred. No. 11;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00881; PROTEIN_SPLICING; UNKNOWN_1.
SEQUENCE 256 AA; 29370 MW; 0A9A3E80AED3B692 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tomato mottle virus.
Viruses; ssDNA viruses; Geminiviridae; Begomovirus
NCBI_raxID=10835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
09AVH0
092W08
092W08
09YF92
09V504
09Y504
09L0X6
09L0X6
09L0X6
09L0X6
09L0X6
09L0X6
09Y2L6
09Y2L6
09Y2L6
09Y2L6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                        Q9GLQ1
Q03863
                                                                                                                                                                                                                                                                                                                                                      Q9N3Q6
Q9H3L7
Q9JUJ7
Q9C6S9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                        Q9LCW4
                                                                                                                             10
                                                                                                                                                           10
                                                                                                                                                                                                                                                        5
10
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%;
80.0%;
                                                                                                                                                                                         17
                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                        1062
1090
1179
1203
                                                                                                                                                                                                                                                                                                     122
162
177
197
212
293
                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRLSYSRRRF 10
777700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q67615
ID Q67615
AC Q67615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  049281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  049281
ID 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     099145 peradorcas
090149 macropus pa
090149 onychogalea
099149 onychogalea
099141 onychogalea
099147 perrogalea
090147 dorcopsulus
099140 betrongia p
090144 dorcopsulus
099140 betrongia p
090143 sminthopsis
094142 lagorcheste
096142 lagorcheste
096141 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q67615 tomato mott
Q49281 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arabidopsis
                                                                                                                             (without alignments)
6.287 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          February 12, 2002, 12:38:39; Search time 232.64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094887
09n9b5
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     096L05
096L09
096L09
096LP8
096LP8
096L01
097UC2
096L04
096L04
097UC3
096L00
097UC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q67615
Q49281
                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094887
Q9N9B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
                                                                                                                                                            US-09-485-571-23
50
                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0

77.0
```

Score

Result

Š

336477777777777777

3 6 7 7 8 8 111 112 113 114 116 117 118

ö

Gaps

ö

Gaps

ö

us-09-485-571-23.rspt

```
SEQUENCE FROM N.A.

BURK A., Springer M.S.;

Burk A., Springer M.S.;

Burk A., Springer M.S.;

J. Mammal. Evol. 0:0-0(2000).

-1- FUNCTION: PROTAMITIES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-1- FUNCTION: PROTAMITIES SUBSTITUTES FOR FOR HISTONES IN THE CHROMATIN OF

SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

SPERM DIN INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onychogalea fraenata (bridled nail-tailed wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBI_TaxID=9318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Length 61;
      DB 6; Length 60; 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA; 8500 MW; A07F5C81C4664B6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SÜBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AR187333; AGG27950.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AA.
                                                                                                                                                                                    61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                       1; Mismatches
        Score 37;
Pred. No.
                                                                                                                                                                                                                   Created)
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                             Macropus parryi (Whiptail wallaby).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00260; protamine_P1; 1. PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%;
70.0%;
      74.0%;
70.0%;
                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, SPERM PROTAMINE P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                         Conservative
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERM PROTAMINE P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 RRRGYSRRRY 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
         Query Match
Best Local Similarity
Matches 7; Conserv
                                                                       1 RRLSYSRRRF 10
                                                                                            61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=114227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9GLQ3;
                                                                                                                                                                                                    09GLQ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09GLQ3
                                                                                                                                                                                  Q9GLQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ
                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GLQ3
                                                                                                                                                       RESULT
                                                                                                                                                                      09GLQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                    δ
                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).
-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DURING THE HARLOID PHASE OF SPERMATOGENESIS. THEY COMPLEX (BY
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE PI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTEE, PSO0048; PROTAMINE_P1; 1.
PROSTEE, PSO0048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condeation; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 60 AA; 8436 MW; B0F0943F6F8BF58B CRC64;
                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                  SECRATIN-CV. COLUMBIA;
Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
Au M., Araulo R., Buehler E., Dewar K., Feng J., Kim C., Li Y.,
Oji O., Osborne B., Theologis A., Davis R.W.;
Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002291; AAC00618.1; -
EMBL; AC002291; Arath;1426;28105.
InterPro: IPR000306; Znf_FYVE.
InterPro: IPR000408; RCCI.
Pfam; PF00415; RCCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Peradorcas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%; Score 38; DB 10; Length 1108; 70.0%; Pred. No. 48; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          121276 MW; B43D6ECABD14615E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 AA
                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00626; RCC1_2; UNKNOWN_3. PROSITE; PS00626; RCC1_3; 7. SMART; SM0064; EYVE; 1. SEQUENCE 1108 AA; 121276 MM· PAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF187538; AAG27955.1; -. Interpro; IPR000221; Protamine_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0
Fra 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel. SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::|||||
| 1053 RRVRFSRRRF 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peradorcas concinna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=69272;
                                                              F22K20.5 PROTEIN.
                                                                                                                                              eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09GLQ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
à
```

ö

Gaps

Euteleostomi;

61;

Length

. 9

DB

m

```
Potorous longipes (long-footed potoroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Potorous
                                                                                                                        Burk A., Springer M.S.;
Burk A., Springer M.S.;
Burk A., Springer M.S.;
J. Mammal. Evol. 0:0-0(2000).
EMBL; AF187548; AAG27965.1; -.
InterPro; IPRO00221; Protamina_P1.
PSEQUENCE 61 AA; 8431 MW; D745F1F638DBBCDC CRC64;
                                                                                                                                                                                                                                                                                                                                                  74.08;
70.08;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
?; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |||||:
45 RRRGYSRRRY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 RRRGYSRRRY 53
                                                                                   NCBI_FaxID=55310;
  PROTAMINE P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0000g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Burk A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-1- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                      -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL, AF187542; AAG27959.1; -.
InterPro: IPRO00221; Protamine_Pl.
Pfam; PF00260; protamine_Pl: 1.
PROSITE; PS00048; PROTAMINE_Pl: 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 61 AA: 8454 MW; CBBBEFC966E44BBA CRC64;
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 61 AA; 8576 MW; 7B324691290717AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aepyprymnus rufescens (rufous rat-kangaroo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Aepyprymnus.
NCBI_TaxID=38598;
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                       74.0%; Score 37; DB 6; Length 61; 70.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 6; Length 61;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-1- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL; AF187547; AAG27964.1; -.
Interpro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1. 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AA.
                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                    SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRLSYSRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRRGYSRRRY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09GLP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09GLP8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9GLP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
09GLP8
ID 09
AC 09
DT 01
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT OF SECULT OF SECURT OF SECULT OF SECURT OF SECULT OF SECURT OF SECULT OF SECULT OF SECULT OF SECULT OF SECULT OF SECURT OF SECULT OF SECULT OF SECULT OF SECULT OF SECULT OF SECURT OF SECURT
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
J. Manimal. Evol. 0:0-0(2000).
-:- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DORING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SFERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onychogalea unguifera (northern nail-tailed wallaby),
Dendrolagus goodfellowi (Goodfellow's tree kangaroo), and
Setonix brachyturs (quokka).
Everorix hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
NCBI_TaxID=65626, 69260, 30670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=O.unguifera, D.goodfellowi, and S.brachyurus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatogenesis; Testis.
8546 MW; F0D55C81C4664B62 CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLUIAK LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
-!- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF187543; AG27960.1; -.
EMBL; AF187537; AG27954.1; -.
EMBL; AF187541; AG27958.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
9
                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                        Mismatches
Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterFro; IPR000221; Protamine_Pl. Pfam; PF00260; protamine_Pl; 1. PROSITE; PS00048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                        Conservative
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
```

```
Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERM PROTAMINE P1 PRM1.
                     RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                           1 RRLSYSRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                     Q9GLQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09GLQ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095100
                                                                                                                                                                 Q9GLQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                        11
                                                            45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                             RESULT
                                                                                                                                            09GLQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09GLQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                       δ
                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                Westerman M.:
"Systemmetr relationships within the dasyurid marsupial tribe
"Systemetic relationships within the dasyurid marsupial tribe
Sminthopsini--a multigene approach.";
MOI. Phylogenet. Evol. 12:140-155(1999).
-I- FUNCTION: PROTAMMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DIA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Petrogale xanthopus (Ring-tailed rock wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Petrogale.
                                                                                                                                                                                   Sminthopsis longioaudata (long-tailed dunnart).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                 Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 37; DB 6; Length 62; ilarity 70.0%; Pred. No. 4.1; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 6; Length 62; Pred. No. 4.1; Lismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burk A., Springer M.S.;
"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).
InterPro; IPR000221; Protamine_P1.
Pfam. PF00260, protamine_P1.
PROSTIE: FS000048; PROTAMINE_P1. UNKNOWN. 1.
SEQUENCE 62 AA; 8656 MW; BEBE685C8089D007 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A9EEA7D7C77964A9 CRC64;
                                                                             (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- TISSUB SPECIFICITY: TESTIS (BY SIMILARITY).
-:- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL: AF089881; AAD55340.1;
                                           62 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AA
                                           PRT;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99310778; PubMed=10381317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleosome core; Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8640 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.vv,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                           PRELIMINARY;
                                                                                                                                              SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 RRRGYSRRRY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 NCBI_TaxID=90764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTAMINE P1
                                                                                 01-MAY-2000
                                                                                                     01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
09GL07
AC 09GL07
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-JUN.
DE PROTAM.
DC C EUKATY.
CO MAMMAI.
CO MAMMAI.
RN 1]
RP SEQUENT
RN 11
RN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09GLQ7
                                           Q9TUC2
9
RESULT
Q9TUC2
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
Burk A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";
J. Mammal. Evol. 0:0-0(2000).

-!- FUNCTION: PROTAMINES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BURK A., Springer M.S.;

"The Chronicle of Kangaroo Evolution.";

J. Mammal. Evol. 0:0-0(2000).

-1- FUNCTION: PROTAMIRES SUBSTITUTES FOR HISTONES IN THE CHROMATIN OF

-2- FUNCTION: THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNR INT A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PR0SITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 62 AA; 8656 MW; 3054825C8089DDB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bettongia penicillata (brush-tailed bettong).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Potoroidae; Bettongia.
NCBI_TaxID=69259;
                                                                                                                                                                                   Dorcopsulus vanheurni (lesser forest wallaby).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Dorcopsulus.
NCBI_TaxID=69270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NAR-2001 (TrEMBLrel. 16, Created)
01-NAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
--- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AR187539; AAG27956.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 6, Pred. No. 4.1; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä.
62 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.0%;
70.0%;
                                                       16,
16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
                                                 01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
SPERM PROTAMINE P1.
```

£

```
1 RRLSYSRRFF 10
                                                                                                                                                                                                                                                                                                                                  II IIIII:
RRRGYSRRRY 55
                                        NCBI_TaxID=75756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                        09GLQ2
                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                         46
                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q9GLQ2
  ŏ
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                        Gaps
-i- SIMILARITY: TO THE PROTAMINE PI FAMILY.

EMBL; AF187546; AAG27963.1; -
InterPro; IPR000221; Protamine_P1.

PROMS Pfam; PR00260; protamine_P1.

PROSITE; PS00048; PROTAMINE_P1; 1.

Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
Nucleosome core: Spermatogenesis; Testis.

SEQUENCE 62 AA; 8633 MW; DEB479472128DDBC CRC64;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis. SEQUENCE 63 AA; 8654 MW; 82A6BEA7CBB76865 CRC64;
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
                                                                                                                                                                                                                                                                                                                    ŚEĞUENCE FROM N.A.
MEDLINE-99310778; PubMed-10381317;
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper S.,
Westerman M.;
                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                               Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 37; DB 6; Length 63; 70.0%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                  Indels
                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-1- TISSUE SPECIFCITIY: TESTIS (BY SIMILARITY).
-1- SIMILARITY: TO THE PROTAMINE P1 FAMILY.
EMBL; AF089873; AAD55332.1; -.
INTERPRO; PROMOD21; FOCAMING_P1.
PROMOD21; FOCAMING_P1.
PROMODS: PSOUD48; PROTAMING_P1, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                               Score 37; DB 6;
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AA.
                                                                                                                                                                                                      63 AA.
                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                      PRT;
                                                                                               74.0%;
70.0%;
                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                              Query Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                   1 RRLSYSRRF 10
                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RRLSYSRRRF 10
                                                                                                                                                                                                                                                                       Sminthopsis bindi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPERM PROTAMINE P1
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=90757;
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TUC3
Q9TUC3;
                                                                                                                                                                                                               Q9TUC4;
                                                                                                                                                                                                    Q9TUC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
Q9TUC3
                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATES
                                                                                                                                     ô
                                                                                                                                                                                                              ò
```

```
ö
                                                                                                                                                                                                  SIMILARITY).

-! SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SISSUE SPECIFICITY: TESTIS (BY SIMILARITY).

-! SIMILARITY: TO THE PROMINE PI FAMILY.

EMBL, AR089878; AAD55337.1; -.

InterPro; IPR000221; Protamine_PI.

Pfon: PF002260; protamine_PI. 1.

PROSITE; PS00048; PROTAMINE_PI; 1.

Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis; Testis.

Nucleosome core; Spermatogenesis; Testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00260; protamine_F1; 1.
PROSITE; PS00048; PROTAMINE_F1; 1.
Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
Nucleosome core; Spermatogenesis; Testis.
SEQUENCE 65 AA, 9052 WW; 2D180858B29D8A0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Sminthopsis griseoventer (gray-bellied dunnart).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.
                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-99310778; PubWed-10381317;
Blacket M.J., Krajewski C., Labrinidis A., Cambron B., Cooper S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lagorchestes hirsutus (rufous hare-wallaby).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Metatheria; Diprotodontia; Macropodidae; Lagorchestes.
NCBI_raxID=65632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
--- SÜBCELLÜLAR LOCATION: NUCLEAR (BY SIMILARITY).
--- TISSUE SPECIFICITY: TESTIS (BY SIMILARITY).
--- SIMILARITY: TO THE PROTAMINE PI FAMILY.
EMBL, AF187544; AAG27961.1; ---
INTERPRO! IPRO00221. PROTAMINE_PI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 37; DB 70.0%; Pred. No. 4.1; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, SPERM PROTAMINE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 74.0
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
```

DB 6; Length 65;

Score 37;

74.0%;

0;

0; Gaps

2; Indels Best Local Similarity 70.0%; Pred. No. 4.3; Matches 7; Conservative 1; Mismatches

1 RRLSYSRRRF 10 || || || || || 1 43 RRRGYSRRRY 52 Qy

Search completed: February 12, 2002, 12:38:40 Job time: 753 sec